NCBI GI BLAST score

E value

Match length



8

```
% identity
 NCBI Description
                   (X98320) peroxidase [Arabidopsis thaliana]
                   >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a
                   [Arabidopsis thaliana]
 Seq. No.
                   259085
 Contig ID
                   345 1.R1011
 5'-most EST
                   fC-zmro700575714 FL
 Method
                   BLASTX
 NCBI GI
                   g2522210
 BLAST score
                   558
 E value
                   4.0e-57
Match length
                   201
 % identity
                   49
NCBI Description (AF023132) choline monooxygenase [Beta vulgaris]
 Seq. No.
                   259086
Contig ID
                   346 1.R1011
5'-most EST
                   fC-zmro700753209 FL
Method
                   BLASTX
NCBI GI
                   q130186
BLAST score
                   1389
E value
                   1.0e-154
Match length
                   313
% identity
                   88
NCBI Description PHYTOCHROME A >gi_82715_pir__JQ0382 phytochrome A - maize
Seq. No.
                   259087
Contig IĐ
                   346 3.R1011
5'-most EST
                   xdb700341355.h1
Method
                   BLASTX
NCBI GI
                   g130186
BLAST score
                   222
E value
                   6.0e-18
Match length
                   46
% identity
                   100
NCBI Description PHYTOCHROME A >gi_82715_pir__JQ0382 phytochrome A - maize
Seq. No.
                   259088
                   347 1.R1011
Contig ID
5'-most EST
                  fC-zmro700832108d4
Method
                  BLASTX
NCBI GI
                  g4154352
BLAST score
                  392
E value
                  1.0e-37
Match length
                  241
% identity
                  39
NCBI Description (AF110333) PrMC3 [Pinus radiata]
Seq. No.
                  259089
Contig ID
                  348 1.R1011
5'-most EST
                  fC-zmro700830011 FL
Method
                  BLASTX
```

35794

q2833378

2.0e-55

544





% identity NCBI Description HEXOKINASE >gi_619928 (U18754) hexokinase [Arabidopsis thaliana] >gi_1582383_prf__2118367A hexokinase [Arabidopsis thaliana] Seq. No. 259090 Contig ID 349 1.R1011 5'-most EST fC-zmro700830067_FL Method BLASTX NCBI GI q4538929 BLAST score 476 E value 4.0e-47 Match length 287 % identity 49 NCBI Description (AL049483) putative nucleic acid binding protein [Arabidopsis thaliana] Seq. No. 259091 Contig ID 350 1.R1011 5'-most EST fC-zmro700830312a1 Method BLASTX NCBI GI g3702332 BLAST score 342 E value 1.0e-31 Match length 193 % identity 34 NCBI Description (AC005397) unknown protein [Arabidopsis thaliana] Seq. No. 259092 Contig ID 351 1.R1011 5'-most EST fC-zmro700830348_FL Method BLASTX NCBI GI g3901012 BLAST score 1101 E value 1.0e-120 Match length 254 % identity 77 NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatical Seq. No. 259093 Contig ID 352 1.R1011 5'-most EST fC-zmro700830504 FL Method BLASTX NCBI GI g4240116 BLAST score 417 E value 9.0e-41 Match length 88 % identity NCBI Description (AB007799) NADH-cytochrome b5 reductase [Arabidopsis thaliana] >gi_4240118_dbj_BAA74838_ (AB007800) NADH-cytochrome b5 reductase [Arabidopsis thaliana]

Seq. No. 259094 Contig ID 353_1.R1011

Method BLASTX



NCBI GI g4191788 BLAST score 690 E value 1.0e-72 Match length 165 % identity 78

NCBI Description (AC005917) putative 1-aminocyclopropane-1-carboxylate

oxidase [Arabidopsis thaliana]

5'-most EST fC-zmro700831325 FL

Method BLASTX
NCBI GI g2088653
BLAST score 691
E value 9.0e-73
Match length 223
% identity 58

NCBI Description (AF002109) Hslpro-1 related protein isolog [Arabidopsis

thaliana]

5'-most EST fC-zmro700831537 FL

Method BLASTX
NCBI GI g3851001
BLAST score 896
E value 1.0e-113
Match length 233
% identity 87

NCBI Description (AF069909) pyruvate dehydrogenase E1 beta subunit isoform 2

[Zea mays]

 Seq. No.
 259097

 Contig ID
 356_1.R1011

5'-most EST fC-zmro700831955 FL

Method BLASTX
NCBI GI g3850630
BLAST score 700
E value 1.0e-73
Match length 199
% identity 62

NCBI Description (AJ012581) cytochrome P450 [Cicer arietinum]

Seq. No. 259098 Contig ID 356_2.R1011

5'-most EST fC-zmro700831544_FL

Method BLASTX
NCBI GI g3850630
BLAST score 419
E value 7.0e-41
Match length 120
% identity 57

NCBI Description (AJ012581) cytochrome P450 [Cicer arietinum]

Seq. No. 259099 Contig ID 357 1.R1011



8

Method BLASTX
NCBI GI g1168470
BLAST score 926
E value 1.0e-100
Match length 259
% identity 73

NCBI Description PROTEIN KINASE APK1A >gi_282877_pir__S28615 protein kinase,

tyrosine/serine/threonine-specific (EC 2.7.1.-) -

Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis

thaliana]

Seq. No. 259100 Contig ID 359_1.R1011

5'-most EST fC-zmro700832181 FL

Method BLASTX
NCBI GI g4585966
BLAST score 1225
E value 1.0e-135
Match length 296
% identity 79

NCBI Description (AC005287) Putative dihyrdolipoamide acetyltransferase

[Arabidopsis thaliana]

Seq. No. 259101 Contig ID 360_1.R1011

5'-most EST fC-zmro700832243_FL

Method BLASTX
NCBI GI g3335378
BLAST score 378
E value 5.0e-36
Match length 158
% identity 51

NCBI Description (AC003028) Myb-related transcription activator [Arabidopsis

thaliana]

Seq. No. 259102 Contig ID 361 1.R1011

Method BLASTX
NCBI GI g2129770
BLAST score 434
E value 1.0e-42
Match length 126
% identity 64

NCBI Description xyloglucan endotransglycosylase-related protein XTR-2 -

Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]

>gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No. 259103 Contig ID 362_1.R1011

5'-most EST fC-zmro700832582 FL

Method BLASTX NCBI GI g2959732 BLAST score 353



E value 3.0e-33 Match length 71 % identity 89 NCBI Description (Y13649) homologous to GATA-binding transcription factors [Arabidopsis thaliana] Seq. No. 259104 Contig ID 363_1.R1011 5'-most EST fC-zmro700832613 FL Method BLASTX NCBI GI a3169883 BLAST score 305 E value 1.0e-27 Match length 136 % identity 47 NCBI Description (AF033194) dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum] >gi 3169888 (AF034411) dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum] 259105 Seq. No. Contig ID 364_1.R1011 5'-most EST fC-zmro700832966_FL Method BLASTX NCBI GI q3204134 BLAST score 707 E value 2.0e-74Match length 182 % identity NCBI Description (AJ006771) beta-galactosidase [Cicer arietinum] Seq. No. 259106 Contig ID 365_1.R1011 5'-most EST fC-zmro700833257 FL Method BLASTX NCBI GI q2494329 BLAST score 376 E value 1.0e-35 Match length 294 % identity 34 NCBI Description GLUCAN 1,3-BETA-GLUCOSIDASE PRECURSOR (EXO-1,3-BETA-GLUCANASE) >gi 1150694 emb CAA86952 (Z46872) exo-1,3-beta-glucanase/1,3-beta-D-glucan glucanohydrolase [Yarrowia lipolytica] Seq. No. 259107 Contig ID 366 1.R1011

5'-most EST fC-zmro700833374 FL

Method BLASTX NCBI GI g1872521 BLAST score 303 E value 3.0e-27Match length 113

% identity 36

NCBI Description (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi 1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis

thaliana]

BLAST score

Match length % identity

E value

1416

86

1.0e-157 319





```
Seq. No.
                   259108
Contig ID
                   367 1.R1011
5'-most EST
                   fC-zmro700833817 FL
Method
                   BLASTX
NCBI GI
                   g2789434
BLAST score
                   252
E value
                   3.0e-21
Match length
                   163
% identity
                   41
NCBI Description (AB001389) CLB1 [Lycopersicon esculentum]
                   259109
Seq. No.
Contig ID
                   368 1.R1011
5'-most EST
                   fC-zmro700833909 FL
Method
                  BLASTX
NCBI GI
                   g3128195
BLAST score
                   204
E value
                   8.0e-16
Match length
                   43
                   88
% identity
NCBI Description
                  (AC004521) putative phosphoribosyl pyrophosphate synthetase
                   [Arabidopsis thaliana] >gi_3341673 (AC003672) putative
                   phosphoribosyl pyrophosphate synthetase [Arabidopsis
                   thaliana }
Seq. No.
                   259110
Contig ID
                   369 1.R1011
5'-most EST
                   fC-zmro700833923 FL
Method
                   BLASTX
NCBI GI
                   g3540200
BLAST score
                   237
E value
                   2.0e-19
Match length
                   186
% identity
                   35
NCBI Description (AC004260) Similar to TINY [Arabidopsis thaliana]
Seq. No.
                  259111
Contig ID
                   370 1.R1011
5'-most EST
                   fC-zmro700834004 FL
Method
                  BLASTX
NCBI GI
                  g2979553
BLAST score
                   511
E value
                   1.0e-51
Match length
                  166
% identity
                   59
NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  259112
                  371 1.R1011
Contig ID
5'-most EST
                  fC-zmro700834049 FL
Method
                  BLASTX
NCBI GI
                  g1915974
```

E value

7.0e-68





```
NCBI Description
                   (U62329) fructokinase [Lycopersicon esculentum] >gi 2102693
                   (U64818) fructokinase [Lycopersicon esculentum]
Seq. No.
                   259113
Contig ID
                   371 2.R1011
5'-most EST
                   fC-zmro700832903d4
Method
                   BLASTX
NCBI GI
                   q1052973
BLAST score
                   406
E value
                   1.0e-39
Match length
                   97
% identity
                   81
NCBI Description (U37838) fructokinase [Beta vulgaris]
Seq. No.
                   259114
Contig ID
                   372 1.R1011
                   fC-zmro700834170_FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2088653
BLAST score
                   684
E value
                   7.0e-72
Match length
                   241
% identity
                   53
NCBI Description
                  (AF002109) Hs1pro-1 related protein isolog [Arabidopsis
                   thaliana]
Seq. No.
                   259115
                   372 2.R1011
Contig ID
5'-most EST
                   fC-zmro700833740d4
Method
                   BLASTX
NCBI GI
                  g2088653
BLAST score
                  253
E value
                   1.0e-21
Match length
                   87
% identity
                   57
NCBI Description (AF002109) Hs1pro-1 related protein isolog [Arabidopsis
                  thaliana]
Seq. No.
                   259116
Contig ID
                   373 1.R1011
5'-most EST
                  fC-zmro700835672:_FL
Method
                  BLASTX
NCBI GI
                  g3450842
BLAST score
                  894
E value
                  3.0e-96
Match length
                  269
% identity
                   62
                  (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                  sativa]
                  259117
Seq. No.
Contig ID
                  374 1.R1011
5'-most EST
                  fC-zmro700835718: FL
Method
                  BLASTX
NCBI GI
                  g2829275
BLAST score
                  649
```





Match length % identity 88 NCBI Description (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] >gi 3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_ (AL049525) nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana] Seq. No. 259118 Contig ID 375 1.R1011 5'-most EST fC-zmro700835944: FL Method BLASTX NCBI GI g3901012 BLAST score 1162 E value 1.0e-128 Match length 274 % identity 75 NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica] Seq. No. 259119 Contig ID 375 2.R1011 5'-most EST fC-zmro700832650a5 Method BLASTX NCBI GI g3901012 BLAST score 623 E value 5.0e-65 Match length 133 % identity 83 NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica] Seq. No. 259120 375 3.R1011 Contig ID 5'-most EST fC-zmro700833207d4 Method BLASTX NCBI GI g3901012 BLAST score 322 E value 8.0e-30 Match length 81 % identity NCBI Description (AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica] Seq. No. 259121 Contig ID 376 1.R1011 5'-most EST xmt700263904.h1 Method BLASTX NCBI GI g3915024 BLAST score 1583

E value 1.0e-177 Match length 400 % identity 77

NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR

(STEAROYL-ACP DESATURASE)





```
259122
Seq. No.
                   376 4.R1011
Contig ID
                  clt700042624.f1
5'-most EST
Method
                  BLASTX
                   g2290400
NCBI GI
BLAST score
                  266
E value
                   3.0e-23
Match length
                  52
% identity
                   94
NCBI Description (U91339) stearoyl-ACP desaturase [Helianthus annuus]
Seq. No.
                   259123
Contig ID
                   376 5.R1011
5'-most EST
                  LIB3078-016-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  g2281099
BLAST score
                   456
E value
                   2.0e-45
Match length
                  108
% identity
                   79
NCBI Description (AC002333) stearoyl-ACP desaturase [Arabidopsis thaliana]
Seq. No.
                   259124
                   377 1.R1011
Contig ID
5'-most EST
                   fC-zmse700615105 FL
Method
                   BLASTX
NCBI GI
                   q4587533
BLAST score
                   311
E value
                   5.0e-28
Match length
                  117
                   57
% identity
                  (AC007060) EST gb AA721821 comes from this gene.
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   259125
                   377 2.R1011
Contig ID
5'-most EST
                  LIB3136-015-Q1-K1-E5
                  BLASTX
Method
NCBI GI
                   g2149640
BLAST score
                   1636
                   0.0e+00
E value
                   677
Match length
                   82
% identity
NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]
                   259126
Seq. No.
                   377 3.R1011
Contig ID
                   wty700167920.h1
5'-most EST
Method
                   BLASTX
                   g1653767
NCBI GI
BLAST score
                   830
                   6.0e-89
E value
                   257
Match length
% identity
```

Seq. No. 259127

NCBI Description

(D90916) oligopeptidase A [Synechocystis sp.]

Seq. No.

Contig ID





```
Contig ID
                   377 4.R1011
5'-most EST
                  LIB3115-020-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   g2149640
BLAST score
                   486
E value
                   6.0e-58
Match length
                   136
% identity
NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]
Seq. No.
                   259128
Contig ID
                   377_6.R1011
5'-most EST
                  uC-zmflb73120h10b1
Seq. No.
                   259129
                   377 7.R1011
Contig ID
5'-most EST
                  LIB3137-049-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  g2149640
BLAST score
                   969
                   1.0e-105
E value
Match length
                  236
% identity
NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]
Seq. No.
                   259130
                   377 8.R1011
Contig ID
5'-most EST
                  uC-zmflb73120a07b1
Method
                  BLASTX
NCBI GI
                   g2149640
BLAST score
                  1865
E value
                   0.0e + 00
Match length
                   551
% identity
NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]
Seq. No.
                   259131
                   377 9.R1011
Contig ID
5'-most EST
                  uC-zmflb73070b01b1
Seq. No.
                   259132
                   377 10.R1011
Contig ID
5'-most EST
                   LIB3137-039-Q1-K1-G1
Method
                   BLASTX
NCBI GI
                   g1871182
BLAST score
                   439
E value
                   5.0e-43
Match length
                  165
                   72
% identity
NCBI Description (U90439) phospholipase D isolog [Arabidopsis thaliana]
Seq. No.
                   259133
                   377 11.R1011
Contig ID
5'-most EST
                  hvj700624488.h1
```

259134

377 17.R1011

Contig ID

5'-most EST





```
5'-most EST
                  wty700169249.h1
                  BLASTX
Method
NCBI GI
                  q1871182
BLAST score
                  291
                  4.0e-36
E value
                  124
Match length
% identity
                 (U90439) phospholipase D isolog [Arabidopsis thaliana]
NCBI Description
                  259135
Seq. No.
                  377_18.R1011
Contig ID
5'-most EST
                  uC-zmflmo17342e11a1
                  259136
Seq. No.
Contig ID
                  377_19.R1011
5'-most EST
                  uC-zmflmo17171a10b1
Method
                  BLASTX
                  g2149640
NCBI GI
                  600
BLAST score
E value
                  2.0e-93
                  300
Match length
                  61
% identity
NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]
Seq. No.
                  259137
Contig ID
                  377 20.R1011
5'-most EST
                  LIB3061-018-Q1-K1-D3
Method
                  BLASTX
                  q1653767
NCBI GI
BLAST score
                   713
E value
                   3.0e-75
Match length
                  284
% identity
NCBI Description (D90916) oligopeptidase A [Synechocystis sp.]
Seq. No.
                   259138
Contig ID
                   377 23.R1011
5'-most EST
                  LIB3076-015-Q1-K1-F11
                  259139
Seq. No.
Contig ID
                   377 24.R1011
5'-most EST
                  uC-zmroteosinte073h02b1
Method
                  BLASTX
NCBI GI
                  g2149640
BLAST score
                  339
E value
                   2.0e-31
Match length
                  120
% identity
NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]
Seq. No.
                   259140
                  377 29.R1011
Contig ID
5'-most EST
                  clt700042028.f1
Seq. No.
                  259141
```

35804

377 30.R1011

ceu700430756.h1

% identity



8

```
Method
                  BLASTX
NCBI GI
                  q1293835
BLAST score
                  227
E value
                  6.0e-22
Match length
                  111
% identity
                  46
NCBI Description (U56965) C15H9.5 gene product [Caenorhabditis elegans]
Seq. No.
                  259142
                  377 31.R1011
Contig ID
5'-most EST
                  ypc700799288.h1
Method
                  BLASTX
NCBI GI
                  g2149640
BLAST score
                  246
E value
                  2.0e-21
Match length
                  80
% identity
                  91
NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]
Seq. No.
                  259143
                  378_1.R1011
Contig ID
5'-most EST
                  fC-zmse700834446 FL
Method
                  BLASTX
NCBI GI
                  q226237
BLAST score
                  608
E value
                  4.0e-63
Match length
                  118
                  100
% identity
NCBI Description lipoxygenase 3 [Glycine max]
Seq. No.
                  259144
Contig ID
                  379 1.R1011
                  fC-zmse700836843_FL
5'-most EST
Method
                  BLASTX
NCBI GI
                  g729882
BLAST score
                  720
                  3.0e-76
E value
Match length
                  142
                  90
% identity
NCBI Description CASEIN KINASE II BETA' CHAIN (CK II)
                  >gi_1076300 pir S47968 casein kinase II (EC 2.7.1.-) beta
                  chain CKB2 - Arabidopsis thaliana >gi_467975 (U03984)
                  casein kinase II beta subunit CKB2 [Arabidopsis thaliana]
                  >gi_2245122_emb_CAB10544_ (Z97343) unnamed protein product
                  [Arabidopsis thaliana]
                  259145
Seq. No.
                  380 1.R1011
Contig ID
5'-most EST
                  fC-zmse700836850 FL
Method
                  BLASTX
NCBI GI
                  g1666096
BLAST score
                  1108
E value
                  1.0e-121
Match length
                  308
```

NCBI Description (Y09113) dioxygenase [Marah macrocarpus]



```
Seq. No.
                   259146
Contig ID
                   381 1.R1011
5'-most EST
                   fC-zmse700836954 FL
Method
                   BLASTX
                   g3128225
NCBI GI
BLAST score
                   1076
E value
                   1.0e-117
Match length
                   322
                   68
% identity
NCBI Description
                  (AC004077) unknown protein [Arabidopsis thaliana]
                   259147
Seq. No.
Contig ID
                   382 1.R1011
5'-most EST
                   fC-zmse700838611 FL
Method
                   BLASTX
NCBI GI
                   g2252846
BLAST score
                   681
                   7.0e-90
E value
Match length
                   310
                   64
% identity
NCBI Description
                  (AF013293) Similar to phospholipase D [Arabidopsis
                   thaliana]
                   259148
Seq. No.
Contig ID
                   383 1.R1011
5'-most EST
                   fC-zmse700838837_FL
                   259149
Seq. No.
                   383 2.R1011
Contig ID
5'-most EST
                   fC-zmse700838864r1
Method
                   BLASTX
NCBI GI
                   g1842251
BLAST score
                   142
E value
                   9.0e-09
Match length
                   64
% identity
                   44
NCBI Description (U73916) rust resistance protein M [Linum usitatissimum]
Seq. No.
                   259150
Contig ID
                   384 1.R1011
5'-most EST
                   fC-zmse700838864 FL
Method
                   BLASTX
NCBI GI
                   g497417
BLAST score
                   283
E value
                   4.0e-25
Match length
                   99
% identity
                   57
NCBI Description (U10111) dehydrin-like protein [Glycine max]
Seq. No.
                   259151
                   385 1.R1011
Contig ID
5'-most EST
                   fC-zmst700332178 FL
Method
                   BLASTX
NCBI GI
```

35806

g2655029

2.0e-34

367

106

BLAST score

Match length

E value

% identity

68





```
% identity
NCBI Description
                  (AF019296) starch synthase isoform zSTSII-1 [Zea mays]
Seq. No.
                  259152
Contig ID
                  386 1.R1011
5'-most EST
                  fC-zmst700332980: FL
Method
                  BLASTX
NCBI GI
                  g4559329
BLAST score
                  521
E value
                  6.0e-53
Match length
                  148
% identity
                  65
                  (AC007087) putative protein kinase MAP3K [Arabidopsis
NCBI Description
                  thaliana]
                  259153
Seq. No.
Contig ID
                  387 1.R1011
5'-most EST
                  fC-zmst700335861 FL
Method
                  BLASTX
NCBI GI
                  g4519936
BLAST score
                  460
E value
                  2.0e-45
Match length
                  304
% identity
                  38
NCBI Description (AB019186) RPR1 [Oryza sativa]
Seq. No.
                  259154
Contig ID
                  388 1.R1011
5'-most EST
                  fC-zmst700336578 FL
Method
                  BLASTX
NCBI GI
                  g4490757
BLAST score
                  400
E value
                  3.0e-38
Match length
                  223
% identity
                  46
NCBI Description (AL035708) homeodomain-like protein [Arabidopsis thaliana]
                  259155
Seq. No.
                  388 2.R1011
Contig ID
5'-most EST
                  LIB3062-012-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  g4490757
BLAST score
                  364
E value
                  2.0e-34
Match length
                  94
                  71
% identity
NCBI Description (AL035708) homeodomain-like protein [Arabidopsis thaliana]
Seq. No.
                  259156
Contig ID
                  388 3.R1011
5'-most EST
                  LIB3156-013-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  g1168548
BLAST score
                  344
                  6.0e-32
E value
Match length
                  95
```





NCBI Description HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-7 (HD-ZIP PROTEIN ATHB-7) >gi_629527_pir__S47137 homeotic protein Athb-7 - Arabidopsis thaliana >gi_499164_emb_CAA47425_ (X67032) orf [Arabidopsis thaliana] 259157 Seq. No. 388 4.R1011 Contig ID 5'-most EST uC-zmflb73177d11b1 Method BLASTX NCBI GI q4490757 BLAST score 180 E value 1.0e-12 169 Match length % identity NCBI Description (AL035708) homeodomain-like protein [Arabidopsis thaliana] Seq. No. 259158 Contig ID 388 5.R1011 5'-most EST wty700170434.h1 Method BLASTX NCBI GI g1168548 BLAST score 352 E value 5.0e-33 Match length 95 % identity 69 NCBI Description HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-7 (HD-ZIP PROTEIN ATHB-7) >gi_629527_pir__S47137 homeotic protein Athb-7 -Arabidopsis thaliana >gi_499164_emb_CAA47425_ (X67032) orf [Arabidopsis thaliana] Seq. No. 259159 389_1.R1011 Contig ID uwc700150082.h1 5'-most EST Method BLASTX NCBI GI q1352081 BLAST score 2929 E value 0.0e+00Match length 550 % identity 98 BETA-GLUCOSIDASE, CHLOROPLAST PRECURSOR (GENTIOBIASE) NCBI Description (CELLOBIASE) (BETA-D-GLUCOSIDE GLUCOHYDROLASE) >gi_799377 (U25157) beta-D-glucosidase [Zea mays] >gi 1399390 (U44773) beta-D-glucosidase [Zea mays] >gi 4096602 (U33816) beta-D-glucosidase [Zea mays] Seq. No. 259160 Contig ID 389 2.R1011 5'-most EST uC-zmflb73100e07b1

Method BLASTX
NCBI GI g1206013
BLAST score 936
E value 0.0e+00
Match length 555
% identity 80

NCBI Description (U44087) beta-D-glucosidase precursor [Zea mays]

Seq. No. 259161





```
Contig ID
                   389 3.R1011
5'-most EST
                   uC-zmflB73043d12b1
Method
                  BLASTX
NCBI GI
                  q626042
BLAST score
                   409
                   5.0e-40
E value
                  92
Match length
% identity
                  86
NCBI Description
                  beta-glucosidase, root meristem (EC 3.2.1.-) precursor -
                  maize >gi_435313_emb_CAA52293_ (X74217) beta-glucosidase
                   [Zea mays]
                   259162
Seq. No.
                   389 5.R1011
Contig ID
5'-most EST
                  LIB83-004-Q1-E2-F6
Method
                  BLASTX
                  q1206013
NCBI GI
BLAST score
                  686
E value
                   2.0e-72
Match length
                  143
% identity
                  89
NCBI Description (U44087) beta-D-glucosidase precursor [Zea mays]
                  259163
Seq. No.
                   389 6.R1011
Contig ID
5'-most EST
                  uC-zmroteosinte095a09b2
Method
                  BLASTX
NCBI GI
                  q626042
                   907
BLAST score
                   1.0e-103
E value
Match length
                   233
                   90
% identity
                  beta-glucosidase, root meristem (EC 3.2.1.-) precursor -
NCBI Description
                  maize >gi 435313 emb CAA52293 (X74217) beta-glucosidase
                  ·[Zea mays]
                   259164
Seq. No.
                   389 7.R1011
Contig ID
5'-most EST
                   pmx700085277.h1
Method
                  BLASTX
NCBI GI
                   g1206013
BLAST score
                  804
E value
                   5.0e-86
Match length
                  190
                   75
% identity
NCBI Description (U44087) beta-D-glucosidase precursor [Zea mays]
                   259165
Seq. No.
                   389 8.R1011
Contig ID
                  uwc700155517.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g626042
BLAST score
                   696
                   2.0e-73
E value
Match length
                  203
% identity
                   99
```

NCBI Description beta-glucosidase, root meristem (EC 3.2.1.-) precursor -





maize >gi 435313 emb CAA52293 (X74217) beta-glucosidase

```
[Zea mays]
                  259166
Seq. No.
                  389 9.R1011
Contig ID
5'-most EST
                  LIB3067-058-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g1352081
BLAST score
                  580
E value
                  8.0e-60
                  139
Match length
                  83
% identity
                  BETA-GLUCOSIDASE, CHLOROPLAST PRECURSOR (GENTIOBIASE)
NCBI Description
                  (CELLOBIASE) (BETA-D-GLUCOSIDE GLUCOHYDROLASE) >gi 799377
                  (U25157) beta-D-glucosidase [Zea mays] >gi 1399390 (U44773)
                  beta-D-glucosidase [Zea mays] >gi_4096602 (U33816)
                  beta-D-glucosidase [Zea mays]
Seq. No.
                  259167
                  389 10.R1011
Contig ID
5'-most EST
                  LIB3136-036-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g1206013
BLAST score
                  485
E value
                  7.0e-49
Match length
                  90
                  100
% identity
NCBI Description (U44087) beta-D-glucosidase precursor [Zea mays]
                  259168
Seq. No.
                  389 12.R1011
Contig ID
5'-most EST
                  LIB3136-035-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  g626042
BLAST score
                  523
E value
                  4.0e-53
                  107
Match length
                  89
% identity
NCBI Description beta-glucosidase, root meristem (EC 3.2.1.-) precursor -
                  maize >gi_435313_emb_CAA52293 (X74217) beta-glucosidase
                  [Zea mays]
                  259169
Seq. No.
Contig ID
                  389 14.R1011
                  ntr700075075.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q626042
BLAST score
                  347
E value
                  6.0e-33
Match length
                  92
                  78
% identity
                  beta-glucosidase, root meristem (EC 3.2.1.-) precursor -
NCBI Description
                  maize >gi 435313 emb CAA52293 (X74217) beta-glucosidase
```

35810

[Zea mays]

389 19.R1011

259170

Seq. No. Contig ID

NCBI GI

BLAST score E value





```
5'-most EST
                  dyk700105284.h1
Method
                  BLASTX
NCBI-GI
                  a626042
BLAST score
                  314
E value
                  4.0e-29
Match length
                  60
                  98
% identity
                  beta-glucosidase, root meristem (EC 3.2.1.-) precursor -
NCBI Description
                  maize >gi_435313_emb_CAA52293_ (X74217) beta-glucosidase
                  [Zea mays]
                  259171
Seq. No.
Contig ID
                  390 1.R1011
                  uC-zmflm017209b06b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3242077
BLAST score
                  267
                  5.0e-23
E value
                  111
Match length
% identity
                  51
                 (AJ003119) protein phosphatase 2C [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  259172
Contig ID
                  390 2.R1011
                  fC-zmst700619527 FL
5'-most EST
Method
                  BLASTX
NCBI GI
                  q499301
BLAST score
                  311
E value
                  1.0e-28
Match length
                  74
% identity
                  80
NCBI Description
                  (X77116) ABI1 [Arabidopsis thaliana] >gi_549981 (U12856)
                  abscisic acid insensitive protein [Arabidopsis thaliana]
                  >gi_4538937_emb_CAB39673.1_ (AL049483) protein phosphatase
                  ABI1 [Arabidopsis thaliana]
Seq. No.
                  259173
Contig ID
                  390 3.R1011
5'-most EST
                  hbs701181178.hl
Method
                  BLASTX
NCBI GI
                  g1352679
BLAST score
                  280
E value
                  1.0e-24
Match length
                  100
                  51
% identity
NCBI Description
                 PROTEIN PHOSPHATASE 2C ABI1 (PP2C) >gi_2129699_pir__A54588
                 , protein phosphatase ABI1 - Arabidopsis thaliana
                   >gi_509419_emb_CAA55484_ (X78886) ABI1 [Arabidopsis
                  thaliana]
Seq. No.
                  259174
                  391 1.R1011
Contig ID
                  fC-zmle700424985f2
5'-most EST
Method
                  BLASTX
```

35811

g1657621 824

3.0e-88

NCBI GI

E value

BLAST score

Match length

% identity

g461498

4.0e-55

538

135

76





```
Match length
% identity
                 (U72505) G6p [Arabidopsis thaliana] >qi 3068711 (AF049236)
NCBI Description
                  putative acyl-coA dehydrogenase [Arabidopsis thaliana]
                  259175
Seq. No.
                  392_1.R1011
Contig ID
                  uC-zmflmo17215a08a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q461498
BLAST score
                  1931
                  0.0e + 00
E value
Match length
                  478
% identity
                  76
NCBI Description ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
                  TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                   (ALAAT-2) >gi_320619_pir__S28429 alanine transaminase (EC
                  2.6.1.2) - proso millet >gi 296204_emb_CAA49199_ (X69421)
                  alanine aminotransferase [Panicum miliaceum]
                  259176
Seq. No.
                  392_2.R1011
Contig ID
5'-most EST
                  uC-zmflb73034f08b2
Method
                  BLASTX
NCBI GI
                  q2632987
BLAST score
                  288
                  1.0e-25
E value
Match length
                  131
% identity
                   46
                 (Z99107) alternate gene name: yerS; similar to RNA
NCBI Description
                  methyltransferase [Bacillus subtilis]
Seq. No.
                   259177
Contig ID
                   392 3.R1011
5'-most EST
                   fC-zmst700620180 FL
Method
                  BLASTX
                  q2766452
NCBI GI
                  210
BLAST score
E value
                   2.0e-16
                   67
Match length
% identity
                   58
NCBI Description (AF029858) cytochrome P450 CYP71E1 [Sorghum bicolor]
Seq. No.
                   259178
                   392 4.R1011
Contig ID
                  LIB3075-048-Q1-K1-A10
5'-most EST
Seq. No.
                   259179
                   392 5.R1011
Contig ID
5'-most EST
                  LIB3078-015-Q1-K1-F4
Method
                  BLASTX
```

35812

NCBI Description ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC





```
TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_320619_pir__ S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421) alanine aminotransferase [Panicum miliaceum]
```

259180 Seq. No. 392 6.R1011 Contig ID 5'-most EST LIB83-005-Q1-E1-A7 Method BLASTX q1703227 NCBI GI BLAST score 210 1.0e-16 E value Match length 44 % identity

NCBI Description ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)

(ALAAT-2) >gi_629770_pir__S42535 alanine transaminase (EC 2.6.1.2) - barley >gi_469148_emb_CAA81231_ (Z26322) alanine

aminotransferase [Hordeum vulgare]

Seq. No. 259181
Contig ID 393_1.R1011

5'-most EST fC-zmst700621688_FL

Method BLASTX
NCBI GI g2829869
BLAST score 310
E value 2.0e-28
Match length 85
% identity 71

NCBI Description (AC002396) pyruvate dehydrogenase E1 alpha subunit

[Arabidopsis thaliana]

NCBI GI g2829869 BLAST score 185 E value 2.0e-13 Match length 48 % identity 67

NCBI Description (AC002396) pyruvate dehydrogenase E1 alpha subunit

[Arabidopsis thaliana]

Seq. No. 259183
Contig ID 394_1.R1011

5'-most EST fC-zmst700621904:_FL

Method BLASTX
NCBI GI g113029
BLAST score 1716
E value 0.0e+00
Match length 452
% identity 74

NCBI Description ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)

>gi_68209_pir__WZCNIU isocitrate lyase (EC 4.1.3.1) upland cotton >gi_18486_emb_CAA36381_ (X52136) isocitrate

lyase (AA 1-576) [Gossypium hirsutum]





259184 Seq. No. 394 2.R1011 Contig ID LIB143-036-Q1-E1-F3 5'-most EST BLASTX Method q1351840 NCBI GI 947 BLAST score 1.0e-103 E value 230 Match length 77 % identity ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) NCBI Description >gi_1084319_pir__S53505 isocitrate lyase - cucumber >gi_1052578_emb_CAA84632_ (Z35499) isocitrate lyase [Cucumis sativus] 259185 Seq. No. 395 1.R1011 Contig ID xjt700092739.h1 5'-most EST BLASTX Method g2760839 NCBI GI 1341 BLAST score 1.0e-148 E value 595 Match length 49 % identity. (AC003105) putative receptor kinase [Arabidopsis thaliana] NCBI Description 259186 Seq. No. 396 1.R1011 Contig ID CPR9206_700072933_FL 5'-most EST BLASTX Method g1708993 NCBI GI BLAST score 1598 1.0e-178 E value 382 Match length 79 % identity CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) NCBI Description (BETA-CYSTATHIONASE) (CYSTEINE LYASE) >gi_2129567_pir__S61429 cystathionine beta-lyase (EC 4.4.1.8) - Arabidopsis thaliana >gi_704397 (L40511) cystathionine beta-lyase [Arabidopsis thaliana] Seq. No. 259187 397 1.R1011 Contig ID CPR22039:2F700076024con_FL 5'-most EST BLASTX Method q3668115 NCBI GI BLAST score 1564 E value 1.0e-175 Match length 333 89 % identity

NCBI Description (Y15069) cinnamoyl-CoA reductase [Zea mays]

259188 Seq. No. 398 1.R1011 Contig ID

CPR22066:2F700094677con_FL 5'-most EST

Method BLASTX g1724110 NCBI GI





```
BLAST score
                   1.0e-113
E value
Match length
                   353
% identity
                   56
                   (U79770) cinnamyl-alcohol dehydrogenase Eli3
NCBI Description
                   [Mesembryanthemum crystallinum]
Seq. No.
                   259189
Contig ID
                   398 2.R1011
5'-most EST
                   ntr700071870.h1
Method
                   BLASTX
NCBI GI
                   g1724110
BLAST score
                   896
E value
                   2.0e-96
Match length
                   350
% identity
                   50
                   (U79770) cinnamyl-alcohol dehydrogenase Eli3
NCBI Description
                   [Mesembryanthemum crystallinum]
Seq. No.
                   259190
Contig ID
                   398 6.R1011
5'-most EST
                   clt700042436.f1
Method
                   BLASTX
NCBI GI
                   q1724110
BLAST score
                   167
E value
                   2.0e-14
Match length
                   63
                   65
% identity
                  (U79770) cinnamyl-alcohol dehydrogenase Eli3
NCBI Description
                   [Mesembryanthemum crystallinum]
                   259191
Seq. No.
                   398 9.R1011
Contig ID
                   uwc700152288.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3913193
BLAST score
                   149
E value
                   5.0e-10
                   39
Match length
                   62
% identity
                   CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_556422 (L36823)
NCBI Description
                   cinnamyl-alcohol dehydrogenase [Stylosanthes humilis]
                   259192
Seq. No.
Contig ID
                   400 1.R1011
                   fwa700097293.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g68029
BLAST score
                   4950
E value
                   0.0e + 00
                   970
Match length
                   99
% identity
```

NCBI Description phosphoenolpyruvate carboxylase (EC 4.1.1.31) - maize >gi_22408_emb_CAA33317_ (X15239) PEP carboxylase [Zea mays] >gi_228619_prf__1807332A phosphoenolpyruvate carboxylase [Zea mays]

- -

Contig ID

5'-most EST





```
Seq. No.
                  259193
Contig ID
                  400 2.R1011
5'-most EST
                  wty700172941.h1
Method
                  BLASTX
NCBI GI
                  g2961176
BLAST score
                  595
E value
                  2.0e-61
Match length
                  186
% identity
NCBI Description
                  (AF050674) ribosomal protein L27 precursor [Oryza sativa]
Seq. No.
                  259194
Contig ID
                  400 3.R1011
5'-most EST
                  LIB83-015-Q1-E1-E11
                  259195
Seq. No.
                  400 4.R1011
Contig ID
5'-most EST
                  LIB36-002-Q1-E1-E7
Method
                  BLASTX
NCBI GI
                  q115608
BLAST score
                  313
                  1.0e-28
E value
Match length
                  77
% identity
                  82
                  PHOSPHOENOLPYRUVATE CARBOXYLASE 1 (PEPCASE)
NCBI Description
                  >gi_22563_emb_CAA33316_ (X15238).phosphoenolpyruvate
                  carboxylase (AA 1 - 970) [Zea mays]
Seq. No.
                  259196
Contig ID
                   400 5.R1011
5'-most EST
                  LIB3078-046-Q1-K1-B8
Method
                  BLASTX
NCBI GI
                  g115608
BLAST score
                  311
E value
                   2.0e-31
Match length
                  93
% identity
                  84
NCBI Description
                  PHOSPHOENOLPYRUVATE CARBOXYLASE 1 (PEPCASE)
                  >gi 22563 emb CAA33316 (X15238) phosphoenolpyruvate
                  carboxylase (AA 1 - 970) [Zea mays]
                  259197
Seq. No.
                   400 7.R1011
Contig ID
5'-most EST
                  LIB189-011-Q1-E1-B3
Method
                  BLASTX
NCBI GI
                  g115608
BLAST score
                  399
                  7.0e-39
E value
Match length
                  144
                   59
% identity
NCBI Description
                  PHOSPHOENOLPYRUVATE CARBOXYLASE 1 (PEPCASE)
                  >gi 22563 emb CAA33316 (X15238) phosphoenolpyruvate
                  carboxylase (AA 1 - 970) [Zea mays]
Seq. No.
                  259198
```

35816

400_8.R1011 uwc700154435.h1

E value

Match length % identity

0.0e+00 799

68





```
Method
                   BLASTX
                   g3132310
NCBI GI
BLAST score
                   776
E value
                   1.0e-82
Match length
                   227
                   73
% identity
                  (AB012228) phosphoenolpyruvate carboxylase [Zea mays]
NCBI Description
                   259199
Seq. No.
                   400 13.R1011
Contig ID
                   uC-\overline{z}mroB73030h08b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3132310
                   937
BLAST score
                   1.0e-102
E value
                   185
Match length
                   100
% identity
                  (AB012228) phosphoenolpyruvate carboxylase [Zea mays]
NCBI Description
                   259200
Seq. No.
                   400_15.R1011
Contig ID
                   uer700578374.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g829295
BLAST score
                   285
                   9.0e-26
E value
Match length
                   58
                   100
% identity
                  (X03613) PEPCase [Zea mays]
NCBI Description
                   259201
Seq. No.
                   401_1.R1011
Contig ID
                   uC-zmflm017025e07b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2459446
BLAST score
                   746
E value
                   7.0e-79
Match length
                   315
                   47
% identity
NCBI Description
                   (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
                   thaliana]
                   259202
Seq. No.
                   401 2.R1011
Contig ID
                   uC-zmflmo17025e07a1
5'-most EST
Seq. No.
                   259203
Contig ID
                   403 1.R1011
5'-most EST
                   fC-zmle700443890a1
Method
                   BLASTX
NCBI GI
                   q2687358
BLAST score
                   2843
```

35817

NCBI Description (AF033263) nonphototropic hypocotyl 1 [Zea mays]

Method

NCBI GI

E value

BLAST score

BLASTX

696

q4056432

1.0e-102





```
Seq. No.
                  259204
                  405 1.R1011
Contig ID
5'-most EST
                  CPR9074:2F700151670.con FL
                  BLASTX
Method
                  q3182921
NCBI GI
BLAST score
                  2731
                  0.0e + 00
E value
                  591
Match length
                  85
% identity
                  ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING)
NCBI Description
                   (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi_1432054
                   (U55873) asparagine synthetase [Oryza sativa]
                  >gi_1902992_dbj_BAA18951_ (D83378) asparagine synthetase
                   [Oryza sativa]
                  259205
Seq. No.
                  405 3.R1011
Contig ID
                  rvt700549316.hl
5'-most EST
                  BLASTX
Method
                  q3182921
NCBI GI
                  321
BLAST score
                  6.0e-30
E value
Match length
                  79
                  80
% identity
                  ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING)
NCBI Description
                   (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi_1432054
                   (U55873) asparagine synthetase [Oryza sativa]
                  >gi 1902992_dbj_BAA18951_ (D83378) asparagine synthetase
                   [Oryza sativa]
                  259206
Seq. No.
                   406 1.R1011
Contig ID
                  CPR22067:2F700152375con FL
5'-most EST
                  BLASTX
Method
                   g4097522
NCBI GI
                   948
BLAST score
                   1.0e-102
E value
Match length
                   354
                   51
% identity
                  (U63534) cinnamyl alcohol dehydrogenase [Fragaria x
NCBI Description
                   ananassa]
Seq. No.
                   259207
                   407 1.R1011
Contig ID
5'-most EST
                   uC-zmrob73002g05a1
                   259208
Seq. No.
Contig ID
                   407 2.R1011
5'-most EST
                   700161669 FL
                   259209
Seq. No.
                   408 1.R1011
Contig ID
5'-most EST
                   CPR22115:2F700169890con FL
```



309 Match length 59 % identity (AC005990) Similar to gi 2245014 glucosyltransferase NCBI Description homolog from Arabidopsis thaliana chromosome 4 contig gb Z97341. ESTs gb_T20778 and gb_AA586281 come from this gene. [Arabidopsis Thaliana] 259210 Seq. No. 409_1.R1011 Contig ID cat700016021.r1 5'-most EST BLASTX Method NCBI GI q2130023 BLAST score 513 2.0e-54 E value 185 Match length 45 % identity DNA-binding protein ABF1 - wild oat (fragment) NCBI Description >gi 1159877 emb CAA88326_ (Z48429) DNA-binding protein [Avena fatua] 259211 Seq. No. 409 2.R1011 Contig ID uC-zmflmo17090d08a1 5'-most EST BLASTX Method q1076685 NCBI GI 451 BLAST score E value 8.0e-45 121 Match length 47 % identity SPF1 protein - sweet potato >gi_484261_dbj_BAA06278_ NCBI Description (D30038) SPF1 protein [Ipomoea batatas] 259212 Seq. No. Contig ID 410 1.R1011 CPR951:2F700203435consensus_FL 5'-most EST Method BLASTX NCBI GI q3250675 BLAST score 989 1.0e-107 E value Match length 375 % identity (AL024486) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 259213 411 1.R1011 Contig ID 5'-most EST qmh700029853.f1Method BLASTX NCBI GI q1418323 BLAST score 256

E value 1.0e-21 167 Match length % identity 36

(X98671) zinc finger protein [Arabidopsis thaliana] NCBI Description >qi 1418333 emb CAA67228 (X98670) zinc finger protein

[Arabidopsis thaliana]

259214 Seq. No.



415 1.R1011 Contig ID CPR9146:2F700220213.CON FL 5'-most EST Method BLASTX g3170601 NCBI GI BLAST score 251 E value 7.0e-21 171 Match length 37 % identity (AF058757) zinc finger protein ID1 [Zea mays] NCBI Description 259215 Seq. No. 415 2.R1011 Contig ID 5'-most EST uC-zmflmo17426e09a1 259216 Seq. No. 416 1.R1011 Contig ID CPR921_700237945_FL 5'-most EST BLASTX Method NCBI GI g2088653 BLAST score 906 E value 5.0e-98 177 Match length 100 % identity (AF002109) Hs1pro-1 related protein isolog [Arabidopsis NCBI Description thaliana] Seq. No. 259217 418 1.R1011 Contig ID 5'-most EST CPR6872_700265919_FL BLASTX Method NCBI GI q3170502 BLAST score 227 3.0e-18E value Match length 163 33 % identity (AF052874) APETALA3 homolog PnAP3-2 [Papaver nudicaule] NCBI Description Seq. No. 259218 419 1.R1011 Contig ID 5'-most EST clt700041944.f1 Method BLASTX NCBI GI g4038043 BLAST score 410 1.0e-81 E value Match length 397 49 % identity NCBI Description (AC005936) putative DNA-binding protein [Arabidopsis thaliana] Seq. No. 259219 Contig ID 419 2.R1011 5'-most EST LIB3062-053-Q1-K1-A4

Contig ID 419_2.R1011
5'-most EST LIB3062-053-Q1-K1-A4
Method BLASTX
NCBI GI g4038043
BLAST score 724
E value 2.0e-76
Match length 176





% identity (AC005936) putative DNA-binding protein [Arabidopsis NCBI Description thaliana] 259220 Seq. No. 419 3.R1011 Contig ID uC-zmflb73267e03b2 5'-most EST BLASTX Method NCBI GI g4204303 BLAST score 534 2.0e-54 E value Match length 126 % identity 78 (AC003027) lcl prt seq No definition line found NCBI Description [Arabidopsis thaliana] 259221 Seq. No. 419 4.R1011 Contig ID LIB3059-040-Q1-K1-G12 5'-most EST 259222 Seq. No. 421_1.R1011 Contig ID CPR22113:2F700381143con_FL 5'-most EST BLASTX Method NCBI GI g4056432 1420 BLAST score E value 1.0e-158 371 Match length 69 % identity (AC005990) Similar to gi_2245014 glucosyltransferase NCBI Description homolog from Arabidopsis thaliana chromosome 4 contig gb Z97341. ESTs gb_T20778 and gb_AA586281 come from this gene. [Arabidopsis thaliana] 259223 Seq. No. Contig ID 424 1.R1011 5'-most EST LIB3136-002-P1-K1-C7 BLASTN Method q2687357 NCBI GI BLAST score 388 0.0e+00E value Match length 446 96 % identity Zea mays nonphototropic hypocotyl 1 (nph1) mRNA, complete NCBI Description Seq. No. 259224 Contig ID 425 1.R1011 5'-most EST pmx700089319.hl Method BLASTX NCBI GI g532623

BLAST score 651 8.0e-68 E value

Match length 288 % identity 52

NCBI Description (L35913) lipase [Zea mays]

E value

Match length

% identity



8

```
Seq. No.
                  259225
Contig ID
                  425 2.R1011
5'-most EST
                  uC-zmflb73130b05b2
                  BLASTX
Method
NCBI GI
                  g532623
BLAST score
                  350
                  1.0e-32
E value
Match length
                  198
% identity
                  59
NCBI Description (L35913) lipase [Zea mays]
                  259226
Seq. No.
                  425 3.R1011
Contig ID
5'-most EST
                  uC-zmflb73020b07b1
Method
                  BLASTX
NCBI GI
                  g532623
BLAST score
                  445
E value
                  1.0e-43
Match length
                  290
% identity
                  44
NCBI Description (L35913) lipase [Zea mays]
Seq. No.
                  259227
Contig ID
                  425 4.R1011
5'-most EST
                  uC-zmroteosinte077e01b1
                  259228
Seq. No.
                  425 6.R1011
Contig ID
5'-most EST
                  uC-zmroteosinte033g04b1
Method
                  BLASTX
NCBI GI
                  g532623
BLAST score
                  233
E value
                  2.0e-20
Match length
                  64
% identity
                  95
NCBI Description (L35913) lipase [Zea mays]
                  259229
Seq. No.
                  425 7.R1011
Contig ID
5'-most EST
                  uC-zmflb73264b10b1
Method
                  BLASTX
NCBI GI
                  g532623
BLAST score
                  500
E value
                  2.0e-50
Match length
                  205
                  57
% identity
NCBI Description (L35913) lipase [Zea mays]
                  259230
Seq. No.
Contig ID
                  425 8.R1011
5'-most EST
                  wyr700236447.h1
Method
                  BLASTX
NCBI GI
                  g532623
BLAST score
                  331
```

1.0e-30

123

61



```
(L35913) lipase [Zea mays]
NCBI Description
Seq. No.
                  259231
                  426 1.R1011
Contig ID
                  uC-zmflmo17163f09b1
5'-most EST
                  BLASTX
Method
                  q2464852
NCBI GI
BLAST score
                  242
E value
                  6.0e-20
Match length
                  167
% identity
                  37
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
                  259232
Seq. No.
                  428 1.R1011
Contig ID
                  xjt700096186.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4586103
BLAST score
                  560
E value
                  6.0e-87
                  233
Match length
% identity
                  72
NCBI Description (AL049638) putative protein [Arabidopsis thaliana]
Seq. No.
                  259233
Contig ID
                  431 1.R1011
                  CPR22093:2F701168881con FL
5'-most EST
Method
                  BLASTX
                  g4206196
NCBI GI
BLAST score
                  509
                  3.0e-51
E value
Match length
                  201
                  51
% identity
NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  259234
                  431 2.R1011
Contig ID
5'-most EST
                  LIB3069-054-Q1-K1-D11
                  259235
Seq. No.
                  432 1.R1011
Contig ID
5'-most EST
                  CPR9051:2F701175695.con FL
                  BLASTX
Method
NCBI GI
                  q730125
BLAST score
                  310
                   6.0e-28
E value
                  223
Match length
                   33
% identity
                  NADPH-CYTOCHROME P450 REDUCTASE >qi 322739 pir S31502
NCBI Description
                   NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Madagascar
                   periwinkle >gi 18139 emb CAA49446 (X69791)
                  NADPH--ferrihemoprotein reductase [Catharanthus roseus]
```

Seq. No. 259236 Contig ID 433 1.R1011 5'-most EST uC-zmflB73010b05b1

Method BLASTX





```
q4406780
NCBI GI
BLAST score
                  469
                  1.0e-46
E value
                  124
Match length
                  70
% identity
                  (AC006532) putative multispanning membrane protein
NCBI Description
                  [Arabidopsis thaliana]
                  259237
Seq. No.
                  433 2.R1011
Contig ID
                  uC-zmflmo17125g05b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4406780
BLAST score
                  1171
                  1.0e-129
E value
                  299
Match length
                  75
% identity
                  (AC006532) putative multispanning membrane protein
NCBI Description
                  [Arabidopsis thaliana]
                  259238
Seq. No.
                  433 3.R1011
Contig ID
                  qmh700028438.fl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4406780
BLAST score
                  1153
                  1.0e-127
E value
                  285
Match length
                  73
% identity
                  (AC006532) putative multispanning membrane protein
NCBI Description
                  [Arabidopsis thaliana]
                  259239
Seq. No.
                  434 1.R1011
Contig ID
                  LIB3075-056-Q1-K1-G10
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1362162
BLAST score
                  1044
E value
                  1.0e-114
Match length
                  335
                  56
% identity
NCBI Description beta-glucosidase BGQ60 precursor - barley >gi 804656
                  (L41869) beta-glucosidase [Hordeum vulgare]
                  259240
Seq. No.
                  435 1.R1011
Contig ID
                  hbs701183357.h1
5'-most EST
Seq. No.
                  259241
                  436 1.R1011
Contig ID
                  pmx700089088.h1
5'-most EST
                  BLASTX
Method
```

5'-most EST pmx700089088.h

Method BLASTX

NCBI GI g3599386

BLAST score 157

E value 4.0e-10

Match length 93

40

% identity





(AF083071) peptidyl-prolyl cis/trans isomerase [Cenarchaeum NCBI Description symbiosum] 259242 Seq. No. 436 2.R1011 Contig ID LIB3076-048-Q1-E1-G6 5'-most EST Seq. No. 259243 Contig ID 436 3.R1011 5'-most EST xsy700217886.h1 259244 Seq. No. 437 1.R1011 Contig ID xsy700217540.hl 5'-most EST 259245 Seq. No. 437 2.R1011 Contig ID 5'-most EST uC-zmflb73227a04a1 Seq. No. 259246 437 3.R1011 Contig ID 5'-most EST ypc700806183.hl Seq. No. 259247 Contig ID 438 1.R1011 yyf700350713.h1 5'-most EST Method BLASTX NCBI GI q3785998 BLAST score 454 E value 2.0e-47 Match length 155 62 % identity NCBI Description (AC005499) unknown protein [Arabidopsis thaliana] 259248 Seq. No. 441 1.R1011 Contig ID 5'-most EST LIB3075-056-Q1-K1-H7 Seq. No. 259249 442 1.R1011 Contig ID LIB3066-055-Q1-K1-E1 5'-most EST Method BLASTX g3785983 NCBI GI BLAST score 362 E value 4.0e-34 Match length 142 49 % identity NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana] 259250 Seq. No. 442 2.R1011 Contig ID LIB148-012-Q1-E1-C10 5'-most EST BLASTX Method

NCBI GI g3785983 BLAST score 376 1.0e-35 E value

143

Match length





% identity (AC005560) hypothetical protein [Arabidopsis thaliana] NCBI Description 259251 Seq. No. Contig ID 442 3.R1011 5'-most EST LIB148-003-Q1-E1-C4 BLASTX Method NCBI GI g3785983 BLAST score 189 E value 4.0e-15 84 Match length 52 % identity (AC005560) hypothetical protein [Arabidopsis thaliana] NCBI Description 259252 Seq. No. Contig ID 442 4.R1011 5'-most EST LIB3066-011-Q1-K1-G9 Method BLASTX NCBI GI g3785983 BLAST score 345 E value 5.0e - 32Match length 164 42 % identity (AC005560) hypothetical protein [Arabidopsis thaliana] NCBI Description 259253 Seq. No. Contig ID 444 1.R1011 uC-zmflmo17221d11b1 5'-most EST Method BLASTX q3152606 NCBI GI BLAST score 355 1.0e-33 E value Match length 71 82 % identity (AC004482) putative ring zinc finger protein [Arabidopsis NCBI Description thaliana] Seq. No. 259254 Contig ID 445 1.R1011 5'-most EST uC-zmflb73251e08b3 Method BLASTX NCBI GI g4432848 BLAST score 435 E value 1.0e-42 Match length 182 % identity 53 NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana] 259255 Seq. No. 446 1.R1011 Contig ID ymt700218630.h1 5'-most EST

Method BLASTX g3309269 NCBI GI BLAST score 1924

0.0e+00E value Match length 443 84 % identity





```
(AF074940) ferric leghemoglobin reductase-2 precursor
NCBI Description
                   [Glycine max]
                  259256
Seq. No.
Contig ID
                  446 2.R1011
5'-most EST
                  uC-zmflb73071b01b3
                  BLASTX
Method
NCBI GI
                  g984678
BLAST score
                  331
E value
                   9.0e-31
                  77
Match length
% identity
                  79
                  (X62995) lipoamide dehydrogenase [Pisum sativum]
NCBI Description
                  259257
Seq. No.
Contig ID
                  446 3.R1011
5'-most EST
                  LIB3059-014-Q1-K1-C6
                  BLASTX
Method
NCBI GI
                  g984678
BLAST score
                  237
E value
                  1.0e-19
                  57
Match length
                  75
% identity
NCBI Description
                  (X62995) lipoamide dehydrogenase [Pisum sativum]
                  259258
Seq. No.
                  446 4.R1011
Contig ID
5'-most EST
                  LIB3158-017-Q1-K1-E3
Method
                  BLASTN
                  g3821780
NCBI GI
BLAST score
                   37
                   2.0e-11
E value
Match length
                   37
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   259259
Contig ID
                   447 1.R1011
5'-most EST
                  LIB3075-056-Q1-K1-F1
Method
                   BLASTX
NCBI GI
                   g2062605
BLAST score
                   177
E value
                   1.0e-12
Match length
                   141
% identity
                   28
NCBI Description
                  (U85946) brain secretory protein hSec10p [Homo sapiens]
Seq. No.
                   259260
```

447 2.R1011 Contig ID nwy700447653.h15'-most EST

Seq. No. 259261 449 1.R1011 Contig ID

5'-most EST LIB3137-008-Q1-K1-F2

Method BLASTX NCBI GI g113621 BLAST score 1825



8

E value 0.0e+00 Match length 355 % identity 99

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase

[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A

cytoplasmic aldolase [Zea mays]

Seq. No. 259262 Contig ID 449 2.R1011

5'-most EST LIB3079-059-Q1-K1-E6

Method BLASTX
NCBI GI g113621
BLAST score 597
E value 9.0e-62
Match length 121
% identity 98

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A

cytoplasmic aldolase [Zea mays]

Seq. No. 259263 Contig ID 449 3.R1011

5'-most EST LIB3150-028-Q1-N1-D9

Method BLASTX
NCBI GI g113621
BLAST score 534
E value 8.0e-58
Match length 130
% identity 92

% identity 92
NCBI Description FRUCTOSE-F

FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_68196_pir_ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850 emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A

cytoplasmic aldolase [Zea mays]

5'-most EST LIB148-003-Q1-E1-C6

Method BLASTX
NCBI GI g464470
BLAST score 677
E value 4.0e-71
Match length 131
% identity 95

NCBI Description PROFILIN 3 >gi_422033_pir_S35798 profilin 3 - maize

>gi_313142_emb_CAA51720_ (X73281) profilin 3 [Zea mays]

Seq. No. 259265 Contig ID 450_2.R1011

5'-most EST LIB148-012-Q1-E1-A11





```
BLASTX
Method
NCBI GI
                   q464470
                   699
BLAST score
                   1.0e-73
E value
Match length
                   131
% identity
                   100
                   PROFILIN 3 >gi_422033_pir__S35798 profilin 3 - maize
NCBI Description
                   >gi 313142 emb CAA51720 (X73281) profilin 3 [Zea mays]
                   259266
Seq. No.
                   450 3.R1011
Contig ID
5'-most EST
                   LIB3067-027-Q1-K1-G7
Method
                   BLASTX
NCBI GI
                   q3914422
BLAST score
                    598
E value
                   7.0e-62
                   131
Match length
                    84
% identity
                   PROFILIN >gi_2154728_emb_CAA69669_ (Y08389) profilin 2
NCBI Description
                    [Cynodon dactylon] >gi 2154730_emb_CAA69670_ (Y08390)
                   profilin 1 [Cynodon dactylon]
                    259267
Seq. No.
                    450 5.R1011
Contig ID
                   LIB148-014-Q1-E1-C10
5'-most EST
Method
                    BLASTX
NCBI GI
                    q464470
                    686
BLAST score
E value
                    4.0e-72
                    131
Match length
                    98
% identity
                   PROFILIN 3 >gi_422033_pir__S35798 profilin 3 - maize
NCBI Description
                    >gi 313142 emb CAA51720 (X73281) profilin 3 [Zea mays]
                    259268
Seq. No.
Contig ID
                    450 9.R1011
5'-most EST
                    wyr700242913.h1
                    BLASTX
Method
NCBI GI
                    q3914422
BLAST score
                    358
                    3.0e - 34
E value
Match length
                    71
                    93
% identity
                    PROFILIN >gi_2154728_emb_CAA69669_ (Y08389) profilin 2 [Cynodon dactylon] >gi_2154730_emb_CAA69670_ (Y08390)
NCBI Description
                    profilin 1 [Cynodon dactylon]
Seq. No.
                    259269
                    451 1.R1011
Contig ID
                    LIB3137-014-Q1-K1-C1
5'-most EST
Method
                    BLASTX
NCBI GI
                    g4558673
BLAST score
                    760
                    1.0e-80
E value
```

35829

(AC007063) hypothetical protein [Arabidopsis thaliana]

304

46

Match length

NCBI Description

% identity

Contig ID





```
Seq. No.
                  259270
Contig ID
                  452 1.R1011
                  uC-zmflb73179f02b1
5'-most EST
Method
                  BLASTX
                  g4455237
NCBI GI
                  710
BLAST score
E value
                  1.0e-94
Match length
                  305
% identity
                  57
                  (AL035523) ubiquitin activating enzyme-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  259271
Seq. No.
                  453 1.R1011
Contig ID
                  LIB148-024-Q1-E1-C9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4454039
BLAST score
                  629
E value
                  2.0e-65
Match length
                  228
% identity
                  (AL035394) putative Na+/H+-exchanging protein [Arabidopsis
NCBI Description
                  thalianal
Seq. No.
                  259272
                  454 1.R1011
Contig ID
5'-most EST
                  wty700169517.hl
Method
                  BLASTX
NCBI GI
                  g3080438
                  394
BLAST score
                   2.0e-44
E value
                  203
Match length
% identity
                   54
NCBI Description (AL022605) putative protein [Arabidopsis thaliana]
                  259273
Seq. No.
                   454 2.R1011
Contig ID
                  uC-zmflb73066b08a1
5'-most EST
                  259274
Seq. No.
                   456 1.R1011
Contig ID
                  LIB3069-050-Q1-K1-D12
5'-most EST
                   259275
Seq. No.
                   457 1.R1011
Contig ID
                  LIB148-014-Q1-E1-G2
5'-most EST
                  BLASTX
Method
                   g2055230
NCBI GI
BLAST score
                   250
                   7.0e-21
E value
Match length
                  285
                   29
% identity
NCBI Description (AB000130) SRC2 [Glycine max]
Seq. No.
                   259276
```

35830

457 2.R1011

Match length





```
5'-most EST
                  LIB148-061-Q1-E1-F5
Method
                  BLASTX
                  a129940
NCBI GI
BLAST score
                  1884
                  0.0e + 00
E value
Match length
                  355
                  100
% identity
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                  (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi_100911_pir__S18570 polygalacturonase (EC 3.2.1.15)
                  precursor - maize >gi_22417_emb_CAA40850_ (X57627)
                  polygalacturonase [Zea mays] >gi_22419_emb_CAA44249_
                   (X62385) polygalacturonase [Zea mays]
                  >gi_288374_emb_CAA46679_ (X65844) polygalacturonase [Zea
                  mays]
Seq. No.
                  259277
                  457 3.R1011
Contig ID
5'-most EST
                  LIB3066-012-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  q129940
BLAST score
                  910
                  1.0e-98
E value
Match length
                  174
% identity
                  98
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                  (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi_100911_pir__S18570 polygalacturonase (EC 3.2.1.15)
                  precursor - maize >gi_22417_emb_CAA40850_ (X57627)
                  polygalacturonase [Zea mays] >gi_22419_emb_CAA44249_
                   (X62385) polygalacturonase [Zea mays]
                  >gi_288374_emb_CAA46679_ (X65844) polygalacturonase [Zea
                  mays]
                  259278
Seq. No.
Contig ID
                  457 4.R1011
5'-most EST
                  LIB3075-035-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  q548493
BLAST score
                  661
E value
                  3.0e-69
Match length
                  129
% identity
                  98
                 EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                   (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi 629854 pir S30067 polygalacturonase - maize
                  >gi 288612 emb CAA47052 (X66422) polygalacturonase [Zea
                  mays]
                  259279
Seq. No.
                  457 5.R1011
Contig ID
                  LIB148-035-Q1-E1-F8
5'-most EST
Method
                  BLASTX
NCBI GI
                  g100912
BLAST score
                  673
E value
                  1.0e-70
```





```
% identity
NCBI Description polygalacturonase (EC 3.2.1.15) - maize
                   259280
Seq. No.
                   457 9.R1011
Contig ID
                   zuv700354690.h1
5'-most EST
                   BLASTX
Method
                   g100912
NCBI GI
BLAST score
                   525
E value
                   2.0e-53
                   113
Match length
                   89
% identity
                   polygalacturonase (EC 3.2.1.15) - maize
NCBI Description
                   259281
Seq. No.
                   457 11.R1011
Contig ID
                   LIB148-014-Q1-E1-A8
5'-most EST
                   BLASTX
Method
                   g100912
NCBI GI
                   772
BLAST score
E value
                   3.0e-82
                   200
Match length
                   77
% identity
NCBI Description polygalacturonase (EC 3.2.1.15) - maize
                   259282
Seq. No.
Contig ID
                   457 12.R1011
                   LIB3075-008-Q1-K1-H12
5'-most EST
                   BLASTX
Method
NCBI GI
                   q548493
BLAST score
                    618
                    2.0e-64
E value
Match length
                   132
                    89
% identity
                   EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                    (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                   >gi_629854_pir__S30067 polygalacturonase - maize
>gi_288612_emb_CAA47052_ (X66422) polygalacturonase [Zea
                   mays]
Seq. No.
                    259283
Contig ID
                    457 14.R1011
5'-most EST
                    LIB148-044-Q1-E1-G8
                    BLASTX
Method
NCBI GI
                    g283049
BLAST score
                    496
E value
                    5.0e-50
Match length
                    121
                    79
% identity
```

NCBI Description p

polygalacturonase (EC 3.2.1.15) precursor (clone W2247) maize (fragment) >gi 481079_pir__S37718 polygalacturonase -

maize >gi 22426 emb CAA44248 (X62384) polygalacturonase

[Zea mays] >gi_\(\bar{2}878\)\(\bar{3}0\)\(\text{emb}\)\(CA\)\(\bar{4}7234\)\((X66692)\)

polygalacturonase [Zea mays]

Seq. No. 259284 Contig ID 462_1.R1011

Match length

308





```
5'-most EST
                  wen700333421.h1
                   259285
Seq. No.
                   462 2.R1011
Contig ID
5'-most EST
                  uC-zmflmo17071g06b1
Method
                  BLASTX
                  g443509
NCBI GI
BLAST score
                  216
                   5.0e-17
E value
Match length
                  139
                   40
% identity
                  Triacylglycerol Acylhydrolase (E.C.3.1.1.3) Complex With
NCBI Description
                   Diethylphosophate
                   259286
Seq. No.
Contig ID
                   462 4.R1011
                  uC\text{-}zmf1b73170f01b2\\
5'-most EST
Method
                  BLASTN
NCBI GI
                  g3341647
BLAST score
                  81
E value
                  1.0e-37
                  237
Match length
                   90
% identity
NCBI Description Zea mays Ama gene encoding single-subunit RNA polymerase
Seq. No.
                  259287
Contig ID
                  463 1.R1011
5'-most EST
                  LIB3066-012-Q1-K1-D3
Seq. No.
                   259288
Contig ID
                   463 2.R1011
5'-most EST
                  LIB148-044-Q1-E1-G2
Seq. No.
                   259289
Contig ID
                   465_1.R1011
5'-most EST
                   zuv700356845.h1
Method
                  BLASTX
                  g3142293
NCBI GI
BLAST score
                   232
                   4.0e-19
E value
Match length
                  104
% identity
                   41
                  (AC002411) Contains similarity to myosin IB heavy chain
NCBI Description
                   gb X70400 from Gallus gallus. [Arabidopsis thaliana]
Seq. No.
                   259290
Contig ID
                   466 1.R1011
5'-most EST
                  LIB148-026-Q1-E1-E1
                   259291
Seq. No.
Contig ID
                   468 1.R1011
5'-most EST
                  uC-zmflmo17220e11b1
Method
                  BLASTX
NCBI GI
                  g3894158
BLAST score
                  468
E value
                   2.0e-46
```





```
% identity
NCBI Description
                  (AC005312) similar to phloem-specific lectin [Arabidopsis
                  thaliana]
                  259292
Seq. No.
                  468 2.R1011
Contig ID
                  LIB3066-029-Q1-K1-A3
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3894158
BLAST score
                  144
E value
                  9.0e-09
Match length
                  106
% identity
                  32
NCBI Description
                  (AC005312) similar to phloem-specific lectin [Arabidopsis
                  thaliana]
                  259293
Seq. No.
Contig ID
                  469 1.R1011
                  pmx700083768.h1
5'-most EST
                  259294
Seq. No.
                  471 1.R1011
Contig ID
5'-most EST
                  LIB3066-004-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  q422032
BLAST score
                  649
E value
                  1.0e-67
                  137
Match length
% identity
                  90
                  profilin 2 - maize >gi_313140_emb_CAA51719_ (X73280)
NCBI Description
                  profilin 2 [Zea mays]
                  259295
Seq. No.
                  473 1.R1011
Contig ID
                  xmt700257947.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3451463
BLAST score
                  325
E value
                  7.0e-30
Match length
                  170
% identity
                   44
NCBI Description (AL031349) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                  259296
                  473 2.R1011
Contig ID
5'-most EST
                  LIB3069-017-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  g1877183
BLAST score
                  168
E value
                  2.0e-11
                  95
Match length
% identity
                   40
                  (Y11586) putative mitochondrial matrix protein
NCBI Description
                   [Chlamydomonas reinhardtii]
Seq. No.
                  259297
```

476_1.R1011

Contig ID

NCBI Description





```
LIB3150-019-Q1-N1-B10
5'-most EST
                  BLASTX
Method
                  g4056502
NCBI GI
                  749
BLAST score
                  7.0e-87
E value
                  205
Match length
                  81
% identity
                  (ACO05896) 40S ribosomal protein S5 [Arabidopsis thaliana]
NCBI Description
                  259298
Seq. No.
                  476 2.R1011
Contig ID
                  uC-zmflb73272b09b1
5'-most EST
                  BLASTX
Method
                  g4056502
NCBI GI
                  866
BLAST score
                  4.0e-93
E value
                  206
Match length
% identity
                  83
                  (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
NCBI Description
                  259299
Seq. No.
                  476 3.R1011
Contig ID
                  LIB3066-026-Q1-K1-G1
5'-most EST
                   259300
Seq. No.
                   476 4.R1011
Contig ID
                  LIB148-023-Q1-E1-G5
5'-most EST
Method
                   BLASTX
                   q4585989
NCBI GI
                   157
BLAST score
                   5.0e-10
E value
Match length
                   149
                   35
% identity
                  (AC005287) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   259301
Seq. No.
Contig ID
                   476 5.R1011
                   LIB3062-046-Q1-K1-B11
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3043428
BLAST score
                   455
                   5.0e-45
E value
                   105
Match length
% identity
                   79
                  (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
NCBI Description
Seq. No.
                   259302
Contig ID
                   476 11.R1011
5'-most EST
                   rvt700552860.hl
                   BLASTX
Method
NCBI GI
                   q1620982
BLAST score
                   233
E value
                   3.0e-19
                   50
Match length
% identity
                   96
```

35835

plumbaginifolia]

(Y08860) 40S ribosomal protein S5 [Nicotiana





Seq. No. 259303 Contig ID 476 12.R1011 5'-most EST uC-zmroteosinte003d07b1 Method BLASTX NCBI GI g3043428 BLAST score 713 E value 2.0e-75 Match length 159 % identity (AJ005346) 40S ribosomal protein S5 [Cicer arietinum] NCBI Description 259304 Seq. No. Contig ID 477 1.R1011 5'-most EST LIB3075-056-Q1-K1-B7 259305 Seq. No. 478 1.R1011 Contig ID 5'-most EST LIB3079-041-Q1-K1-C2 259306 Seq. No. 479 1.R1011 Contig ID 5'-most EST LIB3066-031-Q1-K1-H7 Method BLASTN NCBI GI q4185305 BLAST score 101 2.0e-49 E value Match length 173 90 % identity NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes Seq. No. 259307 481 1.R1011 Contig ID LIB3059-002-Q1-K2-F12 5'-most EST Method BLASTX q136757 NCBI GI BLAST score 375

Method BLASTX
NCBI GI g136757
BLAST score 375
E value 9.0e-36
Match length 91
% identity 82

NCBI Description GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR

>gi_100881_pir__S07314 UDPglucose--starch

glucosyltransferase (EC 2.4.1.11) precursor - maize >gi_168653 (M24258) amyloplast-specific transit protein [Zea mays] >gi_1644339_emb_CAA27574_ (X03935) glucosyl

transferase [Zea mays]

Seq. No. 259308 Contig ID 481_2.R1011 5'-most EST ypc700800096.h1

Method BLASTX
NCBI GI g136757
BLAST score 1070
E value 1.0e-117





Match length 260 % identity GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR NCBI Description >gi_100881_pir__S07314 UDPglucose--starch glucosyltransferase (EC 2.4.1.11) precursor - maize >gi_168653 (M24258) amyloplast-specific transit protein [Zea mays] >gi 1644339 emb CAA27574 (X03935) glucosyl transferase [Zea mays] Seq. No. 259309 Contig ID 481 4.R1011 LIB3075-032-Q1-K1-H4 5'-most EST Method BLASTN NCBI GI q22509 BLAST score 259 E value 1.0e-144 Match length 275 99 % identity Zea mays waxy (wx+) locus for UDP-glucose starch glycosyl NCBI Description transferase 259310 Seq. No. 481 6.R1011 Contig ID 5'-most EST LIB3115-021-P1-K1-H7 Method BLASTN NCBI GI q22509 BLAST score 288 E value 1.0e-161 292 Match length 100 % identity NCBI Description Zea mays waxy (wx+) locus for UDP-glucose starch glycosyl transferase 259311 Seq. No. Contig ID 482 1.R1011 5'-most EST LIB3066-005-Q1-K1-D12 Method BLASTN NCBI GI q3821780 BLAST score 36 E value 2.0e-10 Match length 36 % identity 100 NCBI Description Xenopus laevis cDNA clone 27A6-1 259312 Seq. No. Contig ID 482 2.R1011

5'-most EST LIB3066-056-Q1-K1-F5

Method BLASTN
NCBI GI g22458
BLAST score 753
E value 0.0e+00
Match length 794
% identity 98

NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)

Seq. No. 259313 Contig ID 482 3.R1011

E value

4.0e-43

```
5'-most EST
                  LIB148-060-Q1-E1-E1
                  BLASTN
Method
                  q22458
NCBI GI
BLAST score
                  188
E value
                   1.0e-101
                   320
Match length
                   90
% identity
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                   259314
Seq. No.
                  482_7.R1011
Contig ID
                  LIB148-056-Q1-E1-E8
5'-most EST
                   259315
Seq. No.
                  482 9.R1011
Contig ID
5'-most EST
                  LIB148-061-Q1-E1-D7
                  BLASTN
Method
                   g22458
NCBI GI
                   86
BLAST score
                   2.0e-40
E value
Match length
                   170
                   88
% identity
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                   259316
Seq. No.
                  482 12.R1011
Contig ID
5'-most EST
                   LIB148-005-Q1-E1-A3
                   BLASTN
Method
                   g22458
NCBI GI
                   94
BLAST score
                   1.0e-45
E value
Match length
                   158
                   96
% identity
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
                   259317
Seq. No.
Contig ID
                   486 1.R1011
                   LIB3137-039-Q1-K1-B9
5'-most EST
Method
                   BLASTX
NCBI GI
                   q82733
                   671
BLAST score
E value
                   2.0e-70
Match length
                   155
                   85
% identity
NCBI Description ubiquitin fusion protein UBF9 - maize >gi_168651 (M68937)
                   ubiquitin fusion protein [Zea mays] >gi_902527 (U29161)
                   ubiquitin fusion protein [Zea mays] >gi_1589388_prf__2211240B ubiquitin fusion protein [Zea
                   mays]
                   259318
Seq. No.
Contig ID
                   486 2.R1011
                   LIB3078-034-Q1-K1-B3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g82733
BLAST score
                   437
```



108 Match length 79 % identity ubiquitin fusion protein UBF9 - maize >gi_168651 (M68937) NCBI Description ubiquitin fusion protein [Zea mays] >gi_902527 (U29161) ubiquitin fusion protein [Zea mays] >gi 1589388 prf 2211240B ubiquitin fusion protein [Zea mays] 259319 Seq. No. 486 3.R1011 Contig ID LIB3078-048-Q1-K1-G2 5'-most EST BLASTX Method q82733 NCBI GI BLAST score 562 1.0e-57 E value 137 Match length % identity 81 ubiquitin fusion protein UBF9 - maize >gi_168651 (M68937) NCBI Description ubiquitin fusion protein [Zea mays] >gi_902527 (U29161) ubiquitin fusion protein [Zea mays] >gi 1589388 prf__2211240B ubiquitin fusion protein [Zea mays] 259320 Seq. No. 486 4.R1011 Contig ID LIB3078-053-Q1-K1-B12 5'-most EST Method BLASTX g82733 NCBI GI BLAST score 324 6.0e-30 E value Match length 93 % identity 69 ubiquitin fusion protein UBF9 - maize >gi_168651 (M68937) NCBI Description ubiquitin fusion protein [Zea mays] >gi_902527 (U29161) ubiquitin fusion protein [Zea mays] >gi_1589388_prf__2211240B ubiquitin fusion protein [Zea mays] 259321 Seq. No. 486 6.R1011 Contig ID uC-zmflb73378d04a2 5'-most EST Method BLASTX NCBI GI g133901 BLAST score 237 E value 4.0e-20 Match length 41 % identity 100 40S RIBOSOMAL PROTEIN S27A NCBI Description 259322 Seq. No. Contig ID 486 7.R1011 5'-most EST LIB3150-083-P2-N2-A3

Seq. No. 259322
Contig ID 486_7.R1011
5'-most EST LIB3150-083-P2-N2-F
Method BLASTX
NCBI GI g82733
BLAST score 163
E value 2.0e-11
Match length 28



```
% identity
                    ubiquitin fusion protein UBF9 - maize >gi_168651 (M68937)
NCBI Description
                    ubiquitin fusion protein [Zea mays] >gi 902527 (U29161)
                    ubiquitin fusion protein [Zea mays]
                    >gi 1589388 prf 2211240B ubiquitin fusion protein [Zea
                    mays]
                    259323
Seq. No.
                    487_1.R1011
Contig ID
                    wty700163609.hl
5'-most EST
                    BLASTX
Method
NCBI GI
                    q1518113
                    296
BLAST score
E value
                    2.0e-26
Match length
                    97
% identity
                    63
                   (U66193) SLL2 [Brassica napus]
NCBI Description
                    259324
Seq. No.
                    489 1.R1011
Contig ID
                    cat700017932.rl
5'-most EST
                    259325
Seq. No.
                    489 3.R1011
Contig ID
                    LIB3075-055-Q1-K1-A2
5'-most EST
                    259326
Seq. No.
Contig ID
                    491 1.R1011
                    LIB148-046-Q1-E1-D8
5'-most EST
Method
                    BLASTX
NCBI GI
                    g322571
                    150
BLAST score
                    2.0e-09
E value
Match length
                    60
                    48
% identity
                    proteinase inhibitor II - Arabidopsis thaliana
NCBI Description
                    >gi_16427_emb_CAA48892_ (X69139) protease inhibitor II
[Arabidopsis thaliana] >gi_4038041 (AC005936) proteinase
                    inhibitor II [Arabidopsis thaliana]
                    259327
Seq. No.
Contig ID
                    491 2.R1011
5'-most EST
                    LIB3075-001-Q1-K1-A12
                    BLASTX
Method
NCBI GI
                    g322571
BLAST score
                    178
E value
                    1.0e-12
Match length
                    52
% identity
                    58
                    proteinase inhibitor II - Arabidopsis thaliana
NCBI Description
                    >gi_16427_emb_CAA48892_ (X69139) protease inhibitor II
[Arabidopsis thaliana] >gi_4038041 (AC005936) proteinase
                     inhibitor II [Arabidopsis thaliana]
```

259328 Seq. No. 492 1.R1011 Contig ID

uC-zmflb73053e07b25'-most EST





```
BLASTX
Method
                  g1620986
NCBI GI
                  365
BLAST score
                  2.0e-34
E value
Match length
                  96
                  76
% identity
                  (Y08858) 40S ribosomal protein S17 [Nicotiana
NCBI Description
                  plumbaginifolia]
                  259329
Seq. No.
Contig ID
                  495 1.R1011
                  LIB3075-055-Q1-K1-G6
5'-most EST
Method
                  BLASTX
                   g3901094
NCBI GI
BLAST score
                   596
E value
                   9.0e-62
                   156
Match length
                   70
% identity
                  (Z27090) pollen allergen Phl pI [Phleum pratense]
NCBI Description
                   259330
Seq. No.
                   496_1.R1011
Contig ID
                   uC-zmflmo17321f05b1
5'-most EST
                   BLASTX
Method
                   g3319355
NCBI GI
BLAST score
                   2300
                   0.0e+00
E value
                   528
Match length
                   85
% identity
                   (AF077407) similar to chaperonin containing TCP-1 complex
NCBI Description
                   gamma chain [Arabidopsis thaliana]
                   259331
Seq. No.
                   496 2.R1011
Contig ID
                   ymt700220975.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3024696
BLAST score
                   360
                   3.0e - 34
E value
Match length
                   99
                   72
% identity
                   T-COMPLEX PROTEIN 1, GAMMA SUBUNIT (TCP-1-GAMMA)
NCBI Description
                   (CCT-GAMMA) (CHAPERONIN SUBUNIT CCTV GAMMA)
                   >qi 1906364 emb CAA72704 (Y11967) chaperonin subunit CCTV
                   gamma [Oxytricha granulifera]
Seq. No.
                   259332
                   496 3.R1011
Contig ID
                   LIB3075-006-Q1-K1-C3
5'-most EST
Method
                   BLASTX
                   q3319355
NCBI GI
BLAST score
                   264
E value
                   5.0e-23
                   62
Match length
% identity
                   84
                   (AF077407) similar to chaperonin containing TCP-1 complex
NCBI Description
```

gamma chain [Arabidopsis thaliana]

5'-most EST

Method



8

```
259333
Seq. No.
                   499 1.R1011
Contig ID
                  LIB3075-050-Q1-K1-G8
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3142293
BLAST score
                   376
                   7.0e-36
E value
Match length
                   137
% identity
                   (AC002411) Contains similarity to myosin IB heavy chain
NCBI Description
                   gb X70400 from Gallus gallus. [Arabidopsis thaliana]
                   259334
Seq. No.
Contig ID
                   500 1.R1011
5'-most EST
                   LIB3075-051-Q1-K1-E5
Method
                   BLASTX
NCBI GI
                   q99809
BLAST score
                   1746
E value
                   0.0e + 00
Match length
                   504
                   63 .
% identity
                   gene Bp10 protein - rape >gi_17795_emb_CAA47177_ (X66608)
NCBI Description
                   Bplo [Brassica napus]
Seq. No.
                   259335
                   500 2.R1011
Contig ID
                   LIB3066-045-Q1-K1-C8
5'-most EST
Method
                   BLASTX
NCBI GI
                   q114268
                   1233
BLAST score
                   0.0e + 00
E value
Match length
                   518
% identity
                   L-ASCORBATE OXIDASE HOMOLOG PRECURSOR (ASCORBASE)
NCBI Description
                   >qi 541907 pir S23763 gene Bp10 protein - rape
                   >gi 17789 emb CAA45554 (X64257) protein homologous to
                   ascorbate oxidase [Brassica napus]
                   259336
Seq. No.
                   500 3.R1011
Contig ID
                   LIB148-048-Q1-E1-E10
5'-most EST
                   BLASTX
Method
NCBI GI
                   q128592
BLAST score
                   301
E value
                   4.0e-27
                   79
Match length
                   68
% identity
                   POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR
NCBI Description
                   >gi_82190_pir_ S22495 pollen-specific protein precursor -
                   common tobacco >gi 19902 emb CAA43454 (X61146) pollen
                   specific protein [Nicotiana tabacum]
                   259337
Seq. No.
Contig ID
                   500 4.R1011
```

35842

LIB3067-021-Q1-K1-C10

BLASTX





```
g4204258
NCBI GI
BLAST score
                   424
                   2.0e-41
E value
Match length
                   118
                   64
% identity
                   (AC005223) 14409 [Arabidopsis thaliana]
NCBI Description
                   259338
Seq. No.
                   500 5.R1011
Contig ID
                   LIB148-016-Q1-E1-H5
5'-most EST
                   BLASTX
Method
                   g128592
NCBI GI
                   316
BLAST score
                   6.0e-29
E value
                   90
Match length
                   63
% identity
                   POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR
NCBI Description
                   >gi 82190 pir__S22495 pollen-specific protein precursor -
                   common tobacco >gi 19902 emb CAA43454 (X61146) pollen
                   specific protein [Nicotiana tabacum]
                   259339
Seq. No.
                   500 6.R1011
Contig ID
                   LIB3066-011-Q1-K1-D7
5'-most EST
                   BLASTX
Method
                   g128592
NCBI GI
BLAST score
                   313
E value
                   1.0e-28
                   79
Match length
                   68
% identity
                   POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR
NCBI Description
                   >gi_82190_pir__S22495 pollen-specific protein precursor -
                   common tobacco >gi_19902_emb_CAA43454_ (X61146) pollen
                   specific protein [Nicotiana tabacum]
                   259340
Seq. No.
Contig ID
                   500 8.R1011
                   LIB3066-047-Q1-K1-D6
5'-most EST
                   259341
Seq. No.
                   501 1.R1011
Contig ID
5'-most EST
                   LIB3066-005-Q1-K1-A11
Method
                   BLASTX
NCBI GI
                   g1076791
BLAST score
                   1087
E value
                   1.0e-119
Match length
                   214
% identity
                   calcium-binding protein - maize >gi_2119370_pir__S58170
Calreticulin precursor - maize >gi_577612_emb_CAA86728_
NCBI Description
                   (Z46772) calcium-binding protein [Zea mays]
                   >gi 927572_emb_CAA61939_ (X89813) Calreticulin precursor
                   [Zea mays] >gi_1587033_prf__2205314A calreticulin [Zea
                   mays]
```

259342

501 2.R1011

Seq. No. Contig ID

Match length





```
5'-most EST
                   LIB3075-055-Q1-K1-G5
                   BLASTX
Method
NCBI GI
                   q1076791
BLAST score
                   1393
                   1.0e-155
E value
Match length
                   334
                   79
% identity
                   calcium-binding protein - maize >gi_2119370_pir__S58170
Calreticulin precursor - maize >gi_577612_emb_CAA86728_
NCBI Description
                   (Z46772) calcium-binding protein [Zea mays]
                   >gi_927572_emb_CAA61939_ (X89813) Calreticulin precursor
                   [Zea mays] >gi_1587033 prf _2205314A calreticulin [Zea
                   mays]
Seq. No.
                   259343
                   501 3.R1011
Contig ID
                   nbm700465519.h1
5'-most EST
Method
                   BLASTN
                   q1181332
NCBI GI
BLAST score
                   127
E value
                   6.0e-65
Match length
                   183
% identity
                   97
NCBI Description Z.mays CRH mRNA
                   259344
Seq. No.
                   501 4.R1011
Contig ID
5'-most EST
                   uC-zmroteosinte010h06b1
Method
                   BLASTX
NCBI GI
                   g1658197
BLAST score
                   314
E value
                   1.0e-59
Match length
                   188
% identity
NCBI Description
                   (U74630) calreticulin [Ricinus communis] >gi 1763297
                    (U74631) calreticulin [Ricinus communis]
                   259345
Seq. No.
                   502 1.R1011
Contig ID
                   uC-zmflm017026f02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1084457
BLAST score
                   758
                   2.0e-80
E value
Match length
                   229
% identity
                   67
NCBI Description elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903
                   (D23674) elongation factor 1 beta [Oryza sativa]
                   259346
Seq. No.
                   502 2.R1011
Contig ID
                   LIB3075-014-Q1-K1-E2
5'-most EST
Method
                   BLASTX
                   g1084457
NCBI GI
BLAST score
                   535
E value
                   2.0e-54
```

Method

NCBI GI

BLASTX

g3150402





% identity elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903_ NCBI Description (D23674) elongation factor 1 beta [Oryza sativa] 259347 Seq. No. Contig ID 502 3.R1011 5'-most EST LIB3150-081-P2-N2-F6 259348 Seq. No. 502 4.R1011 Contig ID 5'-most EST LIB3069-030-Q1-K1-E2 Method BLASTX g1084457 NCBI GI BLAST score 369 E value 4.0e-35 Match length 112 69 % identity elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903_ NCBI Description (D23674) elongation factor 1 beta [Oryza sativa] 259349 Seq. No. 502_5.R1011 Contig ID 5'-most EST LIB3070-004-Q1-N1-G1 Method BLASTX g1084457 NCBI GI BLAST score 264 9.0e-28 E value Match length 95 77 % identity NCBI Description elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903_ (D23674) elongation factor 1 beta [Oryza sativa] 259350 Seq. No. Contig ID 502 8.R1011 5'-most EST LIB3156-011-Q1-K1-H8 Method BLASTX NCBI GI g1084457 BLAST score 283 7.0e-25 E value 72 Match length % identity 75 elongation factor 1-beta - Rice >gi 432368 dbj BAA04903 NCBI Description (D23674) elongation factor 1 beta [Oryza sativa] 259351 Seq. No. 502 10.R1011 Contig ID 5'-most EST ypc700800743.h1 259352 Seq. No. 503 1.R1011 Contig ID 5'-most EST LIB3075-055-Q1-K1-F3 259353 Seq. No. 504 1.R1011 Contig ID LIB3062-045-Q1-K1-F12 5'-most EST





```
BLAST score
                   1372
                   1.0e-152
E value
Match length
                   334
                   81
% identity
                   (ACO04165) putative malonyl-CoA: Acyl carrier protein
NCBI Description
                   transacylase [Arabidopsis thaliana]
                   259354
Seq. No.
                   505_1.R1011
Contig ID
                   LIB3150-032-Q1-N1-C1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2431767
BLAST score
                   303
                   3.0e-27
-E value
Match length
                   68
% identity
                   87
                   (U62751) acidic ribosomal protein P3a [Zea mays]
NCBI Description
                   259355
Seq. No.
                   505 2.R1011
Contig ID
5'-most EST
                   uC-zmf1b73030c08b1
                   259356
Seq. No.
                   510 1.R1011
Contig ID
                   LIB3076-007-Q1-K1-G11
5'-most EST
                   259357
Seq. No.
                   510 2.R1011
Contig ID
                   uC-zmroteosinte009b11b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4204262
BLAST score
                   193
                   3.0e-14
E value
Match length
                   80
                   53
 % identity
NCBI Description (AC005223) 37783 [Arabidopsis thaliana]
                   259358
Seq. No.
 Contig ID
                   511 1.R1011
                   LIB3075-004-Q1-K1-B12
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   g2213632
BLAST score
                   166
E value
                   2.0e-11
Match length
                   42
 % identity
NCBI Description (AC000103) F21J9.24 [Arabidopsis thaliana]
                   259359
 Seq. No.
                   512 1.R1011
 Contig ID
                   LIB3075-033-Q1-K1-B10
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   g3157942
 BLAST score
                   405
```

6.0e-39

267 40

E value Match length

% identity





NCBI Description (AC002131) Similar to style development-specific protein 9612 precursor gb_X55193 and pectate lyase P59 precursor gb_X15499 from Lycopersicon esculentum. [Arabidopsis thaliana]

 Seq. No.
 259360

 Contig ID
 515_1.R1011

5'-most EST LIB3066-030-Q1-K1-H7

Method BLASTX
NCBI GI g4455335
BLAST score 1024
E value 1.0e-111
Match length 393
% identity 31

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

5'-most EST LIB3066-026-Q1-K1-D8

Seq. No. 259362 Contig ID 516 2.R1011

5'-most EST LIB3066-002-Q1-K1-F7

Seq. No. 259363 Contig ID 516 3.R1011

5'-most EST LIB3066-026-Q1-K1-E2

Seq. No. 259364 Contig ID 516 4.R1011

5'-most EST LIB148-022-Q1-E1-H1

 Seq. No.
 259365

 Contig ID
 517_1.R1011

 5'-most EST
 mwy700441286.h1

Seq. No. 259366 Contig ID 519 1.R1011

5'-most EST LIB3060-051-Q1-K1-H9

Method BLASTN
NCBI GI g1657759
BLAST score 77

E value 4.0e-35 Match length 155 % identity 88

NCBI Description Zea mays retrotransposon Fourf 5' LTR and primer binding

site DNA sequence

 Seq. No.
 259367

 Contig ID
 521_1.R1011

 5'-most EST
 gwl700613188.h1

5'-most EST LIB3075-055-Q1-K1-E1

Seq. No. 259369

NCBI Description





```
525 1.R1011
Contig ID
                  LIB3066-031-Q1-K1-D3
5'-most EST
Seq. No.
                   259370
                  526 1.R1011
Contig ID
                  ntr700072953.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                   g3935181
BLAST score
                   1664
                   0.0e+00
E value
Match length
                   341
                   87
% identity
                  (AC004557) F17L21.24 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   259371
Contig ID
                   526 2.R1011
5'-most EST
                   uC-zmflb73148f01b1
                   BLASTX
Method
NCBI GI
                   g3935181
BLAST score
                   1600
                   1.0e-179
E value
Match length
                   341
% identity
                  (AC004557) F17L21.24 [Arabidopsis thaliana]
NCBI Description
                   259372
Seq. No.
                   526 3.R1011
Contig ID
                   LIB3079-046-Q1-K1-D5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3935181
BLAST score
                   650
E value
                   7.0e-68
                   149
Match length
% identity
                   83
NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]
                   259373
Seq. No.
                   526 4.R1011
Contig ID
                   LIB3075-003-Q1-K1-H7
5'-most EST
                   BLASTX
Method
                   g3935181
NCBI GI
BLAST score
                   480
                   2.0e-48
E value
                   99
Match length
% identity
                  (AC004557) F17L21.24 [Arabidopsis thaliana]
NCBI Description
                   259374
Seq. No.
                   526_5.R1011
Contig ID
                   ntr700077265.h1
5'-most EST
                   BLASTX
Method
                   g3935181
NCBI GI
BLAST score
                   233
                   3.0e-19
E value
Match length
                   55
                   78
% identity
```

35848

(AC004557) F17L21.24 [Arabidopsis thaliana]





```
Seq. No.
                  527 1.R1011
Contig ID
5'-most EST
                  uC-zmroteosinte075a08b1
                  BLASTX
Method
NCBI GI
                  g1519253
BLAST score
                   613
                   2.0e-63
E value
Match length
                   126
                   94
% identity
                  (U65958) GF14-d protein [Oryza sativa]
NCBI Description
                   259376
Seq. No.
                   527 2.R1011
Contig ID
5'-most EST
                  LIB3061-032-Q1-K1-F11
Method
                   BLASTX
                   q459002
NCBI GI
BLAST score
                   399
                   2.0e-38
E value
Match length
                   194
                   38
% identity
                  (U00036) R151.6 gene product [Caenorhabditis elegans]
NCBI Description
                   259377
Seq. No.
                   527_3.R1011
Contig ID
5'-most EST
                   wty700167237.hl
                   BLASTX
Method
NCBI GI
                   q1519253
BLAST score
                   1196
                   1.0e-131
E value
Match length
                   264
                   90
% identity
NCBI Description (U65958) GF14-d protein [Oryza sativa]
Seq. No.
                   259378
Contig ID
                   527 4.R1011
                   xsy700211218.h1
5'-most EST
Method
                   BLASTX
                   q1389768
NCBI GI
BLAST score
                   667
E value
                   7.0e-70
                   237
Match length
% identity
                   68
                   (U58942) phosphoribosylanthranilate transferase
NCBI Description
                   [Arabidopsis thaliana]
                   259379
Seq. No.
                   527 5.R1011
Contig ID
                   uC-zmroteosinte034f07b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4115936
BLAST score
                   195
                   7.0e-15
E value
Match length
                   95
                   39
% identity
```

NCBI Description (AF118223) No definition line found [Arabidopsis thaliana]

Seq. No.

259385





```
259380
Seq. No.
                   527_6.R1011
Contig ID
                   uC-zmflB73043c08b1
5'-most EST
Method
                   BLASTN
                   g3511235
NCBI GI
BLAST score
                   79
                   3.0e-36
E value
Match length
                   164
% identity
                   87
                   Zea mays starch branching enzyme IIb (ae) gene, complete
NCBI Description
                   259381
Seq. No.
                   527_8.R1011
Contig ID
                   uC-\overline{z}mflmo17012h04b1
5'-most EST
Method
                   BLASTX
                   q1519253
NCBI GI
BLAST score
                   865
                   9.0e-93
E value
Match length
                   207
% identity
                   84
                  (U65958) GF14-d protein [Oryza sativa]
NCBI Description
                   259382
Seq. No.
                   527_9.R1011
Contig ID
5'-most EST
                   uC-zmflmo17238h12b1
Method
                   BLASTX
                   a1519253
NCBI GI
BLAST score
                   782
                   2.0e-83
E value
Match length
                   162
% identity
NCBI Description
                  (U65958) GF14-d protein [Oryza sativa]
                   259383
Seq. No.
Contig ID
                   527_14.R1011
5'-most EST
                   uC-zmflmo17130a02b1
Method
                   BLASTX
NCBI GI
                   g1519253
BLAST score
                   361
E value
                   4.0e-34
Match length
                   171
% identity
                   68
                  (U65958) GF14-d protein [Oryza sativa]
NCBI Description
Seq. No.
                   259384
                   527 21.R1011
Contig ID
                   uC-zmflb73092a03b2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1519253
BLAST score
                   184
E value
                   4.0e-14
                   41
Match length
% identity
                  (U65958) GF14-d protein [Oryza sativa]
NCBI Description
```

BLAST score

E value

412

3.0e-40





```
Contig ID
                  528 1.R1011
                  LIB3066-049-Q1-K1-D3
5'-most EST
Seq. No.
                  259386
Contig ID
                  528 2.R1011
5'-most EST
                  LIB3066-035-Q1-K1-G1
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  2.0e-10
Match length
                  48
                  67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  259387
                  528 3.R1011
Contig ID
5'-most EST
                  LIB3075-030-Q1-K1-D1
                  259388
Seq. No.
Contig ID
                  532 1.R1011
5'-most EST
                  LIB3075-055-Q1-K1-C1
Seq. No.
                  259389
Contig ID
                  534 1.R1011
                  LIB3066-055-Q1-K1-A7
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4454051
BLAST score
                  686
E value
                   4.0e-72
Match length
                  211
% identity
                   58
NCBI Description
                  (AL035394) putative polygalacturonase [Arabidopsis
                  thaliana]
Seq. No.
                  259390
Contig ID
                  534 2.R1011
5'-most EST
                  LIB3150-073-P2-K1-G4
                  BLASTX
Method
NCBI GI
                  g4454051
BLAST score
                  159
E value
                   1.0e-10
Match length
                  73
                   42
% identity
NCBI Description
                  (AL035394) putative polygalacturonase [Arabidopsis
                  thaliana]
                  259391
Seq. No.
                  537 1.R1011
Contig ID
5'-most EST
                  LIB148-037-Q1-E1-F2
Seq. No.
                  259392
                  538 1.R1011
Contig ID
                  LIB3150-048-Q1-N1-A8
5'-most EST
Method
                  BLASTX
NCBI GI
                  g129081
```





Method BLASTX
NCBI GI g1345977
BLAST score 1488
E value 1.0e-166
Match length 386
% identity 69
NCBI Description OMEGA-6 F3

NCBI Description OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

ISOZYME 2 >gi 904154 (L43921) microsomal omega-6 desaturase

[Glycine max]

Seq. No. 259394 Contig ID 538_4.R1011

5'-most EST uC-zmroteosinte088b08b1

Method BLASTX
NCBI GI g1345976
BLAST score 341
E value 8.0e-32
Match length 79
% identity 76

NCBI Description OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

ISOZYME 1 >gi_904152 (L43920) microsomal omega-6 desaturase

[Glycine max]

Seq. No. 259395 Contig ID 538_5.R1011

5'-most EST uC-zmflB73047d03b1

Method BLASTN
NCBI GI g168482
BLAST score 50
E value 6.0e-19
Match length 82

Match length 82 % identity 93

NCBI Description Corn starch branching enzyme II mRNA, complete cds

Method BLASTX

NCBI GI g1345977
BLAST score 440
E value 2.0e-43
Match length 95
% identity 80

NCBI Description OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

ISOZYME 2 >qi_904154 (L43921) microsomal omega-6 desaturase

[Glycine max]

Seq. No. 259397

Match length

244





```
538 7.R1011
Contig ID
                   uC-\overline{z}mflmo17270f03b1
5'-most EST
                   BLASTX
Method
                   q2564237
NCBI GI
                   261
BLAST score
E value
                   1.0e-61
                   164
Match length
                   73
% identity
                   (Y10112) omega-6 desaturase [Gossypium hirsutum]
NCBI Description
                   259398
Seq. No.
                   538 8.R1011
Contig ID
                   fdz701161538.h1
5'-most EST
                   BLASTX
Method
                   g1076818
NCBI GI
BLAST score
                   161
                   3.0e-11
E value
                   70
Match length
                   56
% identity
                   oleosin 17 - maize >gi_687247 (U13702) 17 kDa oleosin [Zea
NCBI Description
                   mays]
                   259399
Seq. No.
                   538 9.R1011
Contig ID
                   uC-\overline{z}mflmo17151c04a1
5'-most EST
Seq. No.
                   259400
                   538 11.R1011
Contig ID
                   uC-zmflb73066h03b1
5'-most EST
Method
                   BLASTX
                   g1054843
NCBI GI
                   673
BLAST score
                   1.0e-72
E value
                   227
Match length
                   61
% identity
NCBI Description
                  (X92847) D12 oleate desaturase [Solanum commersonii]
                   259401
Seq. No.
Contig ID
                   540 1.R1011
5'-most EST
                   xsy700209780.h1
Method
                   BLASTX
NCBI GI
                   g1076812
BLAST score
                   1425
                   1.0e-158
E value
Match length
                   323
                   88
% identity
                   initiator-binding protein - maize >gi_483490_emb_CAA55691_
NCBI Description
                   (X79085) initiator binding protein [Zea mays]
                   259402
Seq. No.
                   540 2.R1011
Contig ID
                   LIB3076-035-Q1-K1-H8
5'-most EST
                   BLASTX
Method
                   g3927827
NCBI GI
BLAST score
                   740
E value
                   3.0e-78
```





```
% identity
                  (AC005727) osmotin-like protein precursor [Arabidopsis
NCBI Description
                  thaliana]
                  259403
Seq. No.
                  540 4.R1011
Contig ID
                  LIB3075-055-Q1-K1-C8
5'-most EST
                  BLASTX
Method
                  g1076813
NCBI GI
BLAST score
                  813
                  3.0e-87
E value
                  173
Match length
                  92
% identity
                  initiator-binding protein - maize
NCBI Description
                  259404
Seq. No.
                  540 6.R1011
Contig ID
                  wty700165473.h1
5'-most EST
                  259405
Seq. No.
                  541_1.R1011
Contig ID
                  uC-zmflmo17a01b1
5'-most EST
                   BLASTX
Method
                   g134668
NCBI GI
                   1140
BLAST score
                   1.0e-125
E value
Match length
                   235
                   92
% identity
                  SUPEROXIDE DISMUTASE 3.1 PRECURSOR (MN)
NCBI Description
                   >gi_22481_emb_CAA31058_ (X12540) superoxide dismutase-3
                   precursor (AA -32 to 203) [Zea mays]
                   259406
Seq. No.
Contig ID
                   541_2.R1011
                   uC-zmflmo17161c07b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1174391
BLAST score
                   481
                   2.0e-48
E value
Match length
                   111
                   86
% identity
                   SUPEROXIDE DISMUTASE 3.4 PRECURSOR (MN)
NCBI Description
                   >gi_539066_pir__B48684 superoxide dismutase (EC 1.15.1.1)
                   (Mn) 3.2 precursor - maize
                   259407
Seq. No.
Contig ID
                   541 3.R1011
                   LIB3069-003-Q1-K1-D7
5'-most EST
Method
                   BLASTX
                   q2245086
NCBI GI
BLAST score
                   1123
E value
                   1.0e-123
                   292
Match length
                   73
% identity
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

259408

Seq. No.





541 4.R1011 Contig ID LIB3066-035-Q1-K1-F8 5'-most EST BLASTX Method g469163 NCBI GI BLAST score 683 9.0e-72E value 130 Match length 96 % identity (L19462) Mn-superoxide dismutase [Zea mays] NCBI Description 259409 Seq. No. 542 1.R1011 Contig ID 5'-most EST LIB148-017-Q1-E1-E10 259410 Seq. No. 543 1.R1011 Contig ID pmx700091766.h1 5'-most EST BLASTX Method g4008159 NCBI GI BLAST score 1659 0.0e+00E value 434 Match length 74 % identity (AB015601) DnaJ homolog [Salix gilgiana] NCBI Description 259411 Seq. No. Contig ID 543_2.R1011 uC-zmroteosinte098h01b2 5'-most EST Method BLASTX g1125691 NCBI GI BLAST score 1049 1.0e-114 E value 239 Match length % identity NCBI Description (X94301) DnaJ protein [Solanum tuberosum] Seq. No. 259412 543 3.R1011 Contig ID uC-zmflmo17219c01a1 5'-most EST Seq. No. 259413 543 4.R1011 Contig ID kem700610911.hl 5'-most EST Method BLASTX NCBI GI g1125691 BLAST score 480 E value 4.0e-48 Match length 114 81 % identity

NCBI Description (X94301) DnaJ protein [Solanum tuberosum]

Seq. No. 259414 544 1.R1011 Contig ID

LIB3068-021-Q1-K1-G2 5'-most EST

Seq. No. 259415 546 1.R1011 Contig ID





```
LIB148-033-Q1-E1-C11
5'-most EST
Method
                  BLASTX
                  q2062421
NCBI GI
                  495
BLAST score
                  9.0e-50
E value
Match length
                  208
                  45
% identity
                  (U82123) expansin [Lycopersicon esculentum]
NCBI Description
                  259416
Seq. No.
                  547 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73241g03b2
                  BLASTX
Method
NCBI GI
                  q82263
BLAST score
                  1206
                  1.0e-133
E value
Match length
                  250
                  90
% identity
                  ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
NCBI Description
                  c1 precursor (clone pC(1)3II) - potato
                  259417
Seq. No.
                   547 2.R1011
Contig ID
                  tzu700204061.hl
5'-most EST
                  BLASTX
Method
                   q82264
NCBI GI
BLAST score
                   315
                   7.0e-29
E value
                   66
Match length
                   86
% identity
                  ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
NCBI Description
                   c1 precursor (clone pC(1)8I) - potato (fragment)
                   >gi_498789_emb_CAA56109_ (X79597) cytochrome c1 [Solanum
                   tuberosum]
                   259418
Seq. No.
Contig ID
                   551_1.R1011
                  LIB189-019-Q1-E1-D7
5'-most EST
Method
                   BLASTX
                   q3033397
NCBI GI
BLAST score
                   1324
E value
                   1.0e-147
                   298
Match length
% identity
                  (AC004238) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   259419
Contig ID
                   552 1.R1011
5'-most EST
                   LIB3066-036-Q1-K1-H1
                   BLASTX
Method
NCBI GI
                   q1707640
BLAST score
                   185
E value
                   3.0e-13
Match length
                   111
% identity
                   42
NCBI Description (X98355) transcription factor GAMyb [Oryza sativa]
```

Seq. No.

Contig ID

259425 557_1.R1011





```
259420
Seq. No.
Contig ID
                   553 1.R1011
5'-most EST
                  uC-zmflb73301a09b2
Method
                  BLASTX
NCBI GI
                   q2463567
BLAST score
                   1441
                   1.0e-160
E value
Match length
                   302
% identity
                   90
NCBI Description
                  (AB007502) squalene synthase [Zea mays]
                   259421
Seq. No.
                   553 2.R1011
Contig ID
                   rvt700550428.h1
5'-most EST
Method
                   BLASTX
                   q2463567
NCBI GI
                   505
BLAST score
                   7.0e-51
E value
                   114
Match length
                   87
% identity
                  (AB007502) squalene synthase [Zea mays]
NCBI Description
                   259422
Seq. No.
                   554 1.R1011
Contig ID
                   LIB148-063-Q1-E1-D4
5'-most EST
Method
                   BLASTX
                   q4490706
NCBI GI
BLAST score
                   209
                   2.0e-16
E value
Match length
                   57
% identity
                   67
                  (AL035680) putative protein [Arabidopsis thaliana]
NCBI Description
                   259423
Seq. No.
Contig ID
                   554 2.R1011
5'-most EST
                   pwr700452531.h1
Method
                   BLASTX
                   g4490706
NCBI GI
BLAST score
                   884
                   4.0e-95
E value
                   274
Match length
                   67
% identity
                  (AL035680) putative protein [Arabidopsis thaliana]
NCBI Description
                   259424
Seq. No.
                   556 1.R1011
Contig ID
                   LIB3137-038-Q1-K1-B6
5'-most EST
                   BLASTX
Method
                   g4321978
NCBI GI
BLAST score
                   2624
E value
                   0.0e+00
Match length
                   488
                   100
% identity
                  (AF068119) beta-amylase [Zea mays]
NCBI Description
```

BLAST score

E value

503

1.0e-50





```
5'-most EST
                  LIB148-046-Q1-E1-F11
                  259426
Seq. No.
                  558 1.R1011
Contig ID
5'-most EST
                  LIB148-065-Q1-E1-F10
                  259427
Seq. No.
                  562 1.R1011
Contig ID
                  LIB148-045-Q1-E1-H7
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4006913
BLAST score
                  1413
                  1.0e-157
E value
                  543
Match length
                  53
% identity
                  (299708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  259428
Seq. No.
                  564 1.R1011
Contig ID
                  dyk700105245.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4115923
BLAST score
                  310
                  1.0e-28
E value
Match length
                  91
% identity
                   62
NCBI Description
                  (AF118222) contains similarity to ubiquitin
                   carboxyl-terminal hydrolase family 2 (Pfam: PF00443,
                   score=40.0, E=5.2e-08, N=1) and (Pfam:PF00442, Score=37.9
                  E=5.3e-10, N=1) [Arabidopsis thaliana]
                   259429
Seq. No.
                   569 1.R1011
Contig ID
5'-most EST
                  LIB3066-013-Q1-K1-F9
Seq. No.
                   259430
Contig ID
                   569 2.R1011
                 LIB3066-017-Q1-K1-A10
5'-most EST
Seq. No.
                   259431
Contig ID
                   570 1.R1011
                   LIB3075-054-Q1-K1-H3
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3335375
BLAST score
                   683
E value
                   6.0e-72
Match length
                   163
% identity
NCBI Description (AC003028) putative amidase [Arabidopsis thaliana]
Seq. No.
                   259432
                   573 1.R1011
Contig ID
                   LIB3078-018-Q1-K1-G4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4371290
```





Match length 123 % identity 71

NCBI Description (AC006260) unknown protein [Arabidopsis thaliana]

5'-most EST LIB148-045-Q1-E1-H6

Method BLASTX
NCBI GI 94371290
BLAST score 412
E value 9.0e-40
Match length 108
% identity 69

NCBI Description (AC006260) unknown protein [Arabidopsis thaliana]

Seq. No. 259434 Contig ID 573 3.R1011

5'-most EST LIB148-063-Q1-E1-B7

Method BLASTX
NCBI GI g4006978
BLAST score 209
E value 2.0e-16
Match length 110
% identity 42

NCBI Description (AJ131335) pollen allergen (group II) [Cynodon dactylon]

Seq. No. 259435 Contig ID 573 5.R1011

5'-most EST LIB148-011-Q1-E1-A6

Method BLASTX
NCBI GI g4006978
BLAST score 152
E value 1.0e-09
Match length 121
% identity 32

NCBI Description (AJ131335) pollen allergen (group II) [Cynodon dactylon]

Seq. No. 259436 Contig ID 574_1.R1011

5'-most EST uC-zmflb73022d03b1

Method BLASTX
NCBI GI g4200122
BLAST score 623
E value 1.0e-64
Match length 159
% identity 74

NCBI Description (AJ009555) hypothetical protein [Arabidopsis thaliana]

 Seq. No.
 259438

 Contig ID
 575_1.R1011

 5'-most EST
 wty700169417.h1

Method BLASTX NCBI GI g2275213

Seq. No.

259444





```
224
BLAST score
                   4.0e-36
E value
Match length
                   223
 % identity
                   45
NCBI Description (AC002337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   259439
Contig ID
                   576 1.R1011
 5'-most EST
                   uC-zmflb73132f06b1
                   BLASTX
Method
NCBI GI
                   q1709798
BLAST score
                   1848
E value
                   0.0e + 00
Match length
                   382
 % identity
                   95
NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG >gi 1155334
                   (U43398) POTATP1 [Solanum tuberosum]
Seq. No.
                   259440
                   576 2.R1011
 Contig ID
 5'-most EST
                   uC-zmflmo17055g12a1
                   BLASTX
Method
NCBI GI
                   g3135751
BLAST score
                   443
 E value
                   6.0e-44
Match length
                   88
 % identity
                   94
                   (AJ006095) 26S protease regulatory subunit 6 [Cicer
 NCBI Description
                   arietinum]
                   259441
 Seq. No.
                   576 5.R1011
 Contig ID
                   rvt700551460.h1
 5'-most EST
 Seq. No.
                   259442
                   578 1.R1011
 Contig ID
                   LIB3079-006-Q1-K1-G3
 5'-most EST
                   BLASTX
 Method
                   q4218116
 NCBI GI
 BLAST score
                   232
                   5.0e-19
 E value
 Match length
                   143
                   38
 % identity
 NCBI Description (AL035353) putative protein [Arabidopsis thaliana]
 Seq. No.
                   259443
                   580 1.R1011
 Contig ID
                   LIB3075-054-Q1-K1-F11
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   q4587990
 BLAST score
                   288
                   1.0e-25
 E value
                   112
. Match length
                    48
 % identity
 NCBI Description (AF085279) hypothetical protein [Arabidopsis thaliana]
```

NCBI Description





```
583 1.R1011
Contig ID
5'-most EST
                  LIB3066-040-Q1-K1-D11
                  BLASTX
Method
                  g3157943
NCBI GI
BLAST score
                  159
                  2.0e-10
E value
                  66
Match length
                  48
% identity
                  (ACO02131) Contains similarity to BAP31 protein gb_X81816
NCBI Description
                  from Mus musculus. [Arabidopsis thaliana]
                  259445
Seq. No.
                  584 1.R1011
Contig ID
                  qmh700027524.fl
5'-most EST
                  259446
Seq. No.
                  585 1.R1011
Contig ID
                  LIB3075-054-Q1-K1-F7
5'-most EST
                  259447
Seq. No.
                  586 1.R1011
Contig ID
                  LIB3136-019-Q1-K1-H11
5'-most EST
                  BLASTX
Method
                  g2982783
NCBI GI
                  414
BLAST score
                   5.0e-40
E value
Match length
                   285
                   34
% identity
                  (AE000670) 3-hydroxyisobutyrate dehydrogenase [Aquifex
NCBI Description
                   aeolicus]
                   259448
Seq. No.
                   589 1.R1011
Contig ID
                   ymt700220364.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2558666
BLAST score
                   878
                   2.0e-94
E value
Match length
                   197
% identity
                   86
                   (U49971) GTP binding protein RoplAt [Arabidopsis thaliana]
NCBI Description
                   >gi 3603426 (AF085480) rac-like GTP binding protein Arac11
                   [Arabidopsis thaliana]
                   259449
Seq. No.
                   589 2.R1011
Contig ID
5'-most EST
                   LIB3066-023-Q1-K1-H7
Method
                   BLASTX
                   g2558666
NCBI GI
BLAST score
                   573
                   7.0e-59
E value
Match length
                   136
% identity
                   83
                  (U49971) GTP binding protein RoplAt [Arabidopsis thaliana]
```

35861

[Arabidopsis thaliana]

>gi 3603426 (AF085480) rac-like GTP binding protein Arac11





```
259450
Seq. No.
                  593 1.R1011
Contig ID
                  LIB3079-010-Q1-K1-C9
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2760334
                  355
BLAST score
                  2.0e-33
E value
                  83
Match length
                  71
% identity
                  (AC002130) F1N21.5 [Arabidopsis thaliana]
NCBI Description
                  259451
Seq. No.
                  593 2.R1011
Contig ID
5'-most EST
                  LIB3067-025-Q1-K1-C8
                  BLASTX
Method
                  g2760334
NCBI GI
                  336
BLAST score
                  4.0e-31
E value
                  83
Match length
                  70
% identity
NCBI Description (AC002130) F1N21.5 [Arabidopsis thaliana]
                  259452
Seq. No.
                  594_1.R1011
Contig ID
5'-most EST
                  LIB3068-030-Q1-K1-B8
Method
                   BLASTX
NCBI GI
                   g131772
                   603
BLAST score
                   3.0e-62
E value
                   139
Match length
                   89
% identity
                   40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                   >gi_82723_pir__A30097 ribosomal protein S14 (clone MCH1) -
                   maize
                   259453
Seq. No.
Contig ID
                   594 2.R1011
                   LIB3059-042-Q1-K1-E12
5'-most EST
                   BLASTX
Method
NCBI GI
                   q131772
BLAST score
                   603
E value
                   2.0e-62
Match length
                   139
                   90
% identity
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                   >gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) -
                   maize
                   259454
Seq. No.
                   594 3.R1011
Contig ID
                   LIB3069-008-Q1-K1-G7
5'-most EST
Method
                   BLASTX
                   g131772
NCBI GI
                   558
BLAST score
                   4.0e-57
E value
Match length
                   168
```

73

% identity





```
40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                  >gi_82723_pir__A30097 ribosomal protein S14 (clone MCH1) -
                  maize
                  259455
Seq. No.
                  594 4.R1011
Contig ID
                  fdz701160436.h1
5'-most EST
                  BLASTX
Method
                  g131772
NCBI GI
                  549
BLAST score
                  5.0e-60
E value
                  144
Match length
                  90
% identity
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                  >gi 82723_pir__A30097 ribosomal protein S14 (clone MCH1) -
                  maize
                  259456
Seq. No.
                  594 5.R1011
Contig ID
                  ymt700222362.h1
5'-most EST
                  BLASTX
Method
                  g131772
NCBI GI
BLAST score
                  414
                  2.0e-40
E value
                  87
Match length
                  95
% identity
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                  >gi 82723_pir__A30097 ribosomal protein S14 (clone MCH1) -
                  maize
                  259457
Seq. No.
                  595 1.R1011
Contig ID
                  LIB3180-054-P2-M1-D3
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4587615
BLAST score
                   2588
                   0.0e+00
E value
Match length
                   673
                   70
% identity
                  (AC006951) putative acyl-CoA synthetase [Arabidopsis
NCBI Description
                  thaliana]
                   259458
Seq. No.
                   595 2.R1011
Contig ID
                  uC-zmflmo17071g02b1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q4587615
BLAST score
                   360
E value
                   6.0e - 34
                   152
Match length
% identity
                  (AC006951) putative acyl-CoA synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   259459
Seq. No.
                   595 3.R1011
Contig ID
5'-most EST
                   uC-zmflMo17087d06b1
```





```
BLASTX
Method
NCBI GI
                   q4587615
                   279
BLAST score
                   2.0e-24
E value
Match length
                   70
                   77
% identity
                   (AC006951) putative acyl-CoA synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   259460
Seq. No.
                   595 4.R1011
Contig ID
5'-most EST
                   uC-zmflb73288a04a1
                   BLASTX
Method
                   g4587615
NCBI GI
BLAST score
                   200
                   3.0e-15
E value
                   47
Match length
                   83
% identity
                   (AC006951) putative acyl-CoA synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   259461
Seq. No.
                   595_5.R1011
Contig ID
5'-most EST
                   uC-zmflb73118b10b1
                   259462
Seq. No.
                   595 8.R1011
Contig ID
5'-most EST
                   gwl700617716.h1
                    259463
Seq. No.
Contig ID
                    596 1.R1011
                   LIB148-032-Q1-E1-D1
5'-most EST
                    BLASTX
Method
                    q19944
NCBI GI
                    280
BLAST score
E value
                    2.0e-24
Match length
                    126
% identity
NCBI Description (X06930) PR-la protein (AA 1 - 168) [Nicotiana tabacum]
                    259464
Seq. No.
Contig ID
                    596 2.R1011
                    LIB148-059-Q1-E1-F2
5'-most EST
                    BLASTX
Method
NCBI GI
                    q3810602
BLAST score
                    159
E value
                    2.0e-10
Match length
                    59
% identity
                    47
                    (ACO05398) PR-1-like protein [Arabidopsis thaliana]
NCBI Description
                    >gi_4263816_gb_AAD15459 (AC006067) putative pathogenesis
related-1 (PR1) protein [Arabidopsis thaliana]
                    259465
Seq. No.
```

596 4.R1011 Contig ID LIB3066-045-Q1-K1-D11 5'-most EST

BLASTX Method

NCBI Description





```
a1351791
NCBI GI
BLAST score
                  492
                  2.0e-49
E value
                  123
Match length
                  34
% identity
                  HYPOTHETICAL 57.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN
NCBI Description
                  CPR4-SSK22 INTERGENIC REGION >gi_83249_pir__S19487
                  hypothetical protein YCR072c - yeast (Saccharomyces
                  cerevisiae) >gi_1907211_emb_CAA42270 (X59720) YCR072c,
                  len:515 [Saccharomyces cerevisiae]
                  259466
Seq. No.
                  598 1.R1011
Contig ID
                  LIB148-036-Q1-E1-A5
5'-most EST
                  259467
Seq. No.
                  598 2.R1011
Contig ID
                  LIB148-051-Q1-E1-E1
5'-most EST
                  BLASTX
Method
                  q416731
NCBI GI
BLAST score
                  681
                  1.0e-71
E value
                  159
Match length
                  84
% identity
                  POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi 82655 pir JQ1107
NCBI Description
                  18.3K protein precursor, pollen - maize
                  >gi_255569_bbs_113677 (S44171) pollen specific protein [Zea
                  mays=corn, Peptide, 170 aa] [Zea mays]
                  >gi 1588669 prf 2209273A Zm13 [Zea mays]
Seq. No.
                   259468
                   598 3.R1011
Contig ID
                   LIB148-048-Q1-E1-F10
5'-most EST
                   BLASTX
Method
                   q416731
NCBI GI
BLAST score
                   794
E value
                   9.0e-85
Match length
                   162
                   94
% identity
                  POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi 82655 pir_ JQ1107
NCBI Description
                   18.3K protein precursor, pollen - maize
                   >gi_255569_bbs_113677 (S44171) pollen specific protein [Zea
                   mays=corn, Peptide, 170 aa] [Zea mays]
                   >gi 1588669 prf 2209273A Zm13 [Zea mays]
                   259469
Seq. No.
Contig ID
                   598 4.R1011
                   LIB148-042-Q1-E1-G8
5'-most EST
                   BLASTX
Method
                   q416731
NCBI GI
BLAST score
                   627
                   4.0e-65
E value
                   150
Match length
                   84
% identity
```

35865

18.3K protein precursor, pollen - maize

POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi 82655_pir__JQ1107

>gi_255569_bbs_113677 (S44171) pollen specific protein [Zea





mays=corn, Peptide, 170 aa] [Zea mays] >gi 1588669 prf 2209273A Zm13 [Zea mays]

259470 Seq. No. 598 5.R1011 Contig ID LIB3066-013-Q1-K1-C12 5'-most EST

BLASTX Method g416731 NCBI GI BLAST score 369 E value 6.0e-35

79 Match length 89 % identity

POLLEN SPECIFIC PROTEIN C13 PRECURSOR >gi_82655_pir__JQ1107 NCBI Description

18.3K protein precursor, pollen - maize

>gi_255569_bbs_113677 (S44171) pollen specific protein [Zea

mays=corn, Peptide, 170 aa] [Zea mays] >gi 1588669 prf 2209273A Zm13 [Zea mays]

259471 Seq. No.

598 10.R1011 Contig ID

LIB148-011-Q1-E1-A11 5'-most EST

259472 Seq. No. 603 1.R1011 Contig ID

5'-most EST LIB3079-049-Q1-K1-B12

Seq. No. 259473 604 1.R1011 Contig ID

LIB3075-032-Q1-K1-D5 5'-most EST

259474 Seq. No. 606 1.R1011 Contig ID

LIB3075-054-Q1-K1-B4 5'-most EST

Method BLASTX q4538926 NCBI GI BLAST score 725 E value 8.0e-77 215 Match length

67 % identity

(AL049483) putative phosphatidylserine decarboxylase NCBI Description

[Arabidopsis thaliana]

Seq. No. 259475 609 1.R1011 Contig ID

5'-most EST uC-zmflb73064h03b1

Method BLASTX NCBI GI q4567282 BLAST score 970 E value 1.0e-105 Match length 304 % identity 62

NCBI Description (AC006841) putative DNAJ protein [Arabidopsis thaliana]

259476 Seq. No. 609 2.R1011 Contig ID

5'-most EST LIB3067-057-Q1-K1-C2

Method BLASTX

E value

Match length

0.0e+00

377





```
q4567282
NCBI GI
BLAST score
                    456
                    3.0e-45
E value
Match length
                    149
% identity
                    62
                    (AC006841) putative DNAJ protein [Arabidopsis thaliana]
NCBI Description
                    259477
Seq. No.
Contig ID
                    609 3.R1011
                    ymt700223602.h1
5'-most EST
                    259478
Seq. No.
                    609_5.R1011
Contig ID
                    wyr700237401.hl
5'-most EST
Method
                    BLASTX
                    q4567282
NCBI GI
                    152
BLAST score
                    2.0e-18
E value
                    69
Match length
                    62
% identity
                    (AC006841) putative DNAJ protein [Arabidopsis thaliana]
NCBI Description
                    259479
Seq. No.
                    611_1.R1011
Contig ID.
5'-most EST
                    hvj700621638.hl
                    BLASTX
Method
NCBI GI
                    q113222
BLAST score
                    1934
                    0.0e+00
E value
                    377
Match length
% identity
                    99
                    ACTIN 1 >gi 295885 emb_CAA33874_ (X15865) actin [Oryza
NCBI Description
                    sativa]
Seq. No.
                    259480
Contig ID
                     611 2.R1011
5'-most EST
                    xsy700211910.h1
Method
                    BLASTX
NCBI GI
                     q1703108
BLAST score
                    1307
E value
                     0.0e+00
Match length
                    376
                     97
% identity
                    ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis
NCBI Description
                     thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis
                    thaliana]
                     259481
Seq. No.
                     611 3.R1011
Contig ID
                    uC-zmflb73196a12b1
5'-most EST
                    {\tt BLASTX}
Method
NCBI GI
                     g1703108
BLAST score
                    1918
```





```
% identity
                     ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis
NCBI Description
                     thaliana]
                     259482
Seq. No.
Contig ID
                     611 4.R1011
                     LIB3066-032-Q1-K1-D5
5'-most EST
Method
                     BLASTX
                     q113222
NCBI GI
                     1934
BLAST score
                     0.0e+00
E value
Match length
                     377
                     99
% identity
NCBI Description ACTIN 1 >gi 295885 emb CAA33874 (X15865) actin [Oryza
                     sativa]
                     259483
Seq. No.
                     611_5.R1011
Contig ID
                     LIB3150-009-Q1-N1-A2
5'-most EST
Method
                     BLASTX
NCBI GI
                     g1669387
                     289
BLAST score
E value
                     4.0e-31
Match length
                     79
% identity
NCBI Description (U41998) actin 2 [Arabidopsis thaliana]
Seq. No.
                     259484
Contig ID
                     611 6.R1011
5'-most EST
                     LIB3066-003-Q1-K1-F8
Method
                     BLASTN
NCBI GI
                     g499011
BLAST score
                     65
E value
                     5.0e-28
Match length
                     282
                     88
% identity
NCBI Description S.vulgare SoAc1 mRNA
                     259485
Seq. No.
                     611 7.R1011
Contig ID
5'-most EST
                     LIB3150-074-P2-K1-G6
Seq. No.
                     259486
                     611 8.R1011
Contig ID
                     xsy700217747.h1
5'-most EST
                     BLASTX
Method
NCBI GI
                     g1703108
BLAST score
                     1919
E value
                     0.0e+00
Match length
                     377
% identity
NCBI Description ACTIN 2/7 >gi 2129525 pir S71210 actin 2 - Arabidopsis
```

thaliana >gi $\overline{2}$ 129528 \overline{p} ir $\overline{5}$ 68107 actin 7 - Arabidopsis thaliana >gi $\overline{104}$ 9307 (U3 $\overline{7}$ 281) actin-2 [Arabidopsis





```
thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]
```

Seq. No. 259487 Contig ID 611_9.R1011

5'-most EST uC-zmflmo17132b07a1

Method BLASTX
NCBI GI g3287695
BLAST score 260
E value 6.0e-22
Match length 126
% identity 44

NCBI Description (AC003979) Similar to hypothetical protein C34B7.2

gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis

thaliana]

Seq. No. 259488

Contig ID 611_10.R1011

5'-most EST uC-zmflb73197f11b1

Method BLASTX
NCBI GI g113222
BLAST score 583
E value 4.0e-60
Match length 108
% identity 100

NCBI Description ACTIN 1 >gi_295885_emb_CAA33874_ (X15865) actin [Oryza

sativa]

Seq. No. 259489

Contig ID 611 19.R1011

5'-most EST uC-zmromo17023b12a1

Seq. No. 259490 Contig ID 611 20.R1011

5'-most EST LIB148-013-Q1-E1-A2

Method BLASTX
NCBI GI g2244734
BLAST score 377
E value 4.0e-36
Match length 142
% identity 88

NCBI Description (D88414) actin [Gossypium hirsutum]

Seq. No. 259491

Contig ID 611_26.R1011 5'-most EST afb700381454.h1

Method BLASTX
NCBI GI g113240
BLAST score 184
E value 5.0e-14
Match length 46
% identity 76

NCBI Description ACTIN 2 > gi_71636_pir__ATRZ2 actin 2 - rice

>gi 20329 emb CAA33873 (X15864) actin [Oryza sativa]

Seq. No. 259492 Contig ID 614 1.R1011





5'-most EST uC-zmflb73185b07b1

Seq. No. 259493 Contig ID 615_1.R1011

5'-most EST uC-zmflb73296f05b2

Seq. No. 259494 Contig ID 617 1.R1011

5'-most EST LIB3075-053-Q1-K1-H3

Method BLASTX
NCBI GI g3511223
BLAST score 359
E value 5.0e-34
Match length 103
% identity 64

NCBI Description (AF069528) plant adhesion molecule 1 [Arabidopsis thaliana]

Seq. No. 259495 Contig ID 618 1.R1011

5'-most EST LIB3279-049-P1-K1-D6

Method BLASTX
NCBI GI g3885884
BLAST score 817
E value 2.0e-87
Match length 164
% identity 93

NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Method BLASTX
NCBI GI g3885884
BLAST score 822
E value 4.0e-88
Match length 164
% identity 95

NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No. 259497 Contig ID 618_3.R1011

5'-most EST uC-zmflb73290h01b1

Method BLASTX
NCBI GI g3885884
BLAST score 821
E value 6.0e-88
Match length 164
% identity 93

NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No. 259498 Contig ID 618 4.R1011

5'-most EST LIB3069-002-Q1-K1-A10

Method BLASTX
NCBI GI g3885884
BLAST score 596
E value 8.0e-80





Match length 165 91 % identity (AF093630) 60S ribosomal protein L21 [Oryza sativa] NCBI Description 259499 Seq. No. 618 5.R1011 Contig ID 5'-most EST wty700165827.hl Method BLASTX NCBI GI g2851508 BLAST score 383 7.0e-37 E value Match length 74 88 % identity 60S RIBOSOMAL PROTEIN L21 >gi 2160162 (AC000132) Similar to NCBI Description ribosomal protein L21 (gb L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana] 259500 Seq. No. Contig ID 624 1.R1011 5'-most EST LIB3075-027-Q1-K1-G4 Method BLASTX NCBI GI g4539417 BLAST score 418 9.0e-41 E value Match length 111 % identity 65 (AL049171) putative protein [Arabidopsis thaliana] NCBI Description 259501 Seq. No. Contig ID 624 2.R1011 LIB3067-025-Q1-K1-D5 5'-most EST Method BLASTX NCBI GI q4539417 BLAST score 421 E value 5.0e-41 Match length 104 % identity 71 (AL049171) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 259502 Contig ID 626 1.R1011 5'-most EST uC-zmflmo17150f02b1 Method BLASTX NCBI GI q2352795 BLAST score 1212 E value 1.0e-133 Match length 240

% identity

NCBI Description (AF007793) retinoblastoma-related protein 1 [Zea mays]

259503 Seq. No. 626 3.R1011 Contig ID

5'-most EST uC-zmroteosinte094c02b2

Method BLASTN NCBI GI g2352794





```
603
BLAST score
                   0.0e + 00
E value
                   622
Match length
                   99
% identity
                   Zea mays retinoblastoma-related protein 1 (RRB1) mRNA,
NCBI Description
                   complete cds
                   259504
Seq. No.
                   626 5.R1011
Contig ID
                   uC-zmromo17100e09a1
5'-most EST
                   BLASTX
Method
                   g2352797
NCBI GI
                   375
BLAST score
                   8.0e-36
E value
                   125
Match length
% identity
                   68
                   (AF007794) retinoblastoma-related protein 2a [Zea mays]
NCBI Description
                   259505
Seq. No.
                   627 1.R1011
Contig ID
                   LIB3066-040-Q1-K1-C10
5'-most EST
                   259506
Seq. No.
                   628 1.R1011
Contig ID
                   LIB3150-097-P1-N1-B9
5'-most EST
                   BLASTX
Method
                   g1519251
NCBI GI
BLAST score
                   1205
                   1.0e-132
E value
                   256
Match length
                   94
% identity
                  (U65957) GF14-c protein [Oryza sativa]
NCBI Description
                   259507
Seq. No.
                   628_2.R1011
Contig ID
                   wyr700240944.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1519251
                   647
BLAST score
                   2.0e-69
E value
                   149
Match length
% identity
                   (U65957) GF14-c protein [Oryza sativa]
NCBI Description
                   259508
Seq. No.
                   628 3.R1011
Contig ID
5'-most EST
                   LIB189-022-Q1-E1-E2
Method
                   BLASTX
NCBI GI
                   q1519251
BLAST score
                   588
                   2.0e-60
E value
Match length
                   237
% identity
                   78
                   (U65957) GF14-c protein [Oryza sativa]
NCBI Description
```

259509

628 4.R1011

Seq. No. Contig ID





```
LIB3066-009-Q1-K1-C10
5'-most EST
                  BLASTX
Method
                  q1519251
NCBI GI
BLAST score
                  486
E value
                  9.0e-49
                  115
Match length
                  84
% identity
                  (U65957) GF14-c protein [Oryza sativa]
NCBI Description
                  259510
Seq. No.
                  629 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73175d08b1
Method
                  BLASTX
NCBI GI
                  g3885329
BLAST score
                  1930
E value
                  0.0e+00
Match length
                  432
% identity
                  84
                  (AC005623) alien-like protein [Arabidopsis thaliana]
NCBI Description
                  259511
Seq. No.
                   629_3.R1011
Contig ID
5'-most EST
                  wyr700242416.h1
                  BLASTX
Method
NCBI GI
                  q3885329
                  201
BLAST score
E value
                   9.0e-16
Match length
                  42
                   88
% identity
                  (AC005623) alien-like protein [Arabidopsis thaliana]
NCBI Description
                   259512
Seq. No.
                   631 1.R1011
Contig ID
5'-most EST
                  dyk700103742.h1
Method
                  BLASTX
NCBI GI
                   g2500497
BLAST score
                   419
E value
                   6.0e-41
Match length
                   81
% identity
                   99
NCBI Description 40S RIBOSOMAL PROTEIN S21 >gi 1419372 emb CAA67225
                   (X98656) ribosomal protein S21 [Zea mays]
                   259513
Seq. No.
                   631 2.R1011
Contig ID
5'-most EST
                   wty700171320.h1
Method
                   BLASTX
                   q2500497
NCBI GI
                   422
BLAST score
                   2.0e-41
E value
Match length
                   81
                   100
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S21 >gi 1419372 emb CAA67225
                   (X98656) ribosomal protein S21 [Zea mays]
Seq. No.
                   259514
```

631 3.R1011

Contig ID





```
yne700378587.h1
5'-most EST
                  BLASTX
Method
                  g2500497
NCBI GI
                  419
BLAST score
                  5.0e-41
E value
                  81
Match length
                   99
% identity
                   40S RIBOSOMAL PROTEIN S21 >gi_1419372_emb_CAA67225_
NCBI Description
                   (X98656) ribosomal protein S21 [Zea mays]
                   259515
Seq. No.
                   634 1.R1011
Contig ID
                   yyf700351540.hl
5'-most EST
                   259516
Seq. No.
                   634 2.R1011
Contig ID
                   wyr700244308.hl
5'-most EST
                   BLASTX
Method
                   g3411152
NCBI GI
                   838
BLAST score
                   6.0e-98
E value
                   205
Match length
                   86
% identity
                   (AF066050) thymidine kinase [Oryza sativa]
NCBI Description
                   259517
Seq. No.
                   635_1.R1011
Contig ID
                   LIB148-044-Q1-E1-C2
5'-most EST
                   259518
Seq. No.
                   636_1.R1011
Contig ID
                   LIB148-044-Q1-E1-C5
5'-most EST
                   BLASTX
Method
                   g2828289
NCBI GI
                   184
BLAST score
                   3.0e-13
E value
Match length
                   149
% identity
                   36
                   (AL021687) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   259519
Seq. No.
                   636 2.R1011
Contig ID
5'-most EST
                   ypc700802274.h1
                   BLASTX
Method
                   q2828289
NCBI GI
                   339
BLAST score
E value
                   2.0e-31
Match length
                   132
 % identity
                   (AL021687) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   259520
 Seq. No.
                   639 1.R1011
 Contig ID
                   LIB3078-008-Q1-K1-G4
 5'-most EST
                   BLASTX
 Method
```

g1172995

284

NCBI GI BLAST score





5.0e-25 E value 108 Match length 58 % identity 60S RIBOSOMAL PROTEIN L22 >gi 1083790 pir__S52084 ribosomal NCBI Description protein L22 - rat >gi_710295_emb_CAA55204 (X78444) ribosomal protein L22 [Rattus norvegicus] >gi 1093952_prf__2105193A ribosomal protein L22 [Rattus norvegicus] 259521 Seq. No. 639 2.R1011 Contig ID LIB3279-008-P1-K1-F2 5'-most EST BLASTX Method g70772 NCBI GI 410 BLAST score 6.0e-40 E value 82 Match length 100 % identity histone H4 - wheat >gi_70773_pir__HSPM4 histone H4 - garden NCBI Description pea 259522 Seq. No. 639 3.R1011 Contig ID LIB3059-056-Q1-K1-F9 5'-most EST BLASTX Method g118204 NCBI GI BLAST score 250 3.0e-21 E value 108 Match length 51 % identity 60S RIBOSOMAL PROTEIN L22 (DEVELOPMENT-SPECIFIC PROTEIN NCBI Description 217) >gi_85392_pir__A30033 development-specific protein 217 - sea urchin (Tripneustes gratilla) >gi 161631 (M22207) 217g protein [Tripneustes gratilla] 259523 Seq. No. Contig ID 639 5.R1011 LIB3157-017-Q1-K1-F9 5'-most EST BLASTX Method NCBI GI g1172995 BLAST score 157 E value 3.0e-16 Match length 89 58 % identity NCBI Description 60S RIBOSOMAL PROTEIN L22 >gi 1083790_pir S52084 ribosomal protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus] >qi 1093952 prf 2105193A ribosomal protein L22 [Rattus norvegicus] 259524 Seq. No. Contig ID 639 7.R1011 LIB3150-089-P2-K1-B11 5'-most EST 259525 Seq. No.

35875

639 8.R1011

LIB3075-015-Q1-K1-C1

Contig ID

5'-most EST





```
BLASTX
Method
                  g118204
NCBI GI
                  154
BLAST score
                  2.0e-10
E value
                  44
Match length
                  68
% identity
                  60S RIBOSOMAL PROTEIN L22 (DEVELOPMENT-SPECIFIC PROTEIN
NCBI Description
                  217) >gi_85392_pir__A30033 development-specific protein 217
                   - sea urchin (Tripneustes gratilla) >gi_161631 (M22207)
                  217g protein [Tripneustes gratilla]
                   259526
Seq. No.
                   642 1.R1011
Contig ID
                  LIB3066-005-Q1-K1-F4
5'-most EST
                   BLASTX
Method
                   q548493
NCBI GI
                   757
BLAST score
                   2.0e-80
E value
                   215
Match length
                   66
% identity
                   EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                   (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                   >gi_629854_pir__S30067 polygalacturonase - maize
                   >gi 288612 emb CAA47052 (X66422) polygalacturonase [Zea
                   mays]
                   259527
Seq. No.
                   642 2.R1011
Contig ID
                   LIB3066-034-Q1-K1-C6
5'-most EST
                   BLASTX
Method
                   g548493
NCBI GI
                   1222
BLAST score
                   1.0e-134
E value
                   366
Match length
                   61
 % identity
                   EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
 NCBI Description
                   (GALACTURAN 1, 4-ALPHA-GALACTURONIDASE)
                   >gi_629854_pir__S30067 polygalacturonase - maize
                   >gi_288612_emb_CAA47052_ (X66422) polygalacturonase [Zea
                   mays]
                   259528
 Seq. No.
                   642 3.R1011
 Contig ID
                   LIB148-029-Q1-E1-A3
 5'-most EST
                   BLASTX
 Method
                   q548492
 NCBI GI
                   243
 BLAST score
                   2.0e-20
 E value
                   98
 Match length
                    50
 % identity
                   EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
 NCBI Description
                    (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                    >gi 629853_pir__S30066 polygalacturonase - maize
```

Seq. No. 259529

mays]

>gi 288379 emb CAA45751 (X64408) polygalacturonase [Zea

NCBI GI





```
642 4.R1011
Contig ID
                  LIB148-014-Q1-E1-B12
5'-most EST
Method
                  BLASTX
NCBI GI
                  q548493
BLAST score
                  422
E value
                  3.0e-41
Match length
                  133
                  60
% identity
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                   (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi_629854_pir__S30067 polygalacturonase - maize
                  >gi 288612 emb CAA47052_ (X66422) polygalacturonase [Zea
                  mays]
                  259530
Seq. No.
Contig ID
                  642 5.R1011
                  LIB148-063-Q1-E1-D3
5'-most EST
                  BLASTX
Method
                  g548493
NCBI GI
BLAST score
                  246
E value
                  7.0e-21
                  79
Match length
                  58
% identity
NCBI Description EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
                   (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                  >gi_629854_pir__S30067 polygalacturonase - maize
                  >gi 288612 emb CAA47052 (X66422) polygalacturonase [Zea
                  mays]
                  259531
Seq. No.
Contig ID
                   642 9.R1011
5'-most EST
                  LIB3066-052-Q1-K1-A9
                   259532
Seq. No.
                   643 1.R1011
Contig ID
5'-most EST
                  LIB3151-050-P1-K1-D7
Method
                  BLASTX
NCBI GI
                   q4185153
BLAST score
                   212
E value
                   2.0e-16
Match length
                   69
% identity
NCBI Description (AC005724) hypothetical protein [Arabidopsis thaliana]
                   259533
Seq. No.
Contig ID
                   644 1.R1011
5'-most EST
                   rvt700549530.h1
                   259534
Seq. No.
                   644 2.R1011
Contig ID
5'-most EST
                   LIB3137-002-Q1-K1-D11
                   259535
Seq. No.
                   646 1.R1011
Contig ID
                   LIB143-038-Q1-E1-E10
5'-most EST
Method
                   BLASTX
```

35877

g3024657





```
BLAST score
                  522
E value
                  9.0e-53
Match length
                  115
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi 2668740 (AF034944) translation initiation factor; GOS2
                  [Zea mays]
                  259536
Seq. No.
                  646 2.R1011
Contig ID
5'-most EST
                  LIB3069-050-Q1-K1-E7
Method
                  BLASTX
                  q1914683
NCBI GI
BLAST score
                  864
E value
                  1.0e-92
Match length
                  401
% identity
                  50
                  (Y12013) RAD23, isoform I [Daucus carota]
NCBI Description
                  259537
Seq. No.
                  646_3.R1011
Contig ID
                  uC-zmflmo17242b08b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1488297
                  265
BLAST score
E value
                   5.0e-23
                  122
Match length
% identity
                   49
NCBI Description (U63530) osRAD23 [Oryza sativa]
Seq. No.
                   259538
                   646_4.R1011
Contig ID
5'-most EST
                  uC-zmflb73232c09b1
                  BLASTX
Method
NCBI GI
                   q1488297
BLAST score
                   278
E value
                   6.0e - 31
Match length
                   145
% identity
                   54
NCBI Description (U63530) osRAD23 [Oryza sativa]
Seq. No.
                   259539
                   646 5.R1011
Contig ID
                   uC-zmflmo17270e02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3024657
BLAST score
                   489
                   4.0e-49
E value
Match length
                   95
                   100
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                   >gi 2668740 (AF034944) translation initiation factor; GOS2
                   [Zea mays]
```

Seq. No. 259540 Contig ID 646_7.R1011

5'-most EST uC-zmroteosinte068h11b1





```
259541
Seq. No.
                  646 9.R1011
Contig ID
                  uC-zmflmo17113q01b1
5'-most EST
                  BLASTX
Method
                  g3024657
NCBI GI
BLAST score
                  434
                  1.0e-42
E value
                  85
Match length
                   99
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                   >qi 2668740 (AF034944) translation initiation factor; GOS2
                   [Zea mays]
                   259542
Seq. No.
                   646 12.R1011
Contig ID
                   LIB3079-049-Q1-K1-F9
5'-most EST
                   BLASTX
Method
                   q1488297
NCBI GI
                   292
BLAST score
                   4.0e-38
E value
                   128
Match length
% identity
                   69
                  (U63530) osRAD23 [Oryza sativa]
NCBI Description
                   259543
Seq. No.
                   646 14.R1011
Contig ID
5'-most EST
                   tfd700573395.h1
Method
                   BLASTX
                   q1914683
NCBI GI
                   393
BLAST score
                   7.0e-38
E value
                   172
Match length
                   55
% identity
                  (Y12013) RAD23, isoform I [Daucus carota]
NCBI Description
                   259544
Seq. No.
Contig ID
                   646 18.R1011
                   pwr700449336.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1488297
BLAST score
                   329
                   8.0e-39
E value
Match length
                   146
                   64
% identity
                  (U63530) osRAD23 [Oryza sativa]
NCBI Description
Seq. No.
                   259545
Contig ID
                   646 20.R1011
                   mwy700440435.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3024657
BLAST score
                   267
                   3.0e-23
E value
Match length
                   68
                   81
% identity
```

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)





>gi_2668740 (AF034944) translation initiation factor; GOS2
[Zea mays]

 Seq. No.
 259546

 Contig ID
 646_21.R1011

 5'-most EST
 vux700156707.h1

 Method
 BLASTN

 NCBI GI
 g2668739

 BLAST score
 244

 E value
 1.0e-135

E value 1.0e-135 Match length 334 % identity 96

NCBI Description Zea mays translation initiation factor GOS2 (TIF) mRNA,

complete cds

 Seq. No.
 259547

 Contig ID
 647_1.R1011

 5'-most EST
 pmx700091634.h1

Seq. No. 259548 Contig ID 648_1.R1011 5'-most EST LIB3060-019-Q1-K1-D11

Seq. No. 259549 Contig ID 652_1.R1011 5'-most EST LIB3115-001-Q1-K1-G1

 Seq. No.
 259550

 Contig ID
 653_1.R1011

 5'-most EST
 LIB3075-045-Q1-K1-A4

 Seq. No.
 259551

 Contig ID
 654_1.R1011

 5'-most EST
 LIB3069-043-Q1-K1-D5

 Method
 BLASTX

 NCBI GI
 g3294469

 BLAST score
 2928

BLAST score 2928
E value 0.0e+00
Match length 583
% identity 98

NCBI Description (U89342) phosphoglucomutase 2 [Zea mays]

 Seq. No.
 259552

 Contig ID
 654_2.R1011

 5'-most EST
 uC-zmflb73073c04a1

 Method
 BLASTX

 NCBI GI
 g3294467

 BLAST score
 323

E value 1.0e-29
Match length 66
% identity 100

NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]

 Seq. No.
 259553

 Contig ID
 654_4.R1011

 5'-most EST
 cyk700050562.f1

 Method
 BLASTX

NCBI GI

g629849





```
NCBI GI
                   g3294467
                   157
BLAST score
                   8.0e-23
E value
Match length
                   54
                   96
% identity
                   (U89341) phosphoglucomutase 1 [Zea mays]
NCBI Description
                   259554
Seq. No.
                   654 8.R1011
Contig ID
                   tzu700203525.h1
5'-most EST
                   BLASTN
Method
                   g3294468
NCBI GI
BLAST score
                   114
                   2.0e-57
E value
Match length
                   144
                   93
% identity
                   Zea mays phosphoglucomutase 2 mRNA, complete cds
NCBI Description
Seq. No.
                   259555
                   655 1.R1011
Contig ID
                   uC-\overline{z}mf1b73245e08b2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4586116
BLAST score
                   1088
                   1.0e-119
E value
Match length
                   291
                   66
% identity
                   (AL049638) putative C-4 sterol methyl oxidase [Arabidopsis
NCBI Description
                   thaliana]
                   259556
Seq. No.
                   658_1.R1011
Contig ID
                   LIB148-035-Q1-E1-E6
5'-most EST
                   BLASTX
Method
                   g4538930
NCBI GI
                   643
BLAST score
                   6.0e-67
E value
Match length
                   289
                   45
% identity
                   (AL049483) putative peroxidase [Arabidopsis thaliana]
NCBI Description
                   259557
Seq. No.
                   659 1.R1011
Contig ID
                   uwc700152625.h1
5'-most EST
                   BLASTX
Method
                   g3132310
NCBI GI
                    3592
BLAST score
                    0.0e+00
E value
                   715
Match length
 % identity
                   (AB012228) phosphoenolpyruvate carboxylase [Zea mays]
NCBI Description
 Seq. No.
                    259558
                    661 1.R1011
 Contig ID
                    LIB148-014-Q1-E1-B11
 5'-most EST
                    BLASTX
Method
```

5'-most EST





```
BLAST score
                  1285
                  1.0e-142
E value
                  450
Match length
                  57
% identity
                  pectate lyase (EC 4.2.2.2) - maize >gi_405535 (L20140)
NCBI Description
                  homology with pectate lyase [Zea mays]
                  259559
Seq. No.
                  661 2.R1011
Contig ID
                  LIB3066-051-Q1-K1-E10
5'-most EST
                  BLASTX
Method
                  g629849
NCBI GI
                  1562
BLAST score
                   1.0e-174
E value
                   405
Match length
                   76
% identity
                  pectate lyase (EC 4.2.2.2) - maize >gi_405535 (L20140)
NCBI Description
                  homology with pectate lyase [Zea mays]
                   259560
Seq. No.
                   661 3.R1011
Contig ID
                   LIB3066-051-Q1-K1-F6
5'-most EST
Method
                   BLASTX
                   g1171161
NCBI GI
BLAST score
                   1240
                   1.0e-137
E value
Match length
                   374
% identity
                   61
                  (U41472) pectate lyase homolog [Medicago sativa]
NCBI Description
                   259561
Seq. No.
                   661 4.R1011
Contig ID
                   LIB3066-038-Q1-K1-A8
5'-most EST
                   BLASTX
Method
                   q629849
NCBI GI
BLAST score
                   1630
                   0.0e + 00
E value
Match length
                   379
                   80
% identity
                   pectate lyase (EC 4.2.2.2) - maize >gi_405535 (L20140)
NCBI Description
                   homology with pectate lyase [Zea mays]
                   259562
Seq. No.
                   661 5.R1011
Contig ID
                   LIB148-012-Q1-E1-F9
5'-most EST
Method
                   BLASTX
NCBI GI
                   g629849
BLAST score
                   753
E value
                   4.0e-80
                   133
Match length
                   100
% identity
                   pectate lyase (EC 4.2.2.2) - maize >gi 405535 (L20140)
NCBI Description
                   homology with pectate lyase [Zea mays]
                   259563
Seq. No.
                   661 6.R1011
Contig ID
```

35882

LIB148-039-Q1-E1-C7





```
Method
                  BLASTX
NCBI GI
                  q730290
BLAST score
                  762
E value
                  7.0e-81
Match length
                  288
                  51
% identity
NCBI Description
                 PECTATE LYASE PRECURSOR >gi 322883 pir S29612 pectate
                  lyase - trumpet lily >gi 19451 emb CAA78976 (Z17328)
                  pectate lyase [Lilium longiflorum] >gi 308902 (L18911)
                  pectate lyase [Lilium longiflorum]
Seq. No.
                  259564
                  661 7.R1011
Contig ID
5'-most EST
                  LIB148-041-Q1-E1-G3
Method
                  BLASTN
                  g405532
NCBI GI
BLAST score
                  132
                  6.0e-68
E value
                  376
Match length
                  97
% identity
NCBI Description Zea mays pollen specific pectate lyase homologue mRNA, 3'
                  end of cds
                  259565
Seq. No.
                  661_14.R1011
Contig ID
5'-most EST
                  LIB148-023-Q1-E1-A3
Seq. No.
                  259566
Contig ID
                  663 1.R1011
5'-most EST
                  LIB3075-008-Q1-K1-C2
                  259567
Seq. No.
                  664 1.R1011
Contig ID
5'-most EST
                  LIB3067-025-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  g1651934
BLAST score
                  260
                  4.0e-22
E value
                  175
Match length
% identity
NCBI Description (D90901) hypothetical protein [Synechocystis sp.]
Seq. No.
                  259568
Contiq ID
                  667 1.R1011
                  LIB3075-010-Q1-K1-B10
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4454032
BLAST score
                  601
```

6.0e-62 E value Match length 239 % identity 47

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 259569 667 2.R1011 Contig ID 5'-most EST bdu700382834.hl





```
259570
Seq. No.
                  667 3.R1011
Contig ID
                  LIB3075-049-Q1-K1-D6
5'-most EST
                  BLASTX
Method
                  q3702332
NCBI GI
```

BLAST score 182 2.0e-13 E value Match length 86 41 % identity

(AC005397) unknown protein [Arabidopsis thaliana] NCBI Description

259571 Seq. No. Contig ID 672_1.R1011

 $uC-\overline{z}mf1b73049e04b1$ 5'-most EST

BLASTX Method g2388561 NCBI GI BLAST score 1229 1.0e-135 E value 403 Match length 60 % identity

(AC000098) Similar to Arabidopsis hypothetical protein NCBI Description

PID:e326839 (gb Z97337). [Arabidopsis thaliana]

259572 Seq. No. Contig ID 672 2.R1011

5'-most EST LIB3069-039-Q1-K1-G4

259573 Seq. No. 672 5.R1011 Contig ID

LIB143-044-Q1-E1-D3 5'-most EST

Method BLASTX q2388561 NCBI GI BLAST score 842 2.0e-90 E value Match length 232

% identity

(AC000098) Similar to Arabidopsis hypothetical protein NCBI Description

PID:e326839 (gb_Z97337). [Arabidopsis thaliana]

259574 Seq. No. Contig ID 674 1.R1011

LIB148-042-Q1-E1-E3 5'-most EST

259575 Seq. No. 674 2.R1011 Contig ID

5'-most EST LIB148-024-Q1-E1-C6

259576 Seq. No. 674 3.R1011 Contig ID

5'-most EST LIB148-046-Q1-E1-H12

Seq. No. 259577 676 1.R1011 Contig ID

uC-zmflb73027e12b1 5'-most EST

BLASTX Method NCBI GI g1708236 BLAST score 1363





0.0e + 00E value Match length 466 72 % identity HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) NCBI Description (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase $(EC^{-}4.1.3.5)$ - \overline{Ar} abidopsis thaliana >gi_1143390_emb_CAA58763_ (X83882)
hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi 1586548 prf 2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana] 259578 Seq. No. 676 2.R1011 Contig ID fC-zmf1700350551r3 5'-most EST BLASTX Method q1655679 NCBI GI 260 BLAST score 2.0e-22 E value 89 Match length 65 % identity (X96386) 3-hydroxy-3-methylglutaryl-CoA-synthase [Pinus NCBI Description sylvestris] 259579 Seq. No. 677 1.R1011 Contig ID LIB83-006-Q1-E1-G4 5'-most EST

BLASTX Method g3298540 NCBI GI 994 BLAST score

1.0e-108 E value Match length 235 78 % identity

NCBI Description (AC004681) unknown protein [Arabidopsis thaliana]

259580 Seq. No. Contig ID 679 1.R1011 zuv700356160.h1 5'-most EST

BLASTX Method q4580389 NCBI GI 827 BLAST score 1.0e-88 E value 218 Match length % identity

NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]

Seq. No. 259581 Contig ID 680 1.R1011 rv1700455880.h1 5'-most EST

259582 Seq. No. 682 1.R1011 Contig ID

LIB3075-052-Q1-K1-G11 5'-most EST

259583 Seq. No. 682 2.R1011 Contig ID

5'-most EST uC-zmflb73136d06b1





```
259584
Seq. No.
                  684 1.R1011
Contig ID
                  ceu700422283.h1
5'-most EST
                  259585
Seq. No.
                  684 2.R1011
Contig ID
                  uC-zmflb73112f09a1
5'-most EST
                  259586
Seq. No.
                  685_1.R1011
Contig ID
                  LIB3075-004-Q1-K1-B11
5'-most EST
                  259587
Seq. No.
                  687 1.R1011
Contig ID
                  LIB3060-035-Q1-K1-D12
5'-most EST
                  BLASTX
Method
                  g729671
NCBI GI
                   463
BLAST score
                   6.0e-46
E value
                   115
Match length
                   83
% identity
                  \tt HISTONE~H2A~>gi\_473603~(U08225)~histone~H2A~[Zea~mays]
NCBI Description
                   259588
Seq. No.
                   687 2.R1011
Contig ID
                   LIB3060-005-Q1-K1-E4
5'-most EST
                   BLASTX
Method
                   g4056488
NCBI GI
                   494
BLAST score
                   2.0e-49
E value
                   227
Match length
                   47
% identity
                  (AC005896) unknown protein [Arabidopsis thaliana]
NCBI Description
                   259589
Seq. No.
                   687_3.R1011
Contig ID
                   uC-zmflmo17029b05b1
5'-most EST
                   BLASTX
Method
                   g4056488
NCBI GI
                   451
BLAST score
                   3.0e-44
E value
                   100
Match length
                   76
% identity
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]
                   259590
Seq. No.
Contig ID
                   687 4.R1011
                   LIB3069-037-Q1-K1-G10
 5'-most EST
                   BLASTX
Method
                   q122007
NCBI GI
BLAST score
                   419
E value
                   8.0e-41
Match length
                   107
                   77
 % identity
 NCBI Description HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley
```

>qi 20448 emb CAA37828 (X53831) H2A histone protein (AA 1





- 149) [Petroselinum crispum]

 Seq. No.
 259591

 Contig ID
 687_5.R1011

 5'-most EST
 LIB3088-020-Q1-K1-H9

 Method
 BLASTX

 NCBI GI
 g122007

 BLAST score
 406

 E value
 3.0e-39

Match length 103 % identity 78

NCBI Description HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley

>gi_20448_emb_CAA37828_ (X $\overline{53}$ 831) H2A histone protein (AA 1

- 149) [Petroselinum crispum]

Seq. No. 259592 Contig ID 687_6.R1011

5'-most EST uC-zmflb73130b01a1

 Seq. No.
 259593

 Contig ID
 687_7.R1011

 5'-most EST
 gwl700615339.h1

Method BLASTX
NCBI GI g4056488
BLAST score 479
E value 1.0e-47
Match length 107
% identity 76

NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

NCBI GI g729671
BLAST score 382
E value 1.0e-36
Match length 103
% identity 75

NCBI Description HISTONE H2A >gi 473603 (U08225) histone H2A [Zea mays]

 Seq. No.
 259595

 Contig ID
 687_10.R1011

 5'-most EST
 gct701174293.h1

Seq. No. 259596

Contig ID 687_11.R1011 5'-most EST uC-zmflb73116a08b2

Method BLASTN
NCBI GI g312180
BLAST score 57
E value 6.0e-23
Match length 124
% identity 87

NCBI Description Z.mays GapC4 gene

Seq. No. 259597





```
687 12.R1011
Contig ID
                  LIB3151-024-Q1-K1-C2
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4056488
BLAST score
                  419
                  9.0e-41
E value
                  100
Match length
                  73
% identity
                  (AC005896) unknown protein [Arabidopsis thaliana]
NCBI Description
                  259598
Seq. No.
                   687 13.R1011
Contig ID
                  LIB3137-023-Q1-K1-H12
5'-most EST
                   259599
Seq. No.
                   687 14.R1011
Contig ID
                  LIB3150-092-P2-K1-G1
5'-most EST
                   BLASTN
Method
                   g473602
NCBI GI
                   62
BLAST score
                   3.0e-26
E value
                   114
Match length
                   89
% identity
NCBI Description Zea mays W-22 histone H2A mRNA, complete cds
                   259600
Seq. No.
                   687 29.R1011
Contig ID
                   fdz701164918.hl
5'-most EST
                   BLASTN
Method
                   q473602
NCBI GI
BLAST score
                   92
                   2.0e-44
E value
                   181
Match length
                   97
% identity
NCBI Description Zea mays W-22 histone H2A mRNA, complete cds
Seq. No.
                   259601
                   688 1.R1011
Contig ID
                   LIB3150-035-Q1-N1-F6
5'-most EST -
                   BLASTX
Method
NCBI GI
                   g4490728
BLAST score
                   301
E value
                   4.0e-27
Match length
                   73
% identity
NCBI Description (AL035709) putative protein [Arabidopsis thaliana]
Seq. No.
                   259602
Contig ID
                   689 1.R1011
                   uC-zmflb73319d05b1
5'-most EST
```

Seq. No. 259603 692 1.R1011 Contig ID LIB3066-046-Q1-K1-B2 5'-most EST

BLASTX Method g2829863 NCBI GI 545 BLAST score





```
2.0e-55
E value
Match length
                   306
                   55
% identity
NCBI Description
                  (AC002396) Putative peroxidase [Arabidopsis thaliana]
                   259604
Seq. No.
Contig ID
                   692 2.R1011
                   LIB148-045-Q1-E1-F10
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2829863
BLAST score
                   571
                   1.0e-58
E value
Match length
                   198
                   54
% identity
```

NCBI Description (AC002396) Putative peroxidase [Arabidopsis thaliana]

Contig ID 696_1.R1011
5'-most EST LIB3066-042-Q1-K1-H5
Method BLASTN
NCBI GI g4140643
BLAST score 57
E value 4.0e-23
Match length 93

259605

% identity 90

Seq. No.

NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

Seq. No. 259606 Contig ID 697 1.R1011

5'-most EST LIB3066-032-Q1-K1-D4

Method BLASTN
NCBI GI g342659
BLAST score 575
E value 0.0e+00
Match length 1092
% identity 99

NCBI Description Maize (Black Mexican Sweet) mitochondrial 1.9 kb plasmid,

complete

Seq. No. 259607 Contig ID 698 1.R1011

5'-most EST LIB3079-013-Q1-K1-C12

Seq. No. 259608 Contig ID 698_2.R1011

5'-most EST LIB36-014-Q1-E1-F4

 Seq. No.
 259609

 Contig ID
 701_1.R1011

 5'-most EST
 tfd700571578.h1

Method BLASTX
NCBI GI g3775993
BLAST score 1676
E value 0.0e+00
Match length 351
% identity 91





```
NCBI Description (AJ010460) RNA helicase [Arabidopsis thaliana]
                  259610
Seq. No.
                  701 2.R1011
Contig ID
                  LIB3066-055-Q1-K1-A3
5'-most EST
                  BLASTX
Method
                   q3047117
NCBI GI
BLAST score
                   664
                   2.0e-69
E value
Match length
                  175
                   91
% identity
                   (AF058919) similar to ATP-dependent RNA helicases
NCBI Description
                   [Arabidopsis thaliana]
                   259611
Seq. No.
Contig ID
                   704 1.R1011
5'-most EST
                   LIB148-039-Q1-E1-B9
                   259612
Seq. No.
                   707 1.R1011
Contig ID
5'-most EST
                  LIB3060-054-Q1-K1-G2
                   259613
Seq. No.
                   707 2.R1011
Contig ID
                  LIB148-016-Q1-E1-C7
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1197461
BLAST score
                   1025
                   1.0e-112
E value
                   235
Match length
                   79
% identity
NCBI Description
                  (X78819) casein kinase I [Arabidopsis thaliana]
                   259614
Seq. No.
                   707 5.R1011
Contig ID
5'-most EST
                   dyk700104995.h1
                   259615
Seq. No.
                   707 6.R1011
Contig ID
                   clt700046463.f1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g260552
BLAST score
                   40
                   6.0e-13
E value
Match length
                   69
                   46
% identity
NCBI Description
                  Wx (wx-B2) {transposable element Tourist-Zm1} [Zea
                   mays=corn, Transposon Mutant, 150 nt]
                   259616
Seq. No.
Contig ID
                   708 1.R1011
```

Seq. No. 259616 Contig ID 708_1.R1011 5'-most EST dyk700106442.h1

Method BLASTX





```
NCBI GI
                  g4586021
                  1995
BLAST score
                  0.0e + 00
E value
Match length
                   433
                  85
% identity
                   (AC007170) putative cytoplasmic aconitate hydratase
NCBI Description
                   [Arabidopsis thaliana]
                   259618
Seq. No.
                   709 2.R1011
Contig ID
                  LIB3115-013-P1-K1-D11
5'-most EST
Method
                   BLASTX
                   g4586021
NCBI GI
                   522
BLAST score
                   6.0e-53
E value
Match length
                   113
                   84
% identity
                   (AC007170) putative cytoplasmic aconitate hydratase
NCBI Description
                   [Arabidopsis thaliana]
                   259619
Seq. No.
                   709 3.R1011
Contig ID
                   cyk700049351.f1
5'-most EST
                   BLASTX
Method
                   q4586021
NCBI GI
                   1308
BLAST score
                   1.0e-145
E value
Match length
                   314
                   80
% identity
                   (AC007170) putative cytoplasmic aconitate hydratase
NCBI Description
                   [Arabidopsis thaliana]
                   259620
Seq. No.
                   710_1.R1011
Contig ID
                   yyf700350616.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2760830
BLAST score
                   1267
                   1.0e-140
E value
                   306
Match length
                   78
% identity
                   (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
                   259621
Seq. No.
Contig ID
                   711 1.R1011
5'-most EST
                   cjh700194387.h1
Seq. No.
                   259622
                   712 1.R1011
Contig ID
                   LIB3066-033-Q1-K1-A7
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2760326
BLAST score
                   747
```

6.0e-79

354

45

E value Match length

% identity





```
(AC002130) F1N21.11 [Arabidopsis thaliana]
NCBI Description
                  259623
Seq. No.
                  716 1.R1011
Contig ID
                  LIB3066-034-Q1-K1-F8
5'-most EST
                  259624
Seq. No.
                  716 2.R1011
Contig ID
                  LIB148-065-Q1-E1-H7
5'-most EST
                  259625
Seq. No.
                  717 1.R1011
Contig ID
                  LIB3078-025-Q1-K1-E4
5'-most EST
                  BLASTX
Method
                   g4585925
NCBI GI
                   670
BLAST score
                   3.0e-70
E value
Match length
                   216
                   60
% identity
                  (AC007211) unknown protein [Arabidopsis thaliana]
NCBI Description
                   259626
Seq. No.
                   718 1.R1011
Contig ID
                   uwc700152914.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4467126
BLAST score
                   304
                   7.0e-27
E value
                   302
Match length
                   32
% identity
                  (AL035538) guanine nucleotide-exchange protein-like
NCBI Description
                   [Arabidopsis thaliana]
                   259627
Seq. No.
                   718 2.R1011
Contig ID
5'-most EST
                   LIB3062-042-Q1-K1-D6
                   259628
Seq. No.
                   718 3.R1011
Contig ID
                   LIB3088-008-Q1-K1-G8
5'-most EST
Seq. No.
                   259629
                   719 1.R1011
Contig ID
5'-most EST
                   uC-zmroteosinte062h09b1
                   259630
Seq. No.
Contig ID
                   722 1.R1011
                   uC-zmflb73193g02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1076809
                   4123
BLAST score
                   0.0e+00
E value
                   925
Match length
% identity
                   88
                   H+-transporting ATPase (EC 3.6.1.35) - maize
NCBI Description
                   >gi 758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase
```

[Zea mays]





```
Seq. No.
                   722 2.R1011
Contig ID
                  LIB3150-100-P2-K1-A5
5'-most EST
Method
                   BLASTX
                   q3668086
NCBI GI
BLAST score
                   401
                   1.0e-70
E value
                   248
Match length
                   63
% identity
                   (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
                   259632
Seq. No.
                   722 3.R1011
Contig ID
                   LIB3066-018-Q1-K1-A12
5'-most EST
                   BLASTX
Method
                   q1621440
NCBI GI
BLAST score
                   2515
                   0.0e + 00
E value
Match length
                   637
                   76
% identity
                   (U72148) plasma membrane H+-ATPase [Lycopersicon
NCBI Description
                   esculentum]
                   259633
Seq. No.
                   722 4.R1011
Contig ID
                   LIB3156-015-Q1-K1-E3
5'-most EST
                   BLASTX
Method
                   g1076511
NCBI GI
                   433
BLAST score
                   1.0e-42
E value
                   101
Match length
                   86
% identity
                   H+-transporting ATPase (EC 3.6.1.35) - kidney bean
NCBI Description
                   >gi_758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase
                   [Phaseolus vulgaris]
Seq. No.
                   259634
                   722 6.R1011
Contig ID
5'-most EST
                   uC-zmflmo17354f12a1
                   259635
Seq. No.
                   722_7.R1011
Contig ID
                   tzu700201641.hl
5'-most EST
                   BLASTX
Method
                   g1076809
NCBI GI
BLAST score
                   606
                   7.0e-63
E value
                   144
Match length
                   81
 % identity
                   H+-transporting ATPase (EC 3.6.1.35) - maize
NCBI Description
                   >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase
                    [Zea mays]
                   259636
 Seq. No.
 Contig ID
                   722 9.R1011
 5'-most EST
                   uC-zmflmo17073a11b1
```

Seq. No.

259642





```
Seq. No.
                  259637
                  722 13.R1011
Contig ID
5'-most EST
                  LIB3067-005-Q1-K1-B9
Method
                  BLASTN
                  q758354
NCBI GI
                  103
BLAST score
                  1.0e-50
E value
Match length
                  188
                  90
% identity
                  Z.mays mRNA for plasma membrane H+ ATPase
NCBI Description
                  259638
Seq. No.
                  724 1.R1011
Contig ID
5'-most EST
                  LIB3076-001-Q1-K1-F5
Method
                  BLASTX
NCBI GI
                  q445612
BLAST score
                  541
E value
                   4.0e-55
Match length
                  121
% identity
                  85
                  ribosomal protein S19 [Solanum tuberosum]
NCBI Description
                   259639
Seq. No.
                  724_2.R1011
Contig ID
5'-most EST
                  uC-zmroteosinte026d07b1
                  BLASTX
Method
NCBI GI
                  q445612
BLAST score
                   539
E value
                   6.0e-55
Match length
                   119
% identity
NCBI Description ribosomal protein S19 [Solanum tuberosum]
Seq. No.
                   259640
Contiq ID
                   724 3.R1011
                   qw1700616890.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q445612
BLAST score
                   550
E value
                   3.0e-56
Match length
                   121
% identity
                   86
NCBI Description ribosomal protein S19 [Solanum tuberosum]
Seq. No.
                   259641
Contig ID
                   724 4.R1011
5'-most EST
                   LIB3078-017-Q1-K1-H2
                   BLASTX
Method
NCBI GI
                   g445612
BLAST score
                   235
                   2.0e-19
E value
                   51
Match length
                   88
% identity
NCBI Description ribosomal protein S19 [Solanum tuberosum]
```



% identity

NCBI Description



```
724 5.R1011
Contig ID
                   uC-\overline{z}mflmo17265e07b1
5'-most EST
                   BLASTX
Method
                   g445612
NCBI GI
                   465
BLAST score
                   3.0e-46
E value
                   120
Match length
                   80
% identity
                   ribosomal protein S19 [Solanum tuberosum]
NCBI Description
                   259643
Seq. No.
                   724_6.R1011
Contig ID
                   xmt700257140.h1
5'-most EST
                   259644
Seq. No.
                   724 8.R1011
Contig ID
                   uC-zmflb73098c06b1
5'-most EST
Method
                   BLASTX
                   g445612
NCBI GI
BLAST score
                   539
                   6.0e-55
E value
                   119
Match length
                   86
% identity
NCBI Description ribosomal protein S19 [Solanum tuberosum]
                   259645
Seq. No.
Contig ID
                   724 12.R1011
                   pmx700085011.h1
5'-most EST
                   BLASTX
Method
                   g445612
NCBI GI
BLAST score
                   351
                   4.0e-33
E value
Match length
                   84
                   77
% identity
                   ribosomal protein S19 [Solanum tuberosum]
NCBI Description
Seq. No.
                   259646
Contig ID
                   725 1.R1011
                   uC-zmrob73066a10b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2347054
BLAST score
                   968
                   1.0e-105
E value
Match length
                   305
                   62
% identity
                   (X96791) arginine decarboxylase [Vitis vinifera]
NCBI Description
Seq. No.
                   259647
                   727 1.R1011
Contig ID
                   LIB3075-052-Q1-K1-A6
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4454031
                   351
BLAST score
                   1.0e-32
E value
                   200
Match length
```

(AL035394) putative protein [Arabidopsis thaliana]





```
      Seq. No.
      259648

      Contig ID
      729 1.R1011

      5'-most EST
      ymt700222430.h1
```

Seq. No. 259649 Contig ID 730 1.R1011

5'-most EST LIB3075-052-Q1-K1-A9

5'-most EST LIB3075-052-Q1-K1-B10

Method BLASTX
NCBI GI g2384758
BLAST score 1430
E value 1.0e-159
Match length 311
% identity 86

NCBI Description (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza

sativa]

Seq. No. 259651 Contig ID 733 1.R1011

5'-most EST uC-zmflb73011b03b1

Method BLASTX
NCBI GI g400650
BLAST score 156
E value 7.0e-10
Match length 96
% identity 33

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (COMPLEX

I-13KD-B) (CI-13KD-B) (B13) >gi_346535_pir_S28244 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B13 - bovine >gi_238_emb_CAA44903_ (X63218) NADH dehydrogenase

[Bos taurus]

 Seq. No.
 259652

 Contig ID
 733_2.R1011

 5'-most EST
 yyf700350106.h1

Method BLASTX
NCBI GI g233598
BLAST score 156
E value 6.0e-10
Match length 96
% identity 33

NCBI Description 13 kDa-B polypeptide of iron-sulfur protein fraction of

NADH:ubiquinone oxidoreductase [cattle, heart, Peptide

Mitochondrial Partial, 114 aa]

 Seq. No.
 259653

 Contig ID
 733_3.R1011

 5'-most EST
 xsy700208007.h1

Seq. No. 259654 Contig ID 736_1.R1011

5'-most EST LIB3151-030-Q1-K1-H10

Method BLASTX

NCBI GI

BLAST score





```
NCBI GI
                  g3142290
BLAST score
                  1414
                  1.0e-157
E value
Match length
                  528
                  59
% identity
                   (AC002411) Contains similarity to gb Z69902 from C.
NCBI Description
                  elegans. [Arabidopsis thaliana]
                  259655
Seq. No.
                  739 1.R1011
Contig ID
5'-most EST
                  ymt700223049.h1
                  259656
Seq. No.
                  739 2.R1011
Contig ID
                  tzu700205641.h1
5'-most EST
                  259657
Seq. No.
                  744 1.R1011
Contig ID
                  LIB83-002-Q1-E1-G8
5'-most EST
                  BLASTX
Method
                   g1841355
NCBI GI
                   300
BLAST score
                   5.0e-27
E value
                   55
Match length
                   93
% identity
                   (D85381) cytochrome c oxidase subunit Vb precursor [Oryza
NCBI Description
                   sativa]
                   259658
Seq. No.
                   744 2.R1011
Contig ID
                   xjt700095967.h1
5'-most EST
                   BLASTX
Method
                   g1841355
NCBI GI
                   534
BLAST score
                   3.0e-54
E value
                   148
Match length
                   70
% identity
                   (D85381) cytochrome c oxidase subunit Vb precursor [Oryza
NCBI Description
                   sativa]
                   259659
Seq. No.
                   745 1.R1011
Contig ID
                   LIB3075-006-Q1-K1-E12
5'-most EST
Method
                   BLASTN
                   g2062705
NCBI GI
                   38
BLAST score
E value
                   8.0e-12
Match length
                   42
% identity
                   98
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                   259660
Contig ID
                   745 2.R1011
5'-most EST
                   LIB3088-035-Q1-K1-E10
                   BLASTX
Method
```

35897

g4586449

Method

NCBI GI

BLASTX

q587566





```
2.0e-36
E value
                   75
Match length
                   87
% identity
                  (AB025187) cytochrome c oxidase subunit 6b-1 [Oryza sativa]
NCBI Description
                   259661
Seq. No.
                   745 3.R1011
Contig ID
                   LIB3066-055-Q1-K1-F9
5'-most EST
                   259662
Seq. No.
Contig ID
                   749 1.R1011
5'-most EST
                   uC-zmflmo17309f01b1
                   259663
Seq. No.
                   749 2.R1011
Contig ID
                   uC-\overline{z}mflb73318d05b1
5'-most EST
Seq. No.
                   259664
                   750 1.R1011
Contig ID
5'-most EST
                   LIB3066-035-Q1-K1-D8
Method
                   BLASTX
NCBI GI
                   g1330401
BLAST score
                   181
                   3.0e-13
E value
Match length
                   82
                   45
% identity
NCBI Description (U58762) T27F7.1 gene product [Caenorhabditis elegans]
                   259665
Seq. No.
                   752 1.R1011
Contig ID
5'-most EST
                   wyr700240846.hl
                   BLASTX
Method
NCBI GI
                   q4582468
BLAST score
                   995
E value
                   1.0e-108
Match length
                   226
% identity
                   87
                   (AC007071) putative 40S ribosomal protein; contains
NCBI Description
                   C-terminal domain [Arabidopsis thaliana]
Seq. No.
                   259666
                   752 2.R1011
Contig ID
                   LIBT43-014-Q1-E1-G10
5'-most EST
Method
                   BLASTX
                   g4582468
NCBI GI
BLAST score
                   579
E value
                   1.0e-59
                   124
Match length
                   90
% identity
                   (AC007071) putative 40S ribosomal protein; contains
NCBI Description
                   C-terminal domain [Arabidopsis thaliana]
                   259667
Seq. No.
                   753 1.R1011
Contig ID
                   ymt700223038.h1
5'-most EST
```





```
BLAST score
                   1718
E value
                   0.0e+00
Match length
                   487
% identity
                   68
NCBI Description
                  (X80237) mitochondrial processing peptidase [Solanum
                  tuberosum]
Seq. No.
                  259668
Contig ID
5'-most EST
                  uC-zmflmo17054f10b1
                  BLASTX
```

753 2.R1011

Method NCBI GI g587564 BLAST score 285 E value 1.0e-24 Match length 87 % identity 70

NCBI Description (X80235) mitochondrial processing peptidase [Solanum

tuberosum]

Seq. No. 259669 Contig ID 753 3.R1011 5'-most EST tfd700571822.hl

Seq. No. 259670 Contig ID 753 4.R1011

5'-most EST uC-zmroteosinte053b09b2

Method BLASTX NCBI GI g477819 BLAST score 538 E value 1.0e-54Match length 180 % identity 58

NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) beta

chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,

530 aal

Seq. No. 259671 Contig ID 757 1.R1011 5'-most EST

LIB148-040-Q1-E1-F5

Method BLASTX NCBI GI g2980781 BLAST score 308 E value 6.0e-28 Match length 114 % identity 50

NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 259672 Contig ID 760 1.R1011 5'-most EST LIB3075-019-Q1-K1-D2

Seq. No. 259673 763 1.R1011 Contig ID 5'-most EST uC-zmflb73236g04b1

Method BLASTX





NCBI GI g4538911 BLAST score 983 E value 1.0e-107 Match length 315 % identity 62

NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]

 Seq. No.
 259674

 Contig ID
 764_1.R1011

5'-most EST LIB3075-050-Q1-K1-H8

 Seq. No.
 259675

 Contig ID
 766_1.R1011

 5'-most EST
 zuv700353424.h1

 Seq. No.
 259676

 Contig ID
 768 1.R1011

 5'-most EST
 fdz701158380.h1

 Seq. No.
 259677

 Contig ID
 776_1.R1011

 5'-most EST
 hvj700624226.h1

Seq. No. 259678 Contig ID 776_2.R1011

5'-most EST LIB3075-050-Q1-K1-F6

 Seq. No.
 259679

 Contig ID
 777_1.R1011

 5'-most EST
 ntr700076231.h1

Method BLASTX
NCBI GI g113116
BLAST score 1437
E value 1.0e-160
Match length 500
% identity 54

NCBI Description ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME)

>gi_111396_pir__A35007 ATP citrate (pro-S)-lyase (EC
4.1.3.8) - rat >gi_203490 (J05210) ATP citrate-lyase

[Rattus norvegicus]

 Seq. No.
 259680

 Contig ID
 777_2.R1011

 5'-most EST
 wty700165379.h1

Method BLASTX
NCBI GI g3402719
BLAST score 906
E value 6.0e-98
Match length 257
% identity 61

NCBI Description (AC004261) unknown protein [Arabidopsis thaliana]

5'-most EST uC-zmflmo17055d05b1

Seq. No. 259682





```
Contig ID
                   777 4.R1011
5'-most EST
                   uC-zmflb73074e05a1
Method
                   BLASTX
NCBI GI
                   g1749596
BLAST score
                   179
E value
                   5.0e-13
Match length
                   45
% identity
                   69
NCBI Description
                  (D89194) similar to Rat ATP citrate-lyase, SWISS-PROT
                   Accession Number P16638 [Schizosaccharomyces pombe]
Seq. No.
                   259683
                   777 5.R1011
Contig ID
5'-most EST
                   LIB3067-009-Q1-K1-G9
Seq. No.
                   259684
Contig ID
                   777 7.R1011
5'-most EST
                   rvt700550685.h1
Method
                   BLASTX
NCBI GI
                   g603074
BLAST score
                   140
E value
                   8.0e-09
Match length
                   61
% identity
                   51
NCBI Description (U18197) ATP:citrate lyase [Homo sapiens]
Seq. No.
                   259685
Contig ID
                   779 1.R1011
5'-most EST
                  uC-zmrob73049a01a1
Method
                  BLASTX
NCBI GI
                  g2213583
BLAST score
                  540
E value
                  1.0e-54
Match length
                  240
% identity
                   45
NCBI Description (AC000348) T7N9.3 [Arabidopsis thaliana]
Seq. No.
                  259686
Contig ID
                  779 2.R1011
5'-most EST
                  LIB3078-048-Q1-K1-A12
Seq. No.
                  259687
Contig ID
                  779 3.R1011
5'-most EST
                  fdz701167039.h1
Method
                  BLASTX
NCBI GI
                  g266944
BLAST score
                  1276
E value
                  1.0e-141
Match length
                  249
% identity
                  94
NCBI Description 60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2)
                  >gi 71078 pir R5TOL8 ribosomal protein L8, cytosolic -
                  tomato >gi_19343_emb_CAA45863_ (X64562) ribosomal protein
                  L2 [Lycopersicon esculentum]
```

Seq. No. 259688 Contig ID 779_4.R1011

% identity





```
5'-most EST
                   uC-zmflmo17286b03b1
Method
                   BLASTX
NCBI GI
                   q2911068
BLAST score
                   739
E value
                   3.0e-78
Match length
                  145
% identity
NCBI Description (AL021960) G10-like protein [Arabidopsis thaliana]
Seq. No.
                   259689
Contig ID
                  779 5.R1011
5'-most EST
                  fwa700097442.h1
Method
                  BLASTX
NCBI GI
                  g4220532
BLAST score
                  287
E value
                   5.0e-25
Match length
                  273
% identity
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                  259690
Contig ID
                  779 6.R1011
                  LIB3067-025-Q1-K1-D9
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3257978
BLAST score
                  451
E value
                  2.0e-44
Match length
                  229
% identity
                  45
NCBI Description
                  (AP000006) 249aa long hypothetical protein [Pyrococcus
                  horikoshii]
Seq. No.
                  259691
Contig ID
                  779 7.R1011
5'-most EST
                  ymt700220386.h1
Seq. No.
                  259692
Contig ID
                  779 8.R1011
5'-most EST
                  uC-zmflb73093e09b2
Method
                  BLASTX
NCBI GI
                  g2213583
BLAST score
                  496
E value
                  7.0e-50
Match length
                  186
% identity
                  52
NCBI Description (AC000348) T7N9.3 [Arabidopsis thaliana]
Seq. No.
                  259693
Contig ID
                  779 9.R1011
5'-most EST
                  uC-zmflb73262h05a2
Method
                  BLASTX
NCBI GI
                  g4335735
BLAST score
                  678
E value
                  6.0e-71
Match length
                  330
```

35902

NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]

% identity

NCBI Description





```
Seq. No.
                   259694
Contig ID
                   779 10.R1011
5'-most EST
                   uC-zmroteosinte088b11b1
Seq. No.
                   259695
Contig ID
                   779 12.R1011
5'-most EST
                   fdz701164148.h1
Seq. No.
                   259696
Contig ID
                   779 13.R1011
5'-most EST
                   LIB83-014-Q1-E1-B4
Method
                   BLASTX
NCBI GI
                   q2911068
BLAST score
                   744
E value
                   8.0e-79
Match length
                   145
                   87
% identity
NCBI Description
                  (AL021960) G10-like protein [Arabidopsis thaliana]
                   259697
Seq. No.
Contig ID
                   779_14.R1011
5'-most EST
                   pmx700085468.h1
                   259698
Seq. No.
Contig ID
                   779 16.R1011
5'-most EST
                   uC-zmflb73351h04a1
Method
                   BLASTN
NCBI GI
                   g1185553
BLAST score
                   77
E value
                   6.0e-35
Match length
                   134
% identity
                   45
NCBI Description
                 Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)
                   gene, complete cds
Seq. No.
                   259699
                   779 17.R1011
Contig ID
                   ymt700218616.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2911068
BLAST score
                   373
E value
                   1.0e-35
Match length
                  77
% identity
NCBI Description
                 (AL021960) G10-like protein [Arabidopsis thaliana]
Seq. No.
                   259700
                   779 18.R1011
Contig ID
5'-most EST
                  LIB3137-016-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g4406816
BLAST score
                  383
E value
                   6.0e-37
Match length
                  70
```

35903

(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

BLAST score

E value

96

2.0e-46





```
Seq. No.
                   259701
Contig ID
                   779 19.R1011
5'-most EST
                   LIB3156-020-Q1-K1-D3
Method
                   BLASTN
NCBI GI
                   g312178
BLAST score
                   100
E value
                   9.0e-49
Match length
                   139
% identity
                   49
NCBI Description Z.mays GapC2 gene
Seq. No.
                   259702
Contig ID
                   779 20.R1011
5'-most EST
                   LIB3067-045-Q1-K1-B10
Seq. No.
                   259703
                   779 23.R1011
Contig ID
5'-most EST
                   mwy700438737.h1
Method
                   BLASTX
                   g1438881
NCBI GI
BLAST score
                   706
E value
                   1.0e-74
Match length
                   184
% identity
                   68
NCBI Description (U43839) GmCK2p [Glycine max]
                   259704
Seq. No.
Contig ID
                   779 25.R1011
                   LIB3067-057-Q1-K1-B1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g1185553
BLAST score
                   116
E value
                   2.0e-58
Match length
                   144
% identity
                   48
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)
                   gene, complete cds
Seq. No.
                   259705
Contig ID
                   779 27.R1011
5'-most EST
                  uC-zmflmo17382h06a1
Method
                  BLASTN
NCBI GI
                  g312178
BLAST score
                  83
E value
                  1.0e-38
Match length
                  146
% identity
                   46
NCBI Description Z.mays GapC2 gene
                  259706
Seq. No.
Contig ID
                  779 28.R1011
5'-most EST
                  uC-zmflmo17057c02a1
Method
                  BLASTN
NCBI GI
                  g1185553
```

5'-most EST

Method





```
Match length
                   139
% identity
                   49
NCBI Description
                   Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)
                   gene, complete cds
Seq. No.
                   259707
Contig ID
                   779 31.R1011
5'-most EST
                   LIB3075-027-Q1-K1-G12
Method
                   BLASTN
NCBI GI
                   g1185553
BLAST score
                   70
E value
                   6.0e-31
Match length
                   133
% identity
                   44
NCBI Description
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)
                   gene, complete cds
Seq. No.
                   259708
Contig ID
                   779 35.R1011
5'-most EST
                   LIB3067-016-Q1-K1-C5
Method
                   BLASTN
NCBI GI
                   g1185553
BLAST score
                   95
E value
                   5.0e-46
Match length
                   140
% identity
                   58
NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)
                   gene, complete cds
                   259709
Seq. No.
Contig ID
                   779 40.R1011
5'-most EST
                   tzu700202754.h1
Method
                   BLASTX
NCBI GI
                   g2911068
BLAST score
                   273
E value
                   3.0e-24
Match length
                  50
% identity
NCBI Description (AL021960) G10-like protein [Arabidopsis thaliana]
Seq. No.
                   259710
Contig ID
                  780 1.R1011
5'-most EST
                  LIB3066-037-Q1-K1-D11
Method
                  BLASTX
NCBI GI
                  g626029
BLAST score
                  571
E value
                  1.0e-58
Match length
                  134
                  78
% identity
NCBI Description
                  pollen allergen Lol p XI - perennial ryegrass
                  >gi_1582249_prf__2118270A allergen Lol p XI [Lolium
                  perenne]
Seq. No.
                  259711
Contig ID
                  782 1.R1011
```

35905

uC-zmflb73120d09b1

BLASTX





NCBI GI g1730990 BLAST score 220 E value 2.0e-17 Match length 153 % identity 33 NCBI Description HYPOTHETICAL 51.7 KD PROTEIN IN DNAJ-RPSU INTEREGENIC REGION >gi_1303812_dbj_BAA12468_ (D84432) YqeV [Bacillus subtilis] >gi_1890061_dbj_BAA12080_ (D83717) YqeV [Bacillus subtilis] >gi_2634989_emb_CAB14485_ (Z99117) similar to hypothetical proteins [Bacillus subtilis] Seq. No. 259712 Contig ID 785 1.R1011 5'-most EST LIB3150-001-01-N1-A6 Method BLASTX NCBI GI g1710530 BLAST score 575

E value 4.0e-59 Match length 135 80 % identity NCBI Description 60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256

ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein

L27a [Arabidopsis thaliana]

Seq. No. 259713 Contig ID 785 2.R1011

5'-most EST LIB36-022-Q1-E1-A2

Method BLASTN NCBI GI g169818 BLAST score 476 E value 0.0e + 00Match length 617 % identity 95

NCBI Description Rice 25S ribosomal RNA gene

Seq. No. 259714 785 3.R1011 Contig ID

5'-most EST LIB148-059-Q1-E1-A9

Seq. No. 259715 785 4.R1011 Contig ID

5'-most EST LIB3066-005-Q1-K1-A2

Method BLASTX NCBI GI q2245066 BLAST score 1352 E value 1.0e-150 Match length 444% identity 59

NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No. 259716 Contig ID 785 5.R1011

5'-most EST LIB148-043-Q1-E1-D12

Method BLASTN NCBI GI g1314407 BLAST score 146

35906



E value 6.0e-76
Match length 162
% identity 98
NCBI Description Zea may

NCBI Description Zea mays ssp. parviglumis USDA PI 331783 ITS1, 5.8S

ribosomal RNA, ITS2

 Seq. No.
 259717

 Contig ID
 785_6.R1011

 5'-most EST
 cat700021586.r1

Method BLASTX
NCBI GI g3608481
BLAST score 571
E value 1.0e-58
Match length 131
% identity 80

NCBI Description (AF088913) ribosomal protein L27a [Petunia x hybrida]

 Seq. No.
 259718

 Contig ID
 785_7.R1011

 5'-most EST
 xyt700346329.h1

Method BLASTX
NCBI GI g4587563
BLAST score 818
E value 2.0e-87
Match length 201
% identity 79

NCBI Description (AC006550) Similar to gb_U51990 pre-mRNA-splicing factor

hPrp18 from Homo sapiens. ESTs gb_T46391 and gb_AA721815

come from this gene. [Arabidopsis thaliana]

Method BLASTX
NCBI GI g3747050
BLAST score 541
E value 4.0e-55
Match length 106
% identity 100

NCBI Description (AF093540) ribosomal protein L26 [Zea mays]

Seq. No. 259720 Contig ID 785 10.R1011

5'-most EST LIB3076-018-Q1-K1-H8

Method BLASTX
NCBI GI g3747050
BLAST score 375
E value 1.0e-35
Match length 75
% identity 97

NCBI Description (AF093540) ribosomal protein L26 [Zea mays]

 Seq. No.
 259721

 Contig ID
 785_11.R1011

5'-most EST LIB3068-055-Q1-K1-C2

Method BLASTN NCBI GI g169818





```
BLAST score
                      217
    E value
                      1.0e-119
    Match length
                      366
    % identity
                      90
   NCBI Description Rice 25S ribosomal RNA gene
    Seq. No.
                      259722
    Contig ID
                      785_12.R1011
    5'-most EST
                      LIB3059-005-Q1-K1-E6
   Method
                      BLASTX
   NCBI GI
                      g2118425
   BLAST score
                      195
   E value
                      1.0e-14
   Match length
                      57
    % identity
                      67
   NCBI Description
                      subtilisin/chymotrypsin inhibitor - maize
                      >gi_475253_emb_CAA55588_ (X78988) proteinase inhibitor [Zea
                      mays] >gi_475922_emb_CAA49593 (X69972) proteinase
                      inhibitor [Zea mays] >gi 559538 emb CAA57677 (X82187)
                      substilin /chymotrypsin-like inhibitor [Zea mays]
   Seq. No.
                      259723
   Contig ID
                      785_13.R1011
   5'-most EST
                      uC-zmflmo170112e12b1
   Method
                      BLASTX
                      q3608481
   NCBI GI
   BLAST score
                      597
                      9.0e-62
   E value
   Match length
                      140
   % identity
                     (AF088913) ribosomal protein L27a [Petunia x hybrida]
   NCBI Description
   Seq. No.
                      259724
   Contig ID
                      785 14.R1011
   5'-most EST
                      LIB148-015-Q1-E1-A1
   Method
                      BLASTX
   NCBI GI
                      g2245066
   BLAST score
                      685
   E value
                      3.0e-72
   Match length
                      192
   % identity
                      65
   NCBI Description
                      (Z97342) Beta-Amylase [Arabidopsis thaliana]
   Seq. No.
                      259725
   Contig ID
                      785 15.R1011
   5'-most EST
                      LIB148-005-Q1-E1-H3
   Seq. No.
                      259726
                      785 16.R1011
   Contig ID
   5'-most EST
                      uwc700152185.h1
   Method
                      BLASTX
   NCBI GI
                      g3747050
   BLAST score
                      532
   E value
                      2.0e-54
Match length
```

(AF093540) ribosomal protein L26 [Zea mays] 35908

106

98

% identity

NCBI Description





```
Seq. No.
                   259727
Contig ID
                   785 17.R1011
5'-most EST
                   LIB3059-041-Q1-K1-B10
Seq. No.
                   259728
Contig ID
                   785 18.R1011
5'-most EST
                   ceu700434224.h1
Method
                   BLASTN
NCBI GI
                   q1314382
BLAST score
                   136
E value
                   3.0e-70
Match length
                   148
                   98
% identity
NCBI Description Tripsacum laxum de Wet 3766 ITS1, 5.8S ribosomal RNA, ITS2
Seq. No.
                   259729
Contig ID
                   785 19.R1011
5'-most EST
                   LIB3088-044-Q1-K1-B2
Method
                   BLASTN
NCBI GI
                   q3282441
BLAST score
                   157
E value
                   6.0e-83
Match length
                   161
                   99
% identity
NCBI Description
                   Zea perennis internal transcribed spacer 1, 5.8S ribosomal
                   RNA gene, and internal transcribed spacer 2, complete
                   sequence
Seq. No.
                   259730
Contig ID
                   785 20.R1011
5'-most EST
                   LIB3136-044-P1-K1-F8
Seq. No.
                   259731
Contig ID
                   785 21.R1011
5'-most EST
                   LIB3067-051-Q1-K1-D11
Method
                   BLASTX
NCBI GI
                   g1710530
BLAST score
                   538
E value
                   7.0e-55
Match length
                   135
% identity
                   76
NCBI Description
                   60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256
                   ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein
                   L27a [Arabidopsis thaliana]
Seq. No.
                   259732
                   785 22.R1011
Contig ID
5'-most EST
                   LIB148-016-Q1-E1-G11
Method
                   BLASTX
NCBI GI
                   g2245066
BLAST score
                   182
```

BLAST score 182
E value 2.0e-13
Match length 56

Match length 56 % identity 55

NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]





```
Seq. No.
                    259733
Contig ID
                    785 25.R1011
5'-most EST
                    LIB3061-054-Q1-K1-H7
Method
                    BLASTX
NCBI GI
                    g4567226
BLAST score
                    221
E value
                    1.0e-17
                    96
Match length
% identity
                    56
NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]
Seq. No.
                    259734
Contig ID
                    785 26.R1011
5'-most EST
                    LIB3079-014-Q1-K1-H10
Method
                    BLASTN
NCBI GI
                    g169818
BLAST score
                    128
E value
                    2.0e-65
Match length
                    170
% identity
                    95
NCBI Description Rice 25S ribosomal RNA gene
Seq. No.
                    259735
Contig ID
                    785 27.R1011
5'-most EST
                    LIB3150-001-Q1-N1-H5
Method
                    BLASTX
NCBI GI
                    q2118425
BLAST score
                    195
E value
                    6.0e-15
Match length
                    57
% identity
                    67
                    subtilisin/chymotrypsin inhibitor - maize
>gi_475253_emb_CAA55588_ (X78988) proteinase inhibitor [Zea
NCBI Description
                    mays] >gi_475922_emb_CAA49593 (X69972) proteinase inhibitor [Zea mays] >gi_559538_emb_CAA57677 (X82187)
                    substilin /chymotrypsin-like inhibitor [Zea mays]
Seq. No.
                    259736
Contig ID
                    785 29.R1011
5'-most EST
                    LIB3078-002-Q1-K1-C2
Seq. No.
                    259737
Contig ID
                    785 30.R1011
5'-most EST
                    LIB3066-042-Q1-K1-C5
Seq. No.
                    259738
                    785 35.R1011
Contig ID
5'-most EST
                    LIB3118-007-Q1-K1-H3
```

Method BLASTN

NCBI GI g3747049 BLAST score 56 E value 2.0e-22 Match length 100 % identity 89

NCBI Description Zea mays ribosomal protein L26 mRNA, partial cds





Seq. No. 259739

Contig ID 785 36.R1011

5'-most EST LIB3067-034-Q1-K1-H6

Method BLASTX
NCBI GI g3747050
BLAST score 425
E value 8.0e-53
Match length 116
% identity 96

NCBI Description (AF093540) ribosomal protein L26 [Zea mays]

Seq. No. 259740 Contig ID 786 1.R1011

5'-most EST LIB3075-050-Q1-K1-G5

Method BLASTX
NCBI GI g606187
BLAST score 181
E value 3.0e-13
Match length 107
% identity 36

NCBI Description (U18997) ORF_f495; orfF of ECMRED, uses 2nd start

[Escherichia coli] >gi_1789645 (AE000404) bundles of

cytoplasmic filaments [Escherichia coli]

Seq. No. 259741 Contig ID 787 1.R1011

5'-most EST uC-zmflb73318g04b1

Method BLASTX
NCBI GI g730645
BLAST score 687
E value 3.0e-72
Match length 149
% identity 88

NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal

protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_(Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_(Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_(AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb R29788, gb ATTS0365 come from this gene. [Arabidopsis

thaliana]

Seq. No. 259742 Contig ID 787_2.R1011

5'-most EST LIB3117-011-Q1-K1-C6

Method BLASTX
NCBI GI 9730645
BLAST score 687
E value 3.0e-72
Match length 149
% identity 88

NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi 313152 emb CAA80679

(Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs





```
gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis
thaliana]
```

 Seq. No.
 259743

 Contig ID
 787_3.R1011

 5'-most EST
 uwc700150852.h1

 Mathed
 DLAGWY

Method BLASTX
NCBI GI g401043
BLAST score 218
E value 8.0e-20
Match length 65
% identity 91

NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_218131_dbj_BAA01746_ (D10962)

unnamed protein product [Oryza sativa]

5'-most EST LIB3067-052-Q1-K1-D2

Method BLASTX
NCBI GI g401043
BLAST score 305
E value 1.0e-27
Match length 58
% identity 100

NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_218131_dbj_BAA01746_ (D10962)

unnamed protein product [Oryza sativa]

 Seq. No.
 259745

 Contig ID
 787_6.R1011

 5'-most EST
 hvj700622933.h1

Method BLASTX
NCBI GI g730645
BLAST score 296
E value 5.0e-27
Match length 74
% identity 80

NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal

protein S15 - Arabidopsis thaliana >\(\frac{\text{gi}}{3\lambda}\) 3\(\frac{13}{13}\) 152 \(\text{emb}\) CAA80679 (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >\(\text{gi}\) 313188 \(\text{emb}\) CAA80681 (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >\(\text{gi}\) 1903366 \(\text{gb}\) AAB70449 (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs \(\text{gb}\) R29788, \(\text{gb}\) ATTS0365 come from this gene. [Arabidopsis

thaliana]

Method BLASTX
NCBI GI g401043
BLAST score 344
E value 2.0e-32
Match length 67
% identity 99

NCBI Description 40S RIBOSOMAL PROTEIN S15 >gi_218131_dbj_BAA01746_ (D10962)

unnamed protein product [Oryza sativa]





```
Seq. No.
                   259747
Contig ID
                   791 1.R1011
5'-most EST
                  LIB3075-050-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  q3063451
BLAST score
                   287
E value
                   2.0e-25
Match length
                  87
% identity
                   66
NCBI Description
                  (AC003981) F22013.13 [Arabidopsis thaliana]
Seq. No.
                  259748
Contig ID
                  792 1.R1011
5'-most EST
                  nbm700467025.h1
Method
                  BLASTX
NCBI GI
                  q3212869
BLAST score
                  2525
                  0.0e+00
E value
Match length
                  591
% identity
                  78
NCBI Description
                  (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  259749
Contig ID
                  792_5.R1011
5'-most EST
                  rvt700549809.h1
Method
                  BLASTX
                  g3212869
NCBI GI
BLAST score
                  356
E value
                  4.0e-34
Match length
                  98
% identity
                  65
NCBI Description
                  (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  259750
Contig ID
                  793 1.R1011
                  pmx700088648.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2133786
BLAST score
                  194
E value
                  4.0e-14
Match length
                  317
                  29
% identity
NCBI Description
                  NF-180 - sea lamprey >gi_632549 (U19361) NF-180 [Petromyzon
                  marinus]
Seq. No.
                  259751
                  795 1.R1011
Contig ID
5'-most EST
                  LIB143-011-Q1-E1-D8
                  259752
Seq. No.
                  795 2.R1011
Contig ID
5'-most EST
                  vux700162532.h1
```

35913

259753

795 3.R1011

uC-zmflmo17271g10b1

Seq. No. Contig ID

5'-most EST





Seq. No. 259754 Contig ID 799 1.R1011

5'-most EST LIB3279-052-P1-K1-F12

259755 Seq. No. Contig ID 804 1.R1011

5'-most EST uC-zmflb73191a10b1

Seq. No. 259756 805 1.R1011 Contig ID

5'-most EST LIB148-044-Q1-E1-D12

Method BLASTX NCBI GI q2781363 BLAST score 585 E value 4.0e-60 Match length 174 % identity 64

NCBI Description (AC003113) F2401.19 [Arabidopsis thaliana]

Seq. No. 259757 Contig ID 805_2.R1011

5'-most EST LIB3075-004-Q1-K1-F6

Method BLASTX NCBI GI q2781363 BLAST score 310 2.0e-28 E value Match length 83 % identity 67

NCBI Description (AC003113) F2401.19 [Arabidopsis thaliana]

Seq. No. 259758 Contig ID 806_1.R1011 5'-most EST ntr700075325.h1

Method BLASTX NCBI GI q548770 BLAST score 1021 E value 0.0e + 00Match length 390 % identity 95

60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630) NCBI Description

ribosomal protein L3 [Oryza sativa]

259759 Seq. No. Contig ID 806 2.R1011

5'-most EST LIB3150-069-P1-N1-B7

Method BLASTX NCBI GI q548770 BLAST score 668 E value 4.0e-70 Match length 136 92 % identity

60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630) ribosomal protein L3 [Oryza sativa] NCBI Description

Seq. No. 259760





```
Contig ID
                   806 3.R1011
5'-most EST
                  uC-zmflmo17060c02a1
Method
                  BLASTX
NCBI GI
                  q548770
BLAST score
                  828
                   9.0e-89
E value
Match length
                  172
% identity
                   91
NCBI Description
                  60S RIBOSOMAL PROTEIN L3 >gi 481228 pir S38359 ribosomal
                  protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                  ribosomal protein L3 [Oryza sativa]
Seq. No.
                  259761
Contig ID
                  806 4.R1011
5'-most EST
                  LIB3150-108-P2-K1-H11
                  BLASTX
Method
NCBI GI
                  a548770
BLAST score
                  384
E value
                  5.0e-37
Match length
                  77
% identity
                  95
NCBI Description
                  60S RIBOSOMAL PROTEIN L3 >gi_481228 pir S38359 ribosomal
                  protein L3 - rice >gi_303853 dbj BAA02155 (D12630)
                  ribosomal protein L3 [Oryza sativa]
                  259762
Seq. No.
Contig ID
                  806 5.R1011
5'-most EST
                  uC-zmromo17025c05a1
Method
                  BLASTX
NCBI GI
                  q548770
BLAST score
                  414
E value
                  2.0e-40
Match length
                  79
                  99
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
                  protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                  ribosomal protein L3 [Oryza sativa]
Seq. No.
                  259763
Contig ID
                  806 6.R1011
5'-most EST
                  uC-zmflmo17025a05a1
Method
                  BLASTX
NCBI GI
                  g548770
BLAST score
                  406
E value
                  1.0e-39
Match length
                  78
% identity
                  97
NCBI Description
```

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)

ribosomal protein L3 [Oryza sativa]

 Seq. No.
 259764

 Contig ID
 806_9.R1011

5'-most EST LIB3180-019-P2-M1-G8

Method BLASTX NCBI GI g548770 BLAST score 420





```
2.0e-41
E value
Match length
                   95
% identity
                   84
NCBI Description
                  60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
                   protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                   ribosomal protein L3 [Oryza sativa]
                   259765
Seq. No.
Contig ID
                   806_12.R1011
5'-most EST
                   LIB3150-089-P2-K1-G2
Method
                   BLASTX
NCBI GI
                   g548770
BLAST score
                   240
                   5.0e-20
E value
Match length
                   95
% identity
                   53
NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
                   protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                   ribosomal protein L3 [Oryza sativa]
                   259766
Seq. No.
Contig ID
                   806_13.R1011
5'-most EST
                   LIB3150-106-P2-K1-H10
Method
                   BLASTX
NCBI GI
                   q548770
BLAST score
                   193
                   8.0e-15
E value
Match length
                   39
                   97
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__ S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                   ribosomal protein L3 [Oryza sativa]
                   259767
Seq. No.
Contig ID
                   807 1.R1011
5'-most EST
                   LIB3059-055-Q1-K1-G8
Method
                   BLASTX
NCBI GI
                   q3935170
BLAST score
                   1320
E value
                   1.0e-146
Match length
                   439
% identity
                   59
NCBI Description (AC004557) F17L21.13 [Arabidopsis thaliana]
Seq. No.
                   259768
Contig ID
                   807 2.R1011
5'-most EST
                   gct701174368.h1
                   259769
Seq. No.
```

Method BLASTX NCBI GI g4514716





```
357
BLAST score
E value
                   7.0e-34
Match length
                   114
                   56
% identity
NCBI Description
                  (AB017533) EPc [Nicotiana tabacum]
                   259771
Seq. No.
Contig ID
                   810_1.R1011
5'-most EST
                  uC-zmroteosinte053f02b2
                   259772
Seq. No.
Contig ID
                   811 1.R1011
5'-most EST
                  LIB3075-050-Q1-K1-D12
                  259773
Seq. No.
Contig ID
                  812 1.R1011
5'-most EST
                  uC-zmflb73120h06b1
Method
                  BLASTX
                  g2459420
NCBI GI
BLAST score
                   714
E value
                   2.0e-75
```

Match length 97 % identity NCBI Description (AC002332) putative ribosomal protein L17 [Arabidopsis thaliana]

Seq. No. 259774 Contig ID 812 2.R1011 5'-most EST LIB3059-059-Q1-K1-D12

140

Method BLASTX

NCBI GI g2459420 BLAST score 714 2.0e-75 E value Match length 140 97 % identity

NCBI Description (AC002332) putative ribosomal protein L17 [Arabidopsis

thaliana]

Seq. No. 259775 Contig ID 814 1.R1011

5'-most EST uC-zmroteosinte023e04b2

Method BLASTX NCBI GI g4101591 BLAST score 727 E value 7.0e-77Match length 297 % identity 51

NCBI Description (AF005051) aspartyl aminopeptidase [Mus musculus]

Seq. No. 259776 Contig ID 815 1.R1011

5'-most EST LIB3078-055-Q1-K1-D7

Method BLASTX NCBI GI g2330816 BLAST score 258 E value 9.0e-22 Match length 325

35917





% identity 25

NCBI Description (Z98602) hypothetical WW domain-containing protein

[Schizosaccharomyces pombe]

 Seq. No.
 259777

 Contig ID
 815_2.R1011

 5'-most EST
 fwa700100934.h1

Method BLASTX
NCBI GI g1330375
BLAST score 291
E value 1.0e-25
Match length 370
% identity 19

NCBI Description (U58758) similar to rat GAP-associated protein p190

(PIR:A38218) [Caenorhabditis elegans]

Seq. No. 259778 Contig ID 816 1.R1011

5'-most EST uC-zmroteosinte080g10b1

Seq. No. 259779 Contig ID 816 2.R1011

5'-most EST LIB3088-010-Q1-K1-B7

Seq. No. 259780 Contig ID 816 3.R1011

5'-most EST LIB3079-040-Q1-K1-B5

Seq. No. 259781 Contig ID 816 4.R1011

5'-most EST LIB3078-013-Q1-K1-F4

Seq. No. 259782 Contig ID 816 5.R1011

5'-most EST LIB3075-012-Q1-K1-D5

 Seq. No.
 259783

 Contig ID
 816_6.R1011

5'-most EST uC-zmflb73069g09a1

Seq. No. 259784 Contig ID 817_1.R1011

5'-most EST LIB3150-049-Q1-N1-D6 Method BLASTX

NCBI GI g3334245
BLAST score 795
E value 7.0e-85
Match length 176
% identity 81

NCBI Description LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)

(ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi_2909424_emb_CAA12028_ (AJ224520) Glyoxalase I [Cicer

arietinum]





```
5'-most EST
                   LIB3066-054-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                   q3337367
BLAST score
                   310
E value
                   2.0e-28
Match length
                   133
% identity
                   42
NCBI Description
                  (AC004481) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   259786
Contig ID
                  820 1.R1011
5'-most EST
                  vux700159915.h1
Method
                  BLASTN
NCBI GI
                  q3241922
BLAST score
                   47
E value
                   4.0e-17
Match length
                  83
% identity
                   89
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MLM24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  259787
Contig ID
                  820 2.R1011
5'-most EST
                  fdz701160794.h1
Method
                  BLASTN
NCBI GI
                  q3241922
BLAST score
                  51
E value
                  1.0e-19
Match length
                  83
% identity
                  90
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MLM24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  259788
                  821 1.R1011
Contig ID
5'-most EST
                  hbs701182955.h1
Method
                  BLASTX
NCBI GI
                  g2708741
BLAST score
                  886
E value
                  1.0e-95
Match length
                  206
                  78
% identity
NCBI Description
                  (AC003952) hypothetical protein [Arabidopsis thaliana]
                  259789
Seq. No.
                  822 1.R1011
Contig ID
5'-most EST
                  LIB3075-013-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g2832632
BLAST score
                  531
E value
                  4.0e-54
Match length
                  195
% identity
NCBI Description
                  (AL021711) hypothetical protein [Arabidopsis thaliana]
```

35919.

259790

824 1.R1011

Seq. No. Contig ID

5'-most EST





```
5'-most EST
                   uwc700152466.h1
Method
                   BLASTX
NCBI GI
                   q3335375
BLAST score
                   2053
E value
                   0.0e + 00
Match length
                   434
% identity
NCBI Description
                  (AC003028) putative amidase [Arabidopsis thaliana]
Seq. No.
                   259791
Contig ID
                   824 2.R1011
5'-most EST
                   LIB3059-048-Q1-K1-D12
Method
                   BLASTX
NCBI GI
                   q3335375
BLAST score
                   534
E value
                   2.0e-54
Match length
                   124
% identity
NCBI Description (AC003028) putative amidase [Arabidopsis thaliana]
Seq. No.
                   259792
Contig ID
                   828_1.R1011
5'-most EST
                   uC-zmroteosinte023b03b2
Method
                   BLASTX
NCBI GI
                   q4455182
BLAST score
                   1163
E value
                   1.0e-128
Match length
                   275
% identity
NCBI Description (AL035521) putative protein [Arabidopsis thaliana]
Seq. No.
                   259793
                   830 1.R1011
Contig ID
5'-most EST
                   LIB3066-031-Q1-K1-D11
Method
                   BLASTX
NCBI GI
                   q4544464
BLAST score
                   319
E value
                   1.0e-28
Match length
                   388
% identity
                   26
                  (AC006580) putative chloroplast nucleoid DNA binding
NCBI Description
                   protein [Arabidopsis thaliana]
Seq. No.
                   259794
Contig ID
                   831 1.R1011
5'-most EST
                   uC-zmflB73111g08b2
Method
                   BLASTX
NCBI GI
                   q3395439
BLAST score
                   358
E value
                   1.0e-33
Match length
                   220
% identity
                  (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   259795
Contig ID
                   832 1.R1011
```

35920

uC-zmf1mo17023g04b1





```
Method
                  BLASTX
NCBI GI
                  g1173218
BLAST score
                  -647
                  1.0e-67
E value
Match length
                  130
                  96
% identity
                  40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                  259796
Seq. No.
Contig ID
                  832 2.R1011
5'-most EST
                  LIB143-041-Q1-E1-A5
Method
                  BLASTX
NCBI GI
                  q1173218
BLAST score
                  646
E value
                  2.0e-67
Match length
                  130
                  95
% identity
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                  259797
Seq. No.
Contig ID
                  832 4.R1011
5'-most EST
                  tzu700206484.h1
                  BLASTX
Method
                  g133793
NCBI GI
BLAST score
                  460
E value
                  6.0e - 46
Match length
                  89
% identity
                  96
                  40S RIBOSOMAL PROTEIN S15A (PPCB8) >gi 99825 pir S20945
NCBI Description
                  ribosomal protein S15a - rape >gi_17863_emb_CAA42599_
                  (X59983) r-protein BnS15a [Brassica napus]
Seq. No.
                  259798
Contig ID
                  833 1.R1011
5'-most EST
                  xmt700267082.h1
                  BLASTX
Method
NCBI GI
                  g913865
BLAST score
                  3294
E value
                  0.0e+00
Match length
                  649
% identity
                  99
NCBI Description
                  branching enzyme II BEII [Zea mays, cultivar B73,
                  endosperms, Peptide, 738 aa]
Seq. No.
                  259799
                  833 2.R1011
Contig ID
5'-most EST
                  LIB3069-025-Q1-K1-F4
```

Method BLASTX

NCBI GI g2340108 BLAST score 772 E value 3.0e-82 Match length 143 % identity 97





```
NCBI Description
                  (U65948) starch branching enzyme IIa [Zea mays]
                   259800
Seq. No.
Contig ID
                   833 3.R1011
5'-most EST
                  LIB3079-025-Q1-K1-F9
Method
                   BLASTX
NCBI GI
                   q3511236
BLAST score
                   468
E value
                   6.0e-50
Match length
                   129
                   76
% identity
NCBI Description
                  (AF072725) starch branching enzyme IIb [Zea mays]
Seq. No.
                   259801
Contig ID
                  834 1.R1011
5'-most EST
                  LIB3075-030-Q1-K1-A9
                   259802
Seq. No.
Contig ID
                   835 1.R1011
5'-most EST
                   uC-zmflmo17249d02a1
Method
                   BLASTX
NCBI GI
                   g2653558
BLAST score
                   1711
                   0.0e+00
E value
Match length
                   333
% identity
                   96
NCBI Description
                  (D50679) ferredoxin-sulfite reductase precursor [Zea mays]
                   259803
Seq. No.
                   835 2.R1011
Contig ID
5'-most EST
                   hvj700623602.h1
Method
                   BLASTX
NCBI GI
                   q4033424
BLAST score
                   1104
                   1.0e-121
E value
Match length
                   214
% identity
                   100
                  SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
NCBI Description
                   PHOSPHO-HYDROLASE) (PPASE) >gi 2668746 (AF034947) inorganic
                  pyrophosphatase [Zea mays]
Seq. No.
                   259804
Contig ID
                   835 3.R1011
5'-most EST
                   uC-zmflb73071f11b3
Method
                   BLASTX
NCBI GI
                   g4033424
BLAST score
                   708
E value
                   6.0e-75
Match length
                   142
                   97
% identity
NCBI Description
                  SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
                   PHOSPHO-HYDROLASE) (PPASE) >gi 2668746 (AF034947) inorganic
                  pyrophosphatase [Zea mays]
```





Method BLASTX NCBI GI g2653558 BLAST score 1984 E value 0.0e + 00Match length 426 % identity 91 NCBI Description (D50679) ferredoxin-sulfite reductase precursor [Zea mays] Seq. No. 259806 Contig ID 835 5.R1011 5'-most EST xsy700211923.h1 Method BLASTX NCBI GI q4033424 BLAST score 642 E value 3.0e-67 Match length 144 90 % identity NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi 2668746 (AF034947) inorqanic pyrophosphatase [Zea mays] Seq. No. 259807 Contig ID 835 6.R1011 5'-most EST LIB3076-007-Q1-K1-B7 Method BLASTX NCBI GI g4033424 BLAST score 596 E value 1.0e-61 Match length 127 % identity 90 NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi 2668746 (AF034947) inorganic pyrophosphatase [Zea mays] Seq. No. 259808 Contig ID 835 7.R1011 5'-most EST LIB3061-035-Q1-K1-C9 Method BLASTX NCBI GI q4033424 BLAST score 656 E value 7.0e-69 Match length 128 % identity 100 NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi 2668746 (AF034947) inorganic pyrophosphatase [Zea mays] 259809 Seq. No. 835 8.R1011 Contig ID 5'-most EST uC-zmflb73257a10b3 Method BLASTX

NCBI GI g4033424 BLAST score 338 E value 1.0e-54

Match length 113 % identity 97

NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE





PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic pyrophosphatase [Zea mays]

 Seq. No.
 259810

 Contig ID
 836_1.R1011

 5'-most EST
 yyf700351568.h1

 Mathod
 BLASTY

Method BLASTX
NCBI GI g3548818
BLAST score 1023
E value 1.0e-111

Match length 242 % identity 81

NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

5'-most EST LIB3150-032-Q1-N1-E2

Method BLASTX
NCBI GI g3548818
BLAST score 177
E value 1.0e-12
Match length 36

% identity 89

NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 259812 Contig ID 836 4.R1011

5'-most EST LIB3059-058-Q1-K1-C12

Method BLASTX
NCBI GI g3548818
BLAST score 886
E value 9.0e-96
Match length 202

% identity 84

NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 259813
Contig ID 837 1.R1011

5'-most EST LIB3066-012-Q1-K1-B1

Method BLASTN
NCBI GI g2062691
BLAST score 34
E value 2.0e-09
Match length 34
% identity 100

NCBI Description Human sodium phosphate transporter (NPT4) mRNA, complete

cds

Seq. No. 259814 Contig ID 837_2.R1011

5'-most EST LIB3066-015-Q1-K1-B4

95

Method BLASTN
NCBI GI g433043
BLAST score 45
E value 4.0e-16
Match length 57

% identity





```
NCBI Description Zea mays W-22 clone PREM-1E retroelement PREM-1, partial
                  sequence
Seq. No.
                  259815
Contig ID
                  838 1.R1011
5'-most EST
                  LIB3279-007-P1-K1-A1
Method
                  BLASTX
                  g3063706
NCBI GI
BLAST score
                  778
E value
                  2.0e-82
Match length
                  367
% identity
                  59
NCBI Description
                 (AL022537) putative protein [Arabidopsis thaliana]
                  259816
Seq. No.
```

Contig ID 838_2.R1011
5'-most EST LIB3067-037-Q1-K1-H10
Method BLASTX
NCBI GI g3063706
BLAST score 185
E value 2.0e-13

Match length 64 % identity 55

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

NCBI GI g3063706 BLAST score 241 E value 3.0e-20 Match length 99 % identity 45

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 259818 Contig ID 840_1.R1011

5'-most EST uC-zmflb73256d04b1

Method BLASTX
NCBI GI g3281870
BLAST score 571
E value 1.0e-66
Match length 496
% identity 36

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

 Seq. No.
 259819

 Contig ID
 840_3.R1011

 5'-most EST
 ypc700803785.h1

 Seq. No.
 259820

 Contig ID
 841_1.R1011

 5° -most EST LIB $\overline{3}$ 061-040-Q1-K1-D7

Method BLASTX
NCBI GI g3643607
BLAST score 1174

35925





```
E value
                  1.0e-129
Match length
                  266
                  80
% identity
NCBI Description
                  (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                  259821
Contig ID
                  841 2.R1011
5'-most EST
                  uC-zmflMo17005c06b1
Method
                  BLASTX
NCBI GI
                  g3643611
BLAST score
                  286
                  1.0e-25
E value
Match length
                  81
% identity
                  67
                 (AC005395) putative casein kinase [Arabidopsis thaliana]
NCBI Description
                  259822
Seq. No.
                  841 3.R1011
Contig ID
5'-most EST
                  uC-zmflb73277e12b1
Method
                  BLASTX
NCBI GI
                  g3643611
BLAST score
                  693
E value
                  4.0e-73
Match length
                  182
                  71
% identity
                 (AC005395) putative casein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  259823
                  844 1.R1011
Contig ID
5'-most EST
                  LIB3075-050-Q1-K1-A5
Method
                  BLASTX
NCBI GI
                  g4204281
BLAST score
                  188
E value
                  1.0e-13
Match length
                  111
% identity
                  33
NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]
                  259824
Seq. No.
Contig ID
                  845 1.R1011
5'-most EST
                  LIB3075-050-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  g113791
BLAST score
                  147
E value
                  7.0e-09
Match length
                  139
```

% identity 30

NCBI Description GLUCOAMYLASE G1 AND G2 PRECURSOR (GLUCAN

> 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) >gi_67393_pir__ALASGR glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - Aspergillus niger >gi_83649_pir__A29166 glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - Aspergillus awamori >gi_2343_emb_CAA25303 (X00712) preproglucoamylase

G1 [Aspergillus niger] >gi_166505 (K02465) preproglucoamylase G1 [Aspergillus awamori]

>gi_732556_emb_CAA25219 (X00548) glucoamylase G1

[Aspergillus niger]



Seq. No.

259825



```
846_1.R1011
Contig ID
5'-most EST
                  LIB148-061-Q1-E1-B1
Method
                  BLASTX
NCBI GI
                  g4587567
BLAST score
                  173
E value
                  5.0e-12
Match length
                  79
% identity
                  41
NCBI Description (AC006550) F1003.7 [Arabidopsis thaliana]
                  259826
Seq. No.
                  847 1.R1011
Contig ID
5'-most EST
                  LIB189-014-Q1-E1-D4
Method
                  BLASTX
NCBI GI
                  q3355476
BLAST score
                  313
E value
                  1.0e-28
Match length
                  150
% identity
                  39
NCBI Description
                 (AC004218) unknown protein [Arabidopsis thaliana]
                  259827
Seq. No.
Contig ID
                  848 1.R1011
5'-most EST
                  LIB3078-026-Q1-K1-E2
                  259828
Seq. No.
Contig ID
                  851 1.R1011
5'-most EST
                  LIB84-017-Q1-E1-F8
Method
                  BLASTX
                  g4454468
NCBI GI
BLAST score
                  643
E value
                  3.0e-67
Match length
                  190
% identity
                  64
                  (AC006234) putative NADH dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  259829
Contig ID
                  852 1.R1011
5'-most EST
                  wyr700242661.h1
Method
                  BLASTX
NCBI GI
                  g2501449
BLAST score
                  466
E value
                  2.0e-46
Match length
                  97
% identity
                  95
NCBI Description UBIQUITIN-LIKE PROTEIN SMT3 >gi 1668773 emb CAA67922
                  (X99608) ubiquitin-like protein [Oryza sativa]
Seq. No.
                  259830
                  852 2.R1011
Contig ID
5'-most EST
                  LIB3062-025-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  g2501449
BLAST score
                  334
```





```
E value
                    5.0e-31
 Match length
                   83
 % identity
                   81
 NCBI Description
                   UBIQUITIN-LIKE PROTEIN SMT3 >gi_1668773_emb_CAA67922
                    (X99608) ubiquitin-like protein [Oryza sativa]
 Seq. No.
                   259831
 Contig ID
                   852_3.R1011
 5'-most EST
                   pwr700450343.h1
 Method
                   BLASTX
 NCBI GI
                   q2501449
 BLAST score
                   426
 E value
                    9.0e-42
 Match length
                   97
 % identity
                   88
 NCBI Description
                   UBIQUITIN-LIKE PROTEIN SMT3 >gi_1668773 emb CAA67922
                    (X99608) ubiquitin-like protein [Oryza sativa]
 Seq. No.
                   259832
 Contig ID
                   853 1.R1011
 5'-most EST
                   LIB3088-050-Q1-K1-G7
 Method
                   BLASTX
 NCBI GI
                   q4008441
 BLAST score
                   448
E value
                   4.0e-44
 Match length
                   144
 % identity
                    60
                   (AL034488) predicted using Genefinder; cDNA EST yk433c6.3
 NCBI Description
                   comes from this gene; cDNA EST EMBL: D72601 comes from this
                   gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST
                   yk433c6.5 comes from this gene [Caenorhabditis elegans]
 Seq. No.
                   259833
 Contig ID
                   853 2.R1011
 5'-most EST
                   uwc700151076.h1
 Method
                   BLASTX
 NCBI GI
                   q4008441
 BLAST score
                   301
 E value
                   3.0e-27
 Match length
                   96
 % identity
                   58
 NCBI Description
                   (AL034488) predicted using Genefinder; cDNA EST yk433c6.3
                   comes from this gene; cDNA EST EMBL: D72601 comes from this
                   gene; cDNA EST EMBL:D75524 comes from this gene; cDNA EST
                   yk433c6.5 comes from this gene [Caenorhabditis elegans]
                   259834
 Seq. No.
                   855 1.R1011
 Contig ID
                   LIB36-005-Q1-E1-F11
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                   g3834310
```

NCBI GI g3834310
BLAST score 704
E value 3.0e-74
Match length 141
% identity 97

NCBI Description (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb D83004 from Homo sapiens. ESTs gb T88233, gb Z24464,





gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]

Seq. No. 259835 Contig ID 855_2.R1011

5'-most EST uC-zmromo17017a09a1

Method BLASTX
NCBI GI g400515
BLAST score 213
E value 8.0e-17
Match length 79
% identity 48

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE B8 SUBUNIT (COMPLEX I-B8)

(CI-B8) >gi_346540_pir__S28249 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B8 - bovine

>gi_246_emb_CAA44904_ (X63219) NADH dehydrogenase [Bos

taurus]

Seq. No. 259836 Contig ID 855_3.R1011

5'-most EST LIB3059-015-Q1-K1-H4

Method BLASTX
NCBI GI g4507793
BLAST score 464
E value 3.0e-46
Match length 110
% identity 78

NCBI Description ubiquitin-conjugating enzyme E2N (homologous to yeast

UBC13) >gi_2501432_sp_Q16781_UBCC_HUMAN

UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_2146981_pir__JC4894

ubiquitin-conjugating enzyme (EC 6.3.2.-) E2 - human >gi_1181558_dbj_BAA11675_ (D83004) ubiquitin-conjugating

enzyme E2 UbcH-ben [Homo sapiens]

 Seq. No.
 259837

 Contig ID
 855_4.R1011

 5'-most EST
 ypc700798932.h1

Method BLASTX
NCBI GI g3834310
BLAST score 700
E value 1.0e-73
Match length 141
% identity 96

NCBI Description (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD

gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122

come from this gene. [Arabidopsis thaliana]

 Seq. No.
 259838

 Contig ID
 855_5.R1011

 5'-most EST
 zuv700355840.h1

Method BLASTX
NCBI GI g3834310
BLAST score 553
E value 2.0e-56
Match length 148



3

% identity 95

NCBI Description (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464,

gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122

come from this gene. [Arabidopsis thaliana]

Seq. No. 259839 Contig ID 855_8.R1011

5'-most EST uC-zmroteosinte030h04b1

Method BLASTX
NCBI GI g400515
BLAST score 208
E value 2.0e-16
Match length 79
% identity 47

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE B8 SUBUNIT (COMPLEX I-B8)

(CI-B8) >gi_346540_pir_ S28249 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B8 - bovine

>gi_246_emb_CAA44904_ (X63219) NADH dehydrogenase [Bos

taurus]

Seq. No. 259840 Contig ID 855 9.R1011

5'-most EST LIB3150-002-Q1-N1-C12

Method BLASTX
NCBI GI g3834310
BLAST score 514
E value 5.0e-56
Match length 127

% identity 89

NCBI Description (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD

gb_D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464, gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122

come from this gene. [Arabidopsis thaliana]

Seq. No. 259841

Contig ID 855 11.R1011

5'-most EST LIB3067-027-Q1-K1-E11

Seq. No. 259842 Contig ID 855 13.R1011

5'-most EST uC-zmflb73237d10b2

Method BLASTX
NCBI GI g4507793
BLAST score 458
E value 1.0e-45
Match length 102
% identity 83

NCBI Description ubiquitin-conjugating enzyme E2N (homologous to yeast

UBC13) >gi_2501432_sp_Q16781_UBCC_HUMAN

UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_2146981_pir__JC4894

ubiquitin-conjugating enzyme (EC 6.3.2.-) E2 - human >gi_1181558_dbj_BAA11675_ (D83004) ubiquitin-conjugating

enzyme E2 UbcH-ben [Homo sapiens]

Seq. No. 259843

Contig ID

Method

5'-most EST





```
Contig ID
                   856 1.R1011
5'-most EST
                   LIB3067-052-Q1-K1-F2
Seq. No.
                   259844
                   858 1.R1011
Contig ID
                   LIB3075-049-Q1-K1-H1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4538947
BLAST score
                   710
                   4.0e-80
E value
Match length
                   269
% identity
                   58
                  (ALO49483) putative mitochondrial carrier protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   259845
Contig ID
                   862 1.R1011
5'-most EST
                   ntr700073840.h1
                   BLASTX
Method
NCBI GI
                   g2911073
BLAST score
                   1007
E value
                   1.0e-109
Match length
                   318
% identity
                   62
                  (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                   259846
Seq. No.
                   862 3.R1011
Contig ID
5'-most EST
                  LIB3075-004-Q1-K1-E10
Seq. No.
                   259847
Contig ID
                   862 5.R1011
5'-most EST
                   LIB148-030-Q1-E1-B4
Method
                   BLASTX
NCBI GI
                   g2911073
BLAST score
                   311
E value
                   2.0e-28
Match length
                   85
% identity
                  (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                   259848
Seq. No.
                   865 1.R1011
Contig ID
5'-most EST
                   LIB3075-027-Q1-K1-F10
Method
                   BLASTX
NCBI GI
                   q3386614
BLAST score
                   698
                   2.0e-73
E value
Match length
                   180
                   37
% identity
NCBI Description
                  (AC004665) putative transcription factor SF3 [Arabidopsis
                   thaliana]
                   259849
Seq. No.
```

35931

865 2.R1011

BLASTX

LIB3066-005-Q1-K1-A7





g3386614 NCBI GI BLAST score 706 2.0e-74E value Match length 173 71 % identity (AC004665) putative transcription factor SF3 [Arabidopsis NCBI Description thaliana] 259850 Seq. No. 865 3.R1011 Contig ID 5'-most EST ${\tt BLASTX}$ Method NCBI GI g3386614

LIB148-048-Q1-E1-F3

BLAST score 526 E value 1.0e-53 Match length 134 45 % identity

(AC004665) putative transcription factor SF3 [Arabidopsis NCBI Description

thaliana]

259851 Seq. No. Contig ID 865 4.R1011

LIB148-018-Q1-E1-G8 5'-most EST

Method BLASTX NCBI GI g3386614 BLAST score 403 E value 3.0e-39 Match length 112 37 % identity

(AC004665) putative transcription factor SF3 [Arabidopsis NCBI Description

thaliana]

Seq. No. 259852 865 5.R1011 Contig ID

LIB148-014-Q1-E1-H6 5'-most EST

Seq. No. 259853 Contig ID 866_1.R1011

uC-zmflmo17309a11b1 5'-most EST

Method BLASTX NCBI GI q2499488 BLAST score 2653 0.0e+00E value Match length 616 80 % identity

PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE NCBI Description

ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))

(PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)

(PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849)

pyrophosphate-dependent phosphofructokinase alpha subunit

[Ricinus communis]

Seq. No. 259854 Contig ID 866 2.R1011

5'-most EST LIB3079-028-Q1-K1-C4

Method BLASTX NCBI GI g2499488

E value





```
BLAST score
                  249
E value
                  3.0e-21
Match length
                  67
                  67
% identity
NCBI Description
                  PYROPHOSPHATE -- FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
                  ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                   (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                   (PPI-PFK) >gi 483547 emb CAA83682 (Z32849)
                  pyrophosphate-dependent phosphofructokinase alpha subunit
                   [Ricinus communis]
Seq. No.
                  259855
Contig ID
                  866 3.R1011
5'-most EST
                  wyr700242667.h1
Method
                  BLASTX
                  g129881
NCBI GI
BLAST score
                  148
                  4.0e-20
E value
Match length
                  66
                  74
% identity
NCBI Description
                  PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
                  ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                  (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                   (PPI-PFK) >gi_482294_pir_ A36094
                  pyrophosphate--fructose-6-phosphate 1-phosphotransferase
                   (EC 2.7.1.90) alpha chain - potato (cv. Kennebec)
                  >gi 169538 (M55190) pyrophosphate-fructose 6-phosphate
                  1-phosphotransferase alpha-subunit [Solanum tuberosum]
                  259856
Seq. No.
Contig ID
                  866 7.R1011
5'-most EST
                  LIB3059-004-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  q2499488
BLAST score
                  387
E value
                  2.0e-37
Match length
                  124
% identity
                  62
NCBI Description
                  PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
                  ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                   (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                   (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849)
                  pyrophosphate-dependent phosphofructokinase alpha subunit
                   [Ricinus communis]
                  259857
Seq. No.
Contig ID
                  866 8.R1011
5'-most EST
                  afb700381747.hl
Method
                  BLASTX
NCBI GI
                  q3790102
BLAST score
                  420
```

Match length 109
% identity 70
NCBI Description (AF095521) pyrophosphate-dependent phosphofructokinase alpha subunit [Citrus X paradisi]

2.0e-41

NCBI Description





```
259858
Seq. No.
Contig ID
                 * 868 1.R1011
5'-most EST
                   LIB3075-049-Q1-K1-F10
Method
                   BLASTX
                   q2982463
NCBI GI
BLAST score
                   218
E value
                   7.0e-36
Match length
                   124
% identity
                   66
NCBI Description
                  (AL022223) putative protein [Arabidopsis thaliana]
                   259859
Seq. No.
Contig ID
                   871 1.R1011
5'-most EST
                   cyk700051068.fl
Method
                   BLASTX
                   g1657855
NCBI GI
BLAST score
                   704
E value
                   4.0e-74
Match length
                   206
% identity
                   67
NCBI Description
                  (U73216) cold acclimation protein WCOR413 [Triticum
                   aestivum]
                   259860
Seq. No.
Contig ID
                   871 2.R1011
5'-most EST
                   wty700166941.h1
Method
                   BLASTX
NCBI GI
                   g1657855
BLAST score
                   257
E value
                   3.0e-23
Match length
                   100
% identity
                   61
NCBI Description
                  (U73216) cold acclimation protein WCOR413 [Triticum
                   aestivum]
Seq. No.
                   259861
Contig ID
                   871 3.R1011
5'-most EST
                   LIB3069-018-Q1-K1-E4
Method
                   BLASTX
NCBI GI
                   g1657855
BLAST score
                   581
E value
                   1.0e-59
Match length
                   262
% identity
                   50
NCBI Description
                   (U73216) cold acclimation protein WCOR413 [Triticum
                   aestivum]
Seq. No.
                   259862
Contig ID
                   872 1.R1011
5'-most EST
                  LIB3075-049-Q1-K1-F3
Method
                   BLASTX
NCBI GI
                   g3876642
BLAST score
                   217
E value
                   2.0e-17
Match length
                   136
                   35
% identity
```

35934

(Z81526) predicted using Genefinder; cDNA EST EMBL:C09939





comes from this gene; cDNA EST EMBL:C12888 comes from this gene; cDNA EST yk265g7.5 comes from this gene; cDNA EST yk412g10.5 comes from this gene; cDNA EST yk224f7.5 co

Seq. No. 259863 Contig ID 873_1.R1011

5'-most EST LIB3075-046-Q1-K1-F4

Seq. No. 259864 Contig ID 875 1.R1011

5'-most EST LIB3066-025-Q1-K1-H11

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 48

Match length 48 % identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 259865 Contig ID 875 2.R1011

5'-most EST LIB148-005-Q1-E1-D11

Method BLASTX
NCBI GI g1808694
BLAST score 386
E value 4.0e-37
Match length 134

% identity 55

NCBI Description (Y10787) hypothetical protein [Sporobolus stapfianus]

Seq. No. 259866 Contig ID 877_1.R1011

5'-most EST LIB3069-043-Q1-K1-E8

Seq. No. 259867 Contig ID 879_1.R1011

5'-most EST uC-zmflb73346c08a2

Method BLASTX
NCBI GI g3880625
BLAST score 378
E value 1.0e-35
Match length 323
% identity 33

NCBI Description (Z93785) predicted using Genefinder; similar to RNA

recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823 comes from this gene; cDNA EST EMBL:D27559 comes from this

ge

Seq. No. 259868 Contig ID 879_2.R1011

5'-most EST LIB3180-041-P2-M2-E2

Seq. No. 259869 Contig ID 880 1.R1011

5'-most EST LIB3075-019-Q1-K1-G2





```
Seq. No. 259870
Contig ID 881_1.R1011
```

5'-most EST uC-zmflMo17002d03b1 Method BLASTX

Method BLASTX
NCBI GI g541849
BLAST score 863
E value 1.0e-92
Match length 201
% identity 77

NCBI Description anthranilate synthase (EC 4.1.3.27) beta chain -

Arabidopsis thaliana >gi_403434 (L22585) anthranilate

synthase beta subunit [Arabidopsis thaliana]

Seq. No. 259871
Contig ID 881 3.R1011
5'-most EST wty700170315.h1
Mothed BIASTY

Method BLASTX
NCBI GI g541849
BLAST score 322
E value 9.0e-30
Match length 83
% identity 67

NCBI Description anthranilate synthase (EC 4.1.3.27) beta chain -

Arabidopsis thaliana >gi_403434 (L22585) anthranilate

synthase beta subunit [Arabidopsis thaliana]

Seq. No. 259872 Contig ID 883 1.R1011

5'-most EST LIB3066-044-Q1-K1-G3

Method BLASTX
NCBI GI g3355308
BLAST score 167
E value 1.0e-11
Match length 139

% identity 33

NCBI Description (AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]

 Seq. No.
 259873

 Contig ID
 885_1.R1011

 5'-most EST
 xjt700096296.h1

Method BLASTX
NCBI GI g2760839
BLAST score 612
E value 1.0e-63
Match length 206
% identity 58

NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 259874 Contig ID 887_1.R1011

5'-most EST LIB143-060-Q1-E1-E6

Method BLASTX
NCBI GI g2853097
BLAST score 272
E value 1.0e-23
Match length 184
% identity 36

NCBI GI

BLAST score





```
NCBI Description
                  (AL021767) hypothetical protein [Schizosaccharomyces pombe]
                  259875
Seq. No.
                  887 3.R1011
Contig ID
5'-most EST
                  LIB3076-004-Q1-K1-E10
                  BLASTX
Method
                  g2853097
NCBI GI
BLAST score
                  175
                  2.0e-12
E value
                  99
Match length
                  42
% identity
                  (AL021767) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                  259876
Seq. No.
                  889 1.R1011
Contig ID
5'-most EST
                  LIB148-038-Q1-E1-F12
                  259877
Seq. No.
                  889 3.R1011
Contig ID
5'-most EST
                  LIB3075-007-Q1-K1-E4
Seq. No.
                  259878
                  890 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73124a06b1
Method
                  BLASTX
NCBI GI
                  g2407800
                  519
BLAST score
                  1.0e-52
E value
Match length
                  115
                   90
% identity
NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
                  259879
Seq. No.
Contig ID
                  890_3.R1011
                  LIB3279-017-P1-K1-A2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2407800
BLAST score
                   378
E value
                  2.0e-36
Match length
                  89
% identity
                  87
NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
                   259880
Seq. No.
Contig ID
                   890 4.R1011
5'-most EST
                  wty700165036.h1
                   259881
Seq. No.
                  890 5.R1011
Contig ID
5'-most EST
                  xyt700347295.h1
Seq. No.
                   259882
                  890 6.R1011
Contig ID
                  xyt700347163.h1
5'-most EST
                  BLASTX
Method
```

35937

g2407800

149



E value

7.0e-10



```
37
  Match length
                     78
  % identity
  NCBI Description
                    (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
                     259883
  Seq. No.
                    894 1.R1011
  Contig ID
  5'-most EST
                    LIB3136-022-Q1-K1-G4
  Method
                    BLASTX
  NCBI GI
                     g1174780
  BLAST score
                     2092
  E value
                     0.0e+00
  Match length
                     410
                     98
  % identity
                    TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR (ORANGE PERICARP
  NCBI Description
                     2) >gi_320135_pir__PQ0450 tryptophan synthase (EC 4.2.1.20)
                    beta-2 chain precursor - maize (fragment) >gi 168574
                     (M76685) tryptophan synthase beta-subunit [Zea mays]
                     259884
  Seq. No.
  Contig ID
                    895 1.R1011
  5'-most EST
                    LIB3076-031-Q1-K1-D2
  Method
                    BLASTX
NCBI GI
                    -g1154954
  BLAST score
                     451
                    1.0e-44
  E value
  Match length
                    111
                     82
  % identity
  NCBI Description (X94693) histone H2A [Triticum aestivum]
  Seq. No.
                     259885
                     896 1.R1011
  Contig ID
  5'-most EST
                    LIB148-044-Q1-E1-B12
  Seq. No.
                     259886
  Contig ID
                     896 2.R1011
  5'-most EST
                    LIB3075-028-Q1-K1-B11
                     259887
  Seq. No.
                     896 3.R1011
  Contig ID
  5'-most EST
                    LIB3075-049-Q1-K1-C12
  Seq. No.
                     259888
  Contig ID
                     896 4.R1011
  5'-most EST
                    LIB148-051-Q1-E1-E8
  Seq. No.
                     259889
                     896 5.R1011
  Contig ID
                    LIB3066-050-Q1-K1-G3
  5'-most EST
                    BLASTN
  Method
  NCBI GI
                    g2062705
  BLAST score
                     39
  E value
                    1.0e-12
                    39
  Match length
                    100
  % identity
```

35938

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

NCBI Description





```
259890
Seq. No.
                   897 1.R1011
Contig ID
5'-most EST
                   LIB143-057-Q1-E1-F9
                   259891
Seq. No.
                   897 2.R1011
Contig ID
                   uC-zmflmo17070c12b1
5'-most EST
Method
                   BLASTX
NCBI GI
                    q4455800
BLAST score
                    357
E value
                    2.0e-33
Match length
                   145
% identity
                   49
                   (Z97343) unnamed protein product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   259892
                   897 3.R1011
Contig ID
5'-most EST
                   uC-zmflmo17070c12a1
                   259893
Seq. No.
                   898 1.R1011
Contig ID
                   LIB3075-049-Q1-K1-B8
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2833311
                   259
BLAST score
E value
                   3.0e-22
Match length
                   86
                    58
% identity
                   HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III
NCBI Description
                   >gi_630728_pir__S43605 R07E5.13 protein (clone R07E5) -
Caenorhabditis elegans >gi_3878946_emb_CAA83622_ (Z32683)
                   R07E5.13 [Caenorhabditis elegans]
Seq. No.
                   259894
Contig ID
                   898 2.R1011
5'-most EST
                   uC-zmflb73098e07b1
Method
                   BLASTX
NCBI GI
                    q2493650
BLAST score
                   2196
E value
                   0.0e + 00
Match length
                   479
% identity
                    94
                   RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD
NCBI Description
                    CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)
                    >gi_1167858_emb_CAA93139_ (Z68903) chaperonin [Secale
                   cereale]
                   259895
Seq. No.
                   898 4.R1011
Contig ID
                   LIB3136-060-Q1-K1-G3
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4584832
BLAST score
                   171
                   7.0e-12
E value
Match length
                   48
% identity
```

(AL031764) hypothetical protein [Schizosaccharomyces pombe]





```
Seq. No.
                  259896
                  898 5.R1011
Contig ID
5'-most EST
                  ntr700073638.h1
Method
                  BLASTX
NCBI GI
                  q1762130
BLAST score
                  616
                  4.0e-64
E value
                  158
Match length
                  85
% identity
                  (U46136) chaperonin-60 beta subunit [Solanum tuberosum]
NCBI Description
                  259897
Seq. No.
                  898 6.R1011
Contig ID
5'-most EST
                  LIB3069-006-Q1-K1-D4
                  259898
Seq. No.
                  898 7.R1011
Contig ID
                  ymt700218704.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2833311
BLAST score
                  200
                  1.0e-15
E value
                  54
Match length
                  65
% identity
                  HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III
NCBI Description
                  >gi_630728_pir S43605 R07E5.13 protein (clone R07E5) -
                  Caenorhabditis elegans >gi 3878946 emb CAA83622 (Z32683)
                  R07E5.13 [Caenorhabditis elegans]
                  259899
Seq. No.
Contig ID
                  898 9.R1011
                  LIB3076-030-Q1-K1-B1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1762130
BLAST score
                  466
E value
                  1.0e-46
Match length
                  125
                  82
% identity
NCBI Description
                  (U46136) chaperonin-60 beta subunit [Solanum tuberosum]
Seq. No.
                  259900
                  898 11.R1011
Contig ID
5'-most EST
                  LIB3062-057-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g2493650
BLAST score
                  429
E value
                  3.0e-42
Match length
                  87
% identity
NCBI Description
                  RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD
                  CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)
                  >gi_1167858_emb_CAA93139_ (Z68903) chaperonin [Secale
                  cereale]
```

35940

259901

898 12.R1011

Seq. No. Contig ID





```
5'-most EST
                  LIB3088-009-Q1-K1-B12
                  259902
Seq. No.
                  898 13.R1011
Contig ID
5'-most EST
                  uC-zmflm017092c04b1
Method
                  BLASTX
NCBI GI
                  g2493650
BLAST score
                  362
E value
                  6.0e-61
                  135
Match length
                  90
% identity
                  RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD
NCBI Description
                  CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)
                  >gi 1167858 emb CAA93139 (Z68903) chaperonin [Secale
                  cereale]
Seq. No.
                  259903
                  899 1.R1011
Contig ID
5'-most EST
                  LIB3075-049-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  g3548808
BLAST score
                  385
                  3.0e-37
E value
Match length
                  137
% identity
                  53
                  (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
                  259904
Seq. No.
                  900 1.R1011
Contig ID
5'-most EST
                  LIB148-005-Q1-E1-E3
                  259905
Seq. No.
                  904_1.R1011
Contig ID
5'-most EST
                  LIB3075-048-Q1-K1-B5
                  BLASTX
Method
NCBI GI
                  g2781363
BLAST score
                  332
                  1.0e-30
E value
Match length
                  93
% identity
                   66
                  (AC003113) F2401.19 [Arabidopsis thaliana]
NCBI Description
                  259906
Seq. No.
                  905 1.R1011
Contig ID
                  LIB3066-035-Q1-K1-D3
5'-most EST
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                   1.0e-10
Match length
                  36
```

100 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

259907 Seq. No. Contig ID 908 1.R1011

LIB3066-027-Q1-K1-B12 5'-most EST

Method BLASTX





NCBI GI g4406787 BLAST score 337 E value 3.0e-31 Match length 92 % identity 71

NCBI Description (AC006532) NADH dehydrogenase [Arabidopsis thaliana]

Seq. No. 259908 Contig ID 909_1.R1011

5'-most EST LIB3075-048-Q1-K1-H2

Seq. No. 259909 Contig ID 910_1.R1011

5'-most EST uC-zmflb73135f02b2

Method BLASTX
NCBI GI g3334441
BLAST score 227
E value 6.0e-33
Match length 184
% identity 28

NCBI Description HYPOTHETICAL 47.9 KD PROTEIN T517.9 IN CHROMOSOME II

>gi_2642161 (AC003000) hypothetical protein [Arabidopsis

thaliana]

 Seq. No.
 259910

 Contig ID
 910_2.R1011

 5'-most EST
 hvj700619392.h1

Method BLASTX
NCBI GI g3334441
BLAST score 354
E value 2.0e-33
Match length 158
% identity 46

NCBI Description HYPOTHETICAL 47.9 KD PROTEIN T517.9 IN CHROMOSOME II

>gi_2642161 (AC003000) hypothetical protein [Arabidopsis

thaliana]

 Seq. No.
 259911

 Contig ID
 911_1.R1011

 5'-most EST
 uwc700154061.h1

Method BLASTX
NCBI GI g2708314
BLAST score 834
E value 4.0e-89
Match length 453
% identity 30

NCBI Description (AF027727) protein disulfide isomerase RB60 [Chlamydomonas

reinhardtii] >gi_4104541 (AF036939) protein disulfide

isomerase [Chlamydomonas reinhardtii]





Method BLASTX g1076793 NCBI GI BLAST score 762 E value 1.0e-80 Match length 305 78 % identity NCBI Description calmodulin cam2 - maize >gi 747917 emb CAA54583 (X77397) calmodulin [Zea mays] 259914 Seq. No. Contig ID 916 1.R1011 5'-most EST LIB3066-047-Q1-K1-C8 Method BLASTX NCBI GI g3176717 BLAST score 504 E value 1.0e-50 Match length 293 % identity 39 NCBI Description (AC002392) putative pectinesterase [Arabidopsis thaliana] 259915 Seq. No. 922 1.R1011 Contig ID 5'-most EST wyr700241154.h1 Method BLASTX NCBI GI g2281115 BLAST score 2027 E value 0.0e+00Match length 517 76 % identity NCBI Description (AC002330) putative cullin-like 1 protein [Arabidopsis thaliana] 259916 Seq. No. 922_2.R1011 Contig ID 5'-most EST $uC-\overline{z}mflmo17285h03b1$ Method BLASTX NCBI GI g2281115 BLAST score 954 E value 1.0e-103 Match length 299 65 % identity (AC002330) putative cullin-like 1 protein [Arabidopsis NCBI Description thaliana] Seq. No. 259917 Contig ID 922 3.R1011

5'-most EST LIB3182-016-P2-M1-G10

Seq. No. 259918 Contig ID 922 5.R1011 5'-most EST ymt700221852.h1

Method BLASTX NCBI GI q2281115 BLAST score 177 E value 6.0e-13 Match length 45 % identity 76





NCBI Description (AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No. 259919
Contig ID 924_1.R1011
5'-most EST LIB3069-042-Q1-K1-F3

 Seq. No.
 259920

 Contig ID
 924_2.R1011

 5'-most EST
 uC-zmflmo17190b06b1

 Seq. No.
 259923

 Contig ID
 924 5.R1011

 5'-most EST
 LIB143-013-Q1-E1-C5

Seq. No. 259924
Contig ID 926_1.R1011
51_most FST 926_7mf[mo17169]

5'-most EST uC-zmflmo17168h09b1

Method BLASTX
NCBI GI g2760543
BLAST score 1728
E value 0.0e+00
Match length 455
% identity 72

NCBI Description (Z97060) L-galactono-1,4-lactone dehydrogenase [Brassica

oleracea]

Seq. No. 259925 Contig ID 929_1.R1011

5'-most EST LIB3061-035-Q1-K1-H2

Method BLASTX
NCBI GI g3660471
BLAST score 2360
E value 0.0e+00
Match length 592
% identity 85

NCBI Description (AJ001809) succinate dehydrogenase flavoprotein alpha

subunit [Arabidopsis thaliana]

Seq. No. 259926 Contig ID 929_2.R1011

5'-most EST $uC-\overline{z}mflb73077e07b2$

Seq. No. 259927 Contig ID 931_1.R1011

5'-most EST LIB3088-029-Q1-K1-B12

Method BLASTX NCBI GI g3776013 BLAST score 150



8

```
3.0e-09
E value
Match length
                  66
% identity
                  45
                  (AJ010470) RNA helicase [Arabidopsis thaliana]
NCBI Description
                  259928
Seq. No.
                  931 2.R1011
Contig ID
                  ntr700074818.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3776029
BLAST score
                  847
E value
                  2.0e-94
Match length
                  222
% identity
                  81
                  (AJ010476) RNA helicase [Arabidopsis thaliana]
NCBI Description
                  259929
Seq. No.
Contig ID
                  933 1.R1011
                  ntr700071881.h1
5'-most EST
Method
                  BLASTX
                  q1352660
NCBI GI
BLAST score
                  216
E value
                  7.0e-17
Match length
                  137
% identity
                  34
                  COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR
NCBI Description
                  >gi_924850 (U26264) CHOp24 [Cricetulus griseus]
                  259930
Seq. No.
                  933 3.R1011
Contig ID
5'-most EST
                  LIB3061-031-Q1-K1-B3
                  259931
Seq. No.
                  934 1.R1011
Contig ID
5'-most EST
                  LIB3066-027-Q1-K1-G2
Method
                  BLASTX
NCBI GI
                  g3193316
BLAST score
                  250
                  3.0e-28
E value
Match length
                  83
                  78
% identity
                  (AF069299) contains similarity to nucleotide sugar
NCBI Description
                  epimerases [Arabidopsis thaliana]
                  259932
Seq. No.
                  934_2.R1011
Contig ID
```

5'-most EST uC-zmf1B73009c08b1

 Seq. No.
 259933

 Contig ID
 934_4.R1011

 5'-most EST
 wyr700242234.h1

Method BLASTX
NCBI GI g3193316
BLAST score 161
E value 1.0e-19
Match length 108
% identity 60





```
(AF069299) contains similarity to nucleotide sugar
NCBI Description
                  epimerases [Arabidopsis thaliana]
                  259934
Seq. No.
                  934 5.R1011
Contig ID
                  LIB3150-060-Q1-N1-D8
5'-most EST
                  BLASTX
Method
                  g2583123
NCBI GI
BLAST score
                  321
                  2.0e-29
E value
Match length
                  153
                  49
% identity
                  (AC002387) putative nucleotide sugar epimerase [Arabidopsis
NCBI Description
                  thaliana]
                  259935
Seq. No.
Contig ID
                  938 1.R1011
5'-most EST
                  LIB3150-023-Q1-N1-F2
Method
                  BLASTX
NCBI GI
                  g476418
BLAST score
                  560
E value
                  3.0e-57
                  107
Match length
                   96
% identity
NCBI Description cytochrome c - maize
Seq. No.
                  259936
Contig ID
                  938 2.R1011
5'-most EST
                  LIB3062-037-Q1-K1-H8
                  BLASTX
Method
NCBI GI
                  g476418
BLAST score
                   585
                  1.0e-60
E value
Match length
                  111
                   97
% identity
NCBI Description cytochrome c - maize
                   259937
Seq. No.
Contig ID
                   938_3.R1011
                   uC-zmflb73255f01b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q118011
BLAST score
                   502
                   7.0e-51
E value
Match length
                   93
                   98
% identity
NCBI Description
                  CYTOCHROME C >gi_625189_pir__CCRZ cytochrome c - rice
                   >gi_169786 (M63704) cytochrome c [Oryza sativa]
                   >gi_218249_dbj_BAA02159_ (D12634) 'cytochrome C' [Oryza
                   sativa]
                   259938
Seq. No.
```

Seq. No. 259938 Contig ID 939_1.R1011 5'-most EST uC-zmflMo17092g02b1

Method BLASTX
NCBI GI g3204125
BLAST score 269





```
3.0e-23
E value
Match length
                   76
                   66
% identity
                   (AJ006766) putative Pi starvation-induced protein [Cicer
NCBI Description
                   arietinum]
                   259939
Seq. No.
                   941 1.R1011
Contig ID
                   uC-zmflb73015h07b1
5'-most EST
                   BLASTX
Method
                   q1143705
NCBI GI
BLAST score
                   1936
                   0.0e+00
E value
Match length
                   592
% identity
                   37
                  (X89760) Hox2a [Zea mays]
NCBI Description
Seq. No.
                   259940
                   941 2.R1011
Contig ID
                   uC-zmflmo17294c12b1
5'-most EST
Method
                   BLASTX
                   g1143705
NCBI GI
BLAST score
                   1136
                   1.0e-125
E value
Match length
                   226
% identity
                   21
                  (X89760) Hox2a [Zea mays]
NCBI Description
                   259941
Seq. No.
                   941 3.R1011
Contig ID
                   uC-\overline{z}mflMo17086h09b1
5'-most EST
                   BLASTX
Method
                   g2130137
NCBI GI
                   519
BLAST score
E value
                   5.0e-64
                   183
Match length
                   26
% identity
NCBI Description homeotic protein Hox2b - maize >gi_1143707_emb_CAA61910_
                   (X89761) Hox2b [Zea mays]
                   259942
Seq. No.
                   941 4.R1011
Contig ID
5'-most EST
                   pmx700090023.hl
Method
                   BLASTX
                   g1143705
NCBI GI
                   501
BLAST score
                   6.0e-65
E value
Match length
                   169
                   45
% identity
NCBI Description (X89760) Hox2a [Zea mays]
                   259943
Seq. No.
Contig ID
                   943 1.R1011
                   uC-zmflmo17205c01a1
5'-most EST
```

35947

BLASTX

672

g232031

Method

NCBI GI BLAST score





E value 2.0e-70 219 Match length 65 % identity ELONGATION FACTOR 1 BETA' >gi_322851_pir_S29224 translation elongation factor eEF-1 beta' chain - rice NCBI Description >gi 218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa] Seq. No. 259944 Contig ID 943_2.R1011 5'-most EST uC-zmflb73190d07b1 Method BLASTX NCBI GI q466172 BLAST score 963 1.0e-104 E value Match length 203 93 % identity GTP-BINDING PROTEIN YPTM2 >gi 283056 pir B38202 ypt family NCBI Description - maize >gi 287835 emb CAA44919 (X6 $\overline{3}$ 278) yptm2 [Zea mays] Seq. No. 259945 943_3.R1011 Contig ID tzu700203296.h1 5'-most EST BLASTX Method NCBI GI q1370166 446 BLAST score E value 2.0e-44 86 Match length 100 % identity NCBI Description (Z73932) RAB1C [Lotus japonicus] 259946 Seq. No. 943 4.R1011 Contig ID hvj700622817.h1 5'-most EST Method BLASTX NCBI GI q466172 BLAST score 933 1.0e-101 E value Match length 198 % identity GTP-BINDING PROTEIN YPTM2 >gi 283056 pir B38202 ypt family NCBI Description - maize >gi_287835_emb_CAA44919_ (X63278) yptm2 [Zea mays] 259947 Seq. No. Contig ID 943 5.R1011 5'-most EST LIB3068-052-Q1-K1-B11 Method BLASTX NCBI GI g4406807 BLAST score 396 E value

3.0e-38 Match length 101 % identity 76

(AC006201) putative elongation factor beta-1 [Arabidopsis NCBI Description

thaliana]

259948 Seq. No. Contig ID 943 12.R1011

BLAST score

2553





```
5'-most EST
                  wyr700243076.h1
                  BLASTX
Method
                  g2245111
NCBI GI
BLAST score
                  265
                  5.0e-23
E value
                  56
Match length
                  96
% identity
                  (Z97343) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                  259949
Seq. No.
                  943 13.R1011 '
Contig ID
5'-most EST
                  uC-zmflb73266e02a2
                  BLASTX
Method
NCBI GI
                  g466172
                  167
BLAST score
                  1.0e-11
E value
Match length
                  37
                  92
% identity
                  GTP-BINDING PROTEIN YPTM2 >gi 283056 pir B38202 ypt family
NCBI Description
                  - maize >gi 287835 emb CAA44919 (X63278) yptm2 [Zea mays]
Seq. No.
                  259950
                  943 14.R1011
Contig ID
                  LIB3079-011-Q1-K1-G11
5'-most EST
                  BLASTX
Method
                  g1370170
NCBI GI
BLAST score
                  312
E value
                  4.0e-54
                  137
Match length
% identity
                  76
NCBI Description
                  (Z73934) RAB1E [Lotus japonicus]
                  259951
Seq. No.
Contig ID
                  944 1.R1011
5'-most EST
                  qmh700029823.f1
Seq. No.
                  259952
Contig ID
                  944_3.R1011
5'-most EST
                  uC-zmflmo17248h04b1
                   259953
Seq. No.
Contig ID
                   945 1.R1011
5'-most EST
                   zuv700355817.h1
Method
                  BLASTX
NCBI GI
                   q4160280
BLAST score
                   423
E value
                   3.0e-54
Match length
                  138
% identity
NCBI Description (AJ006224) purple acid phosphatase [Ipomoea batatas]
Seq. No.
                  259954
Contig ID
                  946 1.R1011
                  xmt700268176.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g417488
```





E value 0.0e+00 Match length 587 % identity 81

NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE

H) >gi_100452_pir__A40995 starch phosphorylase (EC 2.4.1.1) H - potato >gi_169473 (M69038) alpha-glucan phosphorylase

type H isozyme [Solanum tuberosum]

Seq. No. 259955 Contig ID 947 1.R1011

5'-most EST uC-zmflmo17334a01a1

Method BLASTX
NCBI GI g729774
BLAST score 386
E value 1.0e-36
Match length 235
% identity 42

NCBI Description HEAT SHOCK FACTOR PROTEIN HSF30 (HEAT SHOCK TRANSCRIPTION

FACTOR 30) (HSTF 30) (HEAT STRESS TRANSCRIPTION FACTOR) >gi_100265_pir__S25480 heat shock transcription factor HSF30 - Peruvian tomato >gi_19490_emb_CAA47870_ (X67601) heat stress transcription factor HSF30 [Lycopersicon

peruvianum]

Seq. No. 259956 Contig ID 948 1.R1011

5'-most EST LIB3060-041-Q1-K1-A11

Method BLASTX
NCBI GI g4406759
BLAST score 215
E value 5.0e-17
Match length 124
% identity 39

NCBI Description (AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No. 259957 Contig ID 949_1.R1011

5'-most EST uC-zmflB73044e01b1

Seq. No. 259958 Contig ID 949_2.R1011

5'-most EST uC-zmflMo17062f02b1

Seq. No. 259959 Contig ID 949 3.R1011

5'-most EST uC-zmromo17096a12a1

 Seq. No.
 259960

 Contig ID
 950 1.R1011

5'-most EST LIB3150-091-P1-N1-D6

Method BLASTX
NCBI GI g585338
BLAST score 1137
E value 1.0e-124
Match length 240
% identity 90

NCBI Description ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)





```
>gi_391879_dbj_BAA01181_ (D10335) adenylate kinase-b [Oryza
sativa]
```

Seq. No. 259961 Contig ID 950_2.R1011

5'-most EST LIB3150-042-Q1-N1-G1

Method BLASTX
NCBI GI g585338
BLAST score 482
E value 1.0e-48
Match length 102
% identity 91

NCBI Description ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)

>gi_391879_dbj_BAA01181_ (D10335) adenylate kinase-b [Oryza

sativa]

 Seq. No.
 259962

 Contig ID
 950_4.R1011

 5'-most EST
 tfd700569720.h1

Method BLASTX
NCBI GI g585338
BLAST score 364
E value 6.0e-35
Match length 78

% identity

NCBI Description ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)

>gi 391879 dbj BAA01181_ (D10335) adenylate kinase-b [Oryza

~#** · `

sativa]

87

 Seq. No.
 259963

 Contig ID
 950_6.R1011

 5'-most EST
 rv1700457255.h1

Seq. No. 259964 Contig ID 951_1.R1011

5'-most EST uC-zmflb73304d03b1

Seq. No. 259965 Contig ID 951 2.R1011 5'-most EST xyt700346311.h1

 Seq. No.
 259966

 Contig ID
 951_3.R1011

 5'-most EST
 cjh700193056.h1

 Seq. No.
 259967

 Contig ID
 954_1.R1011

5'-most EST LIB3067-044-Q1-K1-G3

Method BLASTX
NCBI GI 94586449
BLAST score 511
E value 1.0e-51
Match length 169
% identity 62

NCBI Description (AB025187) cytochrome c oxidase subunit 6b-1 [Oryza sativa]

Seq. No. 259968





Contig ID 954 2.R1011 5'-most EST LIB143-054-Q1-E1-H1 Method BLASTX NCBI GI g4586449 BLAST score 558 5.0e-57E value Match length 161 68 % identity (AB025187) cytochrome c oxidase subunit 6b-1 [Oryza sativa] NCBI Description 259969 Seq. No. 955 1.R1011 Contig ID 5'-most EST LIB3075-047-Q1-K1-F12 259970 Seq. No. Contig ID 956 1.R1011 5'-most EST uC-zmroteosinte086e02b1 259971 Seq. No. 957 1.R1011 Contig ID 5'-most EST uC-zmflb73030e12b1Method BLASTX NCBI GI g4585966 BLAST score 1599 E value 1.0e-178 Match length 537 % identity 62 (AC005287) Putative dihyrdolipoamide acetyltransferase NCBI Description [Arabidopsis thaliana] Seq. No. 259972 957 2.R1011 Contig ID 5'-most EST LIB3075-041-Q1-K1-B1 259973 Seq. No. Contig ID 958 1.R1011 5'-most EST LIB3075-048-Q1-K1-G10 Method BLASTX NCBI GI q1947152 BLAST score 156 E value 4.0e-10 Match length 86 % identity 35 (AF000265) Similar to beta transducin [Caenorhabditis NCBI Description elegans]

Seq. No. 259974 Contig ID 958 2.R1011 5'-most EST

uC-zmflb73199f11b1

259975 Seq. No. Contig ID 958 3.R1011

5'-most EST LIB3075-047-Q1-K1-F4

Method BLASTX NCBI GI g3123176 BLAST score 265 E value 1.0e-22



Match length 248 % identity 16

NCBI Description HYPOTHETICAL 43.1 KD TRP-ASP REPEATS CONTAINING PROTEIN K04G11.4 IN CHROMOSOME X >gi 3878300 emb CAB01760 (Z78544) predicted using Genefinder; Similarity to C.elegans Guanine nucleotide binding protein (WP:C14B1.4) [Caenorhabditis

elegans]

Method BLASTX
NCBI GI g1346109
BLAST score 1447
E value 1.0e-168
Match length 334
% identity 87

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

PROTEIN (GPB-LR) (RWD) >gi_540535_dbj_BAA07404_ (D38231)

RWD [Oryza sativa]

Seq. No. 259977 Contig ID 959 2.R1011

5'-most EST LIB3115-016-P1-K1-B1

Method BLASTX
NCBI GI g1346109
BLAST score 426
E value 9.0e-42
Match length 94

% identity 81

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

PROTEIN (GPB-LR) (RWD) >gi 540535_dbj_BAA07404_ (D38231)

RWD [Oryza sativa]

Seq. No. 259978 Contig ID 959_5.R1011

5'-most EST uC-zmflmo17205f09a1

Method BLASTX
NCBI GI g1346109
BLAST score 400
E value 7.0e-39
Match length 85
% identity 82

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

PROTEIN (GPB-LR) (RWD) >gi 540535 dbj BAA07404 (D38231)

RWD [Oryza sativa]

Seq. No. 259979 Contig ID 960_1.R1011

5'-most EST uC-zmrob73004h06b1

Method BLASTX
NCBI GI g3122858
BLAST score 411
E value 5.0e-40
Match length 123
% identity 68

NCBI Description D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR

NCBI GI

E value

BLAST score

Match length

g3128180

2.0e-43

439

107





>gi_2189964_dbj_BAA20405_ (AB003280) Phosphoglycerate

```
dehydrogenase [Arabidopsis thaliana]
                       >gi_2804258_dbj_BAA24440_ (AB010407) phosphoglycerate
                       dehydrogenase [Arabidopsis thaliana]
                       259980
     Seq. No.
     Contig ID
                       961_1.R1011
     5'-most EST
                       xjt700094019.h1
    Method
                       BLASTX
    NCBI GI
                       g3128180
    BLAST score
                       1968
                       0.0e + 00
    E value
    Match length
                       472
     % identity
                       78
    NCBI Description
                       (AC004521) citrate synthetase [Arabidopsis thaliana]
    Seq. No.
                       259981
                       961 2.R1011
     Contig ID
                       uC-zmflmo17150b04b1
     5'-most EST
    Method
                       BLASTX
    NCBI GI
                       g3128180
    BLAST score
                       404
    E value
                       2.0e-39
    Match length
                       100
                       78
     % identity
    NCBI Description
                       (AC004521) citrate synthetase [Arabidopsis thaliana]
                       259982
    Seq. No.
     Contig ID
                       961 3.R1011
     5'-most EST
                       xjt700092812.h1
     Method
                       BLASTX
     NCBI GI
                       g3128180
     BLAST score
                       380
     E value
                       3.0e - 36
     Match length
                       185
     % identity
                       74
                      (AC004521) citrate synthetase [Arabidopsis thaliana]
     NCBI Description
                       259983
     Seq. No.
                       961 5.R1011
     Contig ID
     5'-most EST
                       ymt700218803.h1
     Method
                       BLASTX
     NCBI GI
                       g1556429
     BLAST score
                       165
                       3.0e-11
     E value
     Match length
                       43
     % identity
     NCBI Description (X84226) citrate synthase [Nicotiana tabacum]
     Seq. No.
                       259984
    Contig ID
                       961 6.R1011
     5'-most EST
                       LIB3066-007-Q1-K1-G5
Method
                       BLASTX
```





```
% identity
                  (AC004521) citrate synthetase [Arabidopsis thaliana]
NCBI Description
                  259985
Seq. No.
                  961 7.R1011
Contig ID
5'-most EST
                  uC-zmflmo17194g11a1
Method
                  BLASTX
NCBI GI
                  g1556380
BLAST score
                  148
                  2.0e-09
E value
Match length
                  37
                  76
% identity
                  (X84228) citrate (si)-synthase [Beta vulgaris]
NCBI Description
                  259986
Seq. No.
                  965 1.R1011
Contig ID
                  LIB3066-017-Q1-K1-H10
5'-most EST
                  259987
Seq. No.
                   967 1.R1011
Contig ID
5'-most EST
                  LIB148-038-Q1-E1-E9
                  259988
Seq. No.
                  968 1.R1011
Contig ID
                  LIB3062-057-Q1-K1-F3
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3757522
                   579
BLAST score
                   2.0e-59
E value
                  271
Match length
                   49
% identity
NCBI Description
                  (AC005167) putative splicing factor [Arabidopsis thaliana]
                   259989
Seq. No.
                   968_2.R1011
Contig ID
5'-most EST
                  LIB143-014-Q1-E1-G5
Method
                   BLASTX
NCBI GI
                   q3757522
BLAST score
                   280
                   1.0e-24
E value
Match length
                   77
% identity
                   65
                  (AC005167) putative splicing factor [Arabidopsis thaliana]
NCBI Description
                   259990
Seq. No.
                   968_3.R1011
Contig ID
5'-most EST
                  uC-zmflb73012f10b1
Method
                  BLASTX
NCBI GI
                   q3757522
BLAST score
                   323
E value
                   3.0e-29
Match length
                   151
% identity
                   75
                  (AC005167) putative splicing factor [Arabidopsis thaliana]
NCBI Description
```

35955

259991

968 4.R1011

Seq. No.

Contig ID



uC-zmflMo17085d02b1

Method BLASTX
NCBI GI g3757522
BLAST score 693
E value 1.0e-72
Match length 200
% identity 73

5'-most EST

NCBI Description (AC005167) putative splicing factor [Arabidopsis thaliana]

Seq. No. 259992
Contig ID 968_7.R1011

5'-most EST uC-zmflmo17179e04b1

Method BLASTX
NCBI GI g3757522
BLAST score 318
E value 6.0e-29
Match length 155
% identity 72

NCBI Description (AC005167) putative splicing factor [Arabidopsis thaliana]

Seq. No. 259993
Contig ID 972 1.R1011

5'-most EST LIB148-003-Q1-E1-C10

Method BLASTX
NCBI GI g231509
BLAST score 587
E value 2.0e-60
Match length 129
% identity 87

NCBI Description ACTIN DEPOLYMERIZING FACTOR (ADF) >gi 419809 pir S30935

actin-depolymerizing factor - trumpet lily

>gi_22748_emb_CAA78483_ (Z14110) actin depolymerizing

factor [Lilium longiflorum]

Seq. No. 259994 Contig ID 972 2.R1011

5'-most EST LIB3075-007-Q1-K1-D10

Method BLASTX
NCBI GI g231509
BLAST score 585
E value 4.0e-60
Match length 134
% identity 81

NCBI Description ACTIN DEPOLYMERIZING FACTOR (ADF) >gi 419809 pir S30935

actin-depolymerizing factor - trumpet lily

>gi_22748_emb_CAA78483_ (Z14110) actin depolymerizing

factor [Lilium longiflorum]

 Seq. No.
 259995

 Contig ID
 972_3.R1011

5'-most EST LIB148-035-Q1-E1-D6

Method BLASTX
NCBI GI g1168345
BLAST score 643
E value 5.0e-67
Match length 138
% identity 91





```
NCBI Description ACTIN DEPOLYMERIZING FACTOR (ADF) >gi 929918 emb CAA56786
                   (X80820) actin-depolymerizing factor [Zea mays]
                  259996
Seq. No.
Contig ID
                  972 4.R1011
5'-most EST
                  LIB3066-014-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  g231509
BLAST score
                  407
E value
                  4.0e-55
                  132
Match length
                  84
% identity
NCBI Description
                  ACTIN DEPOLYMERIZING FACTOR (ADF) >gi 419809 pir $30935
                  actin-depolymerizing factor - trumpet lily
                  >gi 22748_emb_CAA78483_ (Z14110) actin depolymerizing
                  factor [Lilium longiflorum]
                  259997
Seq. No.
Contig ID
                  972 5.R1011
5'-most EST
                  LIB148-013-Q1-E1-H8
Method
                  BLASTX
NCBI GI
                  g1419368
BLAST score
                  653
                  1.0e-68
E value
Match length
                  126
% identity
                  98
NCBI Description
                  (X97725) actin depolymerizing factor [Zea mays]
                  259998
Seq. No.
                  973 1.R1011
Contig ID
5'-most EST
                  wyr700236001.hl
Method
                  BLASTX
NCBI GI
                  q4646233
BLAST score
                  589
                  2.0e-60
E value
Match length
                  289
% identity
                  47
NCBI Description
                  (AC007266) putative G9a protein [Arabidopsis thaliana]
Seq. No.
                  259999
Contig ID
                  975 1.R1011
5'-most EST
                  LIB3075-047-Q1-K1-E2
Seq. No.
                  260000
                  977 1.R1011
Contig ID
5'-most EST
                  LIB3075-047-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  g4559388
```

Method BLASTX
NCBI GI 94559388
BLAST score 289
E value 5.0e-26
Match length 89

% identity 60

NCBI Description (AC006526) hypothetical protein [Arabidopsis thaliana]

Seq. No. 260001 Contig ID 979_1.R1011

5'-most EST LIB3075-047-Q1-K1-B3



Method BLASTX
NCBI GI g728867
BLAST score 220
E value 6.0e-18
Match length 81
% identity 52

NCBI Description ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR >gi 99694 pir S21961 proline-rich protein APG -

Arabidopsis thaliana >gi_22599_emb_CAA42925_ (X60377) APG

[Arabidopsis thaliana]

 Seq. No.
 260002

 Contig ID
 980_1.R1011

5'-most EST LIB3075-047-Q1-K1-B4

Seq. No. 260003 Contig ID 982 1.R1011

5'-most EST LIB3075-047-Q1-K1-B6

Method BLASTX
NCBI GI g2138180
BLAST score 144
E value 6.0e-09
Match length 102

Match length 102 % identity 39

NCBI Description (U69108) TNF receptor associated factor 5 [Homo sapiens]

Seq. No. 260004 Contig ID 983_1.R1011

5'-most EST LIB189-026-Q1-E1-E12

Method BLASTX
NCBI GI g3341697
BLAST score 822
E value 9.0e-88
Match length 264
% identity 61

NCBI Description (AC003672) hypothetical protein [Arabidopsis thaliana]

Seq. No. 260005 Contig ID 984 1.R1011

5'-most EST LIB3075-047-Q1-K1-B8

Method BLASTX
NCBI GI g3249086
BLAST score 495
E value 6.0e-50
Match length 146
% identity 71

NCBI Description (AC004473) Contains similarity to 21 KD subunit of the

Arp2/3 protein complex (ARC21) gb_AF006086 from Homo sapiens. EST gb_Z37222 comes [Arabidopsis thaliana]

Seq. No. 260006 Contig ID 985_1.R1011

5'-most EST LIB3070-013-Q1-N1-A8

 Seq. No.
 260007

 Contig ID
 985_2.R1011

 5'-most EST
 xyt700344935.h1



```
260008
Seq. No.
Contig ID
                  987 1.R1011
5'-most EST
                  hvj700624679.h1
Method
                  BLASTX
                  g2118423
NCBI GI
BLAST score
                  592
                  4.0e-61
E value
                  134
Match length
                  87
% identity
                  cystatin - maize >gi_1498133_dbj_BAA09666_ (D63342)
NCBI Description
                  cysteine proteinase inhibitor [Zea mays]
                  260009
Seq. No.
                  987 2.R1011
Contig ID
                  wyr700244310.hl
```

5'-most EST BLASTX Method NCBI GI g399334 BLAST score 528 E value 1.0e-53Match length 111 % identity 94

NCBI Description

CYSTATIN I PRECURSOR (CORN KERNEL CYSTEINE PROTEINASE INHIBITOR) >gi_322868_pir__S27239 cysteine proteinase inhibitor - maize >gi_217962_dbj_BAA01472_ (D10622) corn

cystatin I [Zea mays]

260010 Seq. No. Contig ID 987 3.R1011

5'-most EST LIB3137-018-Q1-K1-D6

BLASTX Method NCBI GI g399334 BLAST score 465 1.0e-46 E value Match length 116 % identity 81

NCBI Description CYSTATIN I PRECURSOR (CORN KERNEL CYSTEINE PROTEINASE

cystatin I [Zea mays]

Seq. No. 260011 Contig ID 987 4.R1011 5'-most EST yd1700405449.h1

Method BLASTX NCBI GI q399334 BLAST score 338 E value 2.0e-31 Match length 68 % identity

NCBI Description CYSTATIN I PRECURSOR (CORN KERNEL CYSTEINE PROTEINASE

> INHIBITOR) >gi_322868_pir__S27239 cysteine proteinase inhibitor - maize >gi_217962_dbj_BAA01472_ (D10622) corn

cystatin I [Zea mays]

260012 Seq. No. Contig ID 992 1.R1011



5

```
LIB3075-046-Q1-K1-H5
5'-most EST
                  BLASTX
Method
                  g4567247
NCBI GI
                  847
BLAST score
                  6.0e-91
E value
Match length
                  246
                  67
% identity
                  (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
                  260013
Seq. No.
                  992 3.R1011
Contig ID
                  wyr700238512.h1
5'-most EST
                  BLASTX
Method
                  g4567247
NCBI GI
                  150
BLAST score
                  6.0e-10
E value
Match length
                  57
                  54
% identity
                  (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
                  260014
Seq. No.
                  993 1.R1011
Contig ID
                  LIB143-002-Q1-E1-H4
5'-most EST
                  BLASTX
Method
                  g1351856
NCBI GI
                  4159
BLAST score
                  0.0e + 00
E value
Match length
                  894
                   88
% identity
NCBI Description ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
                   (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase
                   [Cucurbita sp.]
                   260015
Seq. No.
                   993_2.R1011
Contig ID
5'-most EST
                   uC-zmflmo17175d01b1
Method
                   BLASTX
NCBI GI
                   q1169238
BLAST score
                   2027
                   0.0e + 00
E value
                   493
Match length
                   77
% identity
NCBI Description GLUTAMATE DECARBOXYLASE (GAD) >gi_1076648_pir__A48767
                   glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding -
                   garden petunia >gi_294112 (L16797) glutamate decarboxylase
                   [Petunia hybrida] >gi_309680 (L16977) glutamate
                   decarboxylase [Petunia hybrida]
Seq. No.
                   260016
                   993 3.R1011
Contig ID
                   uC-zmflB73106a07b1
5'-most EST
```

Match length 754 % identity 76





NCBI Description ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase [Cucurbita sp.] 260017 Seq. No. 993 4.R1011 Contig ID uC-zmflmo17131f10b1 5'-most EST BLASTX Method g2494174 NCBI GI BLAST score 686 3.0e-72 E value Match length 144 91 % identity NCBI Description GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi_497979 (U10034) glutamate decarboxylase [Arabidopsis thaliana] Seq. No. 260018 993 5.R1011 Contig ID uC-zmflmo17072h05b1 5'-most EST BLASTX Method g4586021 NCBI GI BLAST score 774 3.0e-82 E value 191 Match length 74 % identity (AC007170) putative cytoplasmic aconitate hydratase NCBI Description [Arabidopsis thaliana] 260019 Seq. No. 993 7.R1011 Contig ID LIB143-004-Q1-E1-D2 5'-most EST BLASTX Method g4455220 NCBI GI BLAST score 338 E value 1.0e-31 Match length 71 % identity 86 NCBI Description (AL035440) putative aconitase [Arabidopsis thaliana]

260020 Seq. No.

993 11.R1011 Contig ID 5'-most EST cyk700048870.f1

Method BLASTX NCBI GI q3309243 BLAST score 799 E value 2.0e-85 Match length 247 % identity 67

NCBI Description (AF073507) aconitase-iron regulated protein 1 [Citrus

limon]

Seq. No. 260021

993 18.R1011 Contig ID

uC-zmflmo17057h03a1 5'-most EST

260022 Seq. No.

993 22.R1011 Contig ID





```
5'-most EST
                  LIB143-060-Q1-E1-H12
                  BLASTX
Method
                  q4586021
NCBI GI
                  171
BLAST score
                  4.0e-12
E value
Match length
                  43
                  79
% identity
                   (AC007170) putative cytoplasmic aconitate hydratase
NCBI Description
                   [Arabidopsis thaliana]
                  260023
Seq. No.
                  993 23.R1011
Contig ID
                   fdz701161794.h1
5'-most EST
                  BLASTX
Method
                  g3121731
NCBI GI
                  195
BLAST score
                   4.0e-17
E value
Match length
                  64
                   60
% identity
                  ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
NCBI Description
                   (ACONITASE) > gi_2145473 \text{ emb } CAA65735  (X97012) \text{ aconitate}
                  hydratase [Solanum tuberosum]
                   260024
Seq. No.
                   994 1.R1011
Contig ID
5'-most EST
                  LIB3060-022-Q1-K1-H7
Method
                   BLASTX
NCBI GI
                   g1706260
BLAST score
                   1753
                   0.0e + 00
E value
Match length
                   371
                   91
% identity
                  CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597
NCBI Description
                   cysteine proteinase 1 precursor - maize
                  >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                  mays]
                   260025
Seq. No.
Contig ID
                   994 2.R1011
                  LIB3062-032-Q1-K1-H2
5'-most EST
Method
                  BLASTX
NCBI GI
                   q1352200
BLAST score
                   1586
                   1.0e-177
E value
Match length
                   357
% identity
NCBI Description
                  CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)
                   >gi_480909_pir__S37497 triose
                   phosphate/3-phosphoglycerate/phosphate translocator - maize
                   >gi_405635_emb_CAA81349_ (Z26595) triose
                   phosphate/phosphate translocator [Zea mays]
                   260026
```

 Seq. No.
 260026

 Contig ID
 994_3.R1011

 5'-most EST
 xsy700210614.h1

 Method
 BLASTX

 NCBI GI
 q3914685



BLAST score 878 E value 1.0e-94 Match length 171 % identity 99 60S RIBOSOMAL PROTEIN L17 >gi 2668748 (AF034948) ribosomal NCBI Description protein L17 [Zea mays] 260027 Seq. No. Contig ID 994 4.R1011 LIB3078-007-Q1-K1-H9 5'-most EST Method BLASTX NCBI GI q729478 BLAST score 1217 1.0e-134 E value Match length 276 82 % identity FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) NCBI Description >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+ reductase [Oryza sativa] 260028 Seq. No. 994 5.R1011 Contig ID 5'-most EST LIB3067-026-Q1-K1-H6 Method BLASTX NCBI GI g3914685 * BLAST score 886 1.0e-95 E value Match length 171 100 % identity NCBI Description 60S RIBOSOMAL PROTEIN L17 >gi 2668748 (AF034948) ribosomal protein L17 [Zea mays]

Seq. No. 260029 Contig ID 994 6.R1011

5'-most EST uC-zmflB73021a10b1

Method BLASTX NCBI GI q729478 BLAST score 331 E value 4.0e-36 Match length 95 % identity 87

FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) NCBI Description

>gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+

reductase [Oryza sativa]

Seq. No. 260030 994 7.R1011 Contig ID

5'-most EST fC-zmle700441928a1

BLASTX Method NCBI GI q729478 BLAST score 624 E value 7.0e-65 Match length 142 85 % identity

FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) NCBI Description

>gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+

reductase [Oryza sativa]



260031 Seq. No. Contig ID 994 8.R1011

5'-most EST uC-zmflmo17157f06a1

260032

Method BLASTN NCBI GI q405634 BLAST score 119 E value 3.0e-60 Match length 131 % identity 98

NCBI Description Z.mays zmcpt mRNA triose phosphate/phosphate translocator

Seq. No. Contig ID 994_9.R1011 xtj700377607.h1 5'-most EST Method BLASTX NCBI GI q1352200 BLAST score 235

E value 2.0e-19 Match length 62 % identity 81

NCBI Description CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)

>gi_480909_pir__S37497 triose

phosphate/3-phosphoglycerate/phosphate translocator - maize

>gi_405635_emb_CAA81349_ (Z26595) triose phosphate/phosphate translocator [Zea mays]

Seq. No. 260033 Contig ID 994 10.R1011

5'-most EST uC-zmflmo17330d01a1

Method BLASTX NCBI GI g1706260 BLAST score 171 E value 4.0e-12 Match length 38 % identity 87

NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597

cysteine proteinase 1 precursor - maize

>gi 643597 dbj BAA08244 (D45402) cysteine proteinase [Zea

mays]

260034 Seq. No.

Contig ID 994 12.R1011 5'-most EST pmx700088785.h1

Method BLASTX NCBI GI q729478 BLAST score 272 E value 4.0e-24 Match length 54 % identity 91

NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)

>gi_442481 dbj BAA04616 (D17790) ferredoxin-NADP+

reductase [Oryza sativa]

Seq. No. 260035

Contig ID 994 13.R1011

5'-most EST LIB3060-010-Q1-K1-C7



Method BLASTX NCBI GI q729477 BLAST score 440 E value 2.0e-43Match length 119 % identity 71

FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) NCBI Description

>gi_320548_pir_A44974 ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - common ice plant >gi 167256 (M25528) ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1) [Mesembryanthemum crystallinum] >gi_226768_prf__1604475A ferredoxin NADP reductase [Mesembryanthemum crystallinum]

260036 Seq. No. Contig ID 994 15.R1011 5'-most EST LIB3078-008-Q1-K1-G10 Method BLASTN

g405634 NCBI GI BLAST score 358 E value 0.0e+00398

Match length 98 % identity

NCBI Description Z.mays zmcpt mRNA triose phosphate/phosphate translocator

Seq. No. 260037 994 22.R1011 Contig ID

5'-most EST LIB36-007-Q1-E1-B1

Method BLASTX NCBI GI q1352200 BLAST score 583 3.0e-60

E value Match length 119 98 % identity

NCBI Description CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT)

>gi_480909_pir__S37497 triose
phosphate/3-phosphoglycerate/phosphate translocator - maize

>gi_405635_emb_CAA81349_ (Z26595) triose phosphate/phosphate translocator [Zea mays]

260038 Seq. No.

Contig ID 994 27.R1011 ymt700224661.h1 5'-most EST

Method BLASTX NCBI GI g3914685 BLAST score 191 E value 2.0e-14 Match length 42 % identity 86

NCBI Description 60S RIBOSOMAL PROTEIN L17 >gi 2668748 (AF034948) ribosomal

protein L17 [Zea mays]

Seq. No. 260039 995 1.R1011 Contig ID

5'-most EST LIB148-014-Q1-E1-D7

Seq. No. 260040 Contig ID 996 1.R1011



5'-most EST uC-zmflmo17236a04b1
Method BLASTX

NCBI GI g3551425
BLAST score 174
E value 7.0e-12
Match length 184

% identity 34
NCBI Description (AB015291) pyrrolidone carboxyl peptidase [Pyrococcus

furiosus]

Seq. No. 260041 Contig ID 997_1.R1011

5'-most EST uC-zmroteosinte103e06b2

 Seq. No.
 260042

 Contig ID
 997_2.R1011

 5'-most EST
 ntr700076088.h1

Method BLASTX
NCBI GI g913248
BLAST score 167
E value 4.0e-11
Match length 226
% identity 29

NCBI Description (S76155) leucine-rich motif (LRR) protein homology to

interleukin 1 receptor cytoplasmic domain=tlr [Drosophila melanogaster=fruit flies, Peptide, 1385 aa] [Drosophila

melanogaster]

Seq. No. 260043 Contig ID 998_1.R1011

5'-most EST LIB3075-013-Q1-K1-D3

Seq. No. 260044 Contig ID 999 1.R1011

5'-most EST LIB3075-015-Q1-K1-H7

Method BLASTX
NCBI GI g2398679
BLAST score 997
E value 1.0e-129
Match length 279
% identity 82

NCBI Description (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate

synthase [Morinda citrifolia]

Method BLASTX
NCBI GI g4567207
BLAST score 319

BLAST score 319
E value 2.0e-29
Match length 104
% identity 53

NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]

Seq. No. 260046

Contig ID 1003 1.R1011



5'-most EST uC-zmflmo17321h09b1

Method BLASTX
NCBI GI g1086252
BLAST score 690
E value 3.0e-72
Match length 240
% identity 55

NCBI Description sucrose cleavage protein - Potato >gi_707001_bbs_157931

(S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa]

[Solanum tuberosum]

Seq. No. 260047

Contig ID 1003_2.R1011 5'-most EST cyk700048820.f1

Method BLASTX
NCBI GI g1086252
BLAST score 318
E value 2.0e-38
Match length 169
% identity 50

NCBI Description sucrose cleavage protein - Potato >gi_707001_bbs_157931

(S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa]

[Solanum tuberosum]

Seq. No. 260048

Contig ID 1005 1.R1011

5'-most EST LIB3075-047-Q1-K1-A9

Method BLASTX
NCBI GI g3123261
BLAST score 235
E value 3.0e-19
Match length 226
% identity 29

NCBI Description MEIOTIC RECOMBINATION PROTEIN REC12

>gi 2370483_emb_CAB11511_ (Z98849) meiotic recombination

protein [Schizosaccharomyces pombe]

Seq. No. 260049

Contig ID 1007_1.R1011

5'-most EST LIB83-015-Q1-E1-H4

Method BLASTX
NCBI GI g2213602
BLAST score 211
E value 3.0e-16
Match length 273
% identity 38

NCBI Description (AC000348) T7N9.22 [Arabidopsis thaliana]

Seq. No. 260050

Contig ID 1008 1.R1011

5'-most EST uC-zmflmo17184g05b1

Seq. No. 260051

Contig ID 1008 2.R1011

5'-most EST uC-zmroteosinte032h10b1



260052 Seq. No.

1008 3.R1011 Contig ID

LIB3151-061-Q1-K1-G8 5'-most EST

260053 Seq. No.

1008 5.R1011 Contig ID wty700170261.hl 5'-most EST

260054 Seq. No.

1010 1.R1011 Contig ID

LIB84-026-Q1-E1-A9 5'-most EST

BLASTXMethod g417103 NCBI GI BLAST score 679 E value 2.0e-71 136 Match length 100 % identity

HISTONE H3.2, MINOR >gi 282871 pir S24346 histone NCBI Description

H3.3-like protein - Arabidopsis thaliana

>gi 16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] $>gi_488577$ (U09465) histone H3.2

[Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1 $\overline{4}$ 351 $\overline{5}$ 7_emb_CA \overline{A} 58445_ (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum]

>gi 2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AFO93633) histone H3 [Oryza sativa] >gi 4038469 gb AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_

(AL035708) Histon H3 [Arabidopsis thaliana]

260055 Seq. No.

1010 2.R1011 Contig ID

5'-most EST LIB3151-020-Q1-K1-G7

BLASTX Method g417103 NCBI GI BLAST score 679 3.0e-71E value Match length 136 100 % identity NCBI Description

HISTONE H3.2, MINOR >gi_282871_pir__\$24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] $>gi_488567$ ($\overline{U}09460$) histone H3.2 [Medicago sativa] >gi 488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911 emb_CAA56153_ (X79714) histone



H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

```
260056
Seq. No.
                   1013 1.R1011
Contig ID
                   LIB3\overline{1}36-060-Q1-K1-B5
5'-most EST
                   BLASTX
Method
                   q1001309
NCBI GI
BLAST score
                   498
                   1.0e-49
E value
Match length
                   372
                   33
% identity
                   (D64006) aspartate aminotransferase [Synechocystis sp.]
NCBI Description
                   260057
Seq. No.
Contig ID
                   1013 2.R1011
                   dyk700106601.h1
5'-most EST
                   260058
Seq. No.
                   1013 4.R1011
Contig ID
5'-most EST
                   xsy700210490.h1
                   260059
Seq. No.
                   1013 5.R1011
Contig ID
                   LIB3\overline{1}36-011-Q1-K1-F9
5'-most EST
                   260060
Seq. No.
                   1019 1.R1011
Contig ID
                   uC-zmflmo17037d01b1
5'-most EST
                   BLASTX
Method
                   g421960
NCBI GI
BLAST score
                   606
                   3.0e-70
E value
Match length
                   221
% identity
                   small nuclear ribonucleoprotein U2B'' - potato >gi_169589
NCBI Description
                   (M72892) spliceosomal protein [Solanum tuberosum]
                   260061
Seq. No.
                   1019_2.R1011
Contig ID
5'-most EST
                   xmt700266673.h1
                   BLASTX
Method
                   g421960
NCBI GI
                   337
BLAST score
```

small nuclear ribonucleoprotein U2B'' - potato >gi_169589

(M72892) spliceosomal protein [Solanum tuberosum]

2.0e-31

101

E value Match length

% identity

NCBI Description



```
260062
Seq. No.
                  1019 3.R1011
Contig ID
                  LIB3180-045-P2-M2-H6
5'-most EST
                  BLASTX
Method
                  q421960
NCBI GI
                  321
BLAST score
                  1.0e-29
E value
                   96
Match length
                   66
% identity
                   small nuclear ribonucleoprotein U2B'' - potato >gi_169589
NCBI Description
                   (M72892) spliceosomal protein [Solanum tuberosum]
                   260063
Seq. No.
                   1022 1.R1011
Contig ID
                   uwc700152769.h1
5'-most EST
Method
                  BLASTX
                   q1458245
NCBI GI
BLAST score
                   526
                   7.0e-53
E value
                   373
Match length
                   35
% identity
                  (U64834) coded for by C. elegans cDNA cm17a1; coded for by
NCBI Description
                   C. elegans cDNA cm7g1; coded for by C. elegans cDNA
                   CEMSE26F; similar to methyltransferases [Caenorhabditis
                   elegans]
                   260064
Seq. No.
Contig ID
                   1022 3.R1011
                   LIB3075-008-Q1-K1-A3
5'-most EST
                   260065
Seq. No.
                   1024 1.R1011
Contig ID
                   uC-z\overline{m}rob73077d10b1
5'-most EST
                   BLASTX
Method
                   g1076821
NCBI GI
                   1314
BLAST score
                   1.0e-145
E value
Match length
                   253
                   100
% identity
                   probable 1-acyl-glycerol-3-phosphate acyltransferase -
NCBI Description
                   maize >gi_575960_emb_CAA82638_ (Z29518)
                   1-acyl-glycerol-3-phosphate acyltransferase (putative) [Zea
                   mays]
                   260066
Seq. No.
Contig ID
                   1025 1.R1011
5'-most EST
                   LIB3066-009-Q1-K1-E11
Method
                   BLASTX
NCBI GI
                   g2880046
BLAST score
                   156
E value
                   4.0e-10
                   87
Match length
% identity
                   43
                  (AC002340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

260067

1029_1.R1011

Seq. No. Contig ID



```
LIB3066-051-Q1-K1-C4
5'-most EST
                  BLASTN
Method
                  q3821780
NCBI GI
                  34
BLAST score
                  2.0e-09
E value
Match length
                  34
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  260068
Seq. No.
                  1033 1.R1011
Contig ID
                  uC-zmflmo17127h05b1
5'-most EST
Method
                  BLASTX
                  q2493131
NCBI GI
BLAST score
                  2449
                  0.0e+00
E value
Match length
                  552
% identity
                  98
                  VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B
NCBI Description
                  SUBUNIT) >qi 167108 (L11862) vacuolar ATPase B subunit
                   [Hordeum vulgare]
                  260069
Seq. No.
                  1033_2.R1011
Contig ID
                  ymt700220112.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2493131
BLAST score
                  387
                  3.0e-37
E value
Match length
                  77
                   97
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B
NCBI Description
                   SUBUNIT) >gi 167108 (L11862) vacuolar ATPase B subunit
                   [Hordeum vulgare]
                   260070
Seq. No.
Contig ID
                  1033 3.R1011
5'-most EST
                  LIB3059-058-Q1-K1-B7
                  BLASTX
Method
                  g141605
NCBI GI
BLAST score
                   287
                   2.0e-25
E value
Match length
                   84
% identity
                   71
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                   >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize > gi_168\overline{68}0 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                   260071
                   1033 4.R1011
Contig ID
                   LIB36-002-Q1-E1-G8
5'-most EST
```

Method BLASTX NCBI GI q2493132 BLAST score 678

E value 3.0e-71Match length 137 % identity 96



VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B NCBI Description SUBUNIT) >qi 167110 (L11873) vacuolar ATPase B subunit [Hordeum vulgare]

260072 Seq. No.

1033 5.R1011 Contig ID

5'-most EST LIB3115-028-P1-K1-A10

BLASTX Method NCBI GI g2493130 -BLAST score 200 E value 3.0e-15 Match length 61 70

VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 2 (V-ATPASE B NCBI Description

SUBUNIT) >gi_459200 (U07053) vacuolar H+-ATPase subunit B

[Gossypium hirsutum]

260073 Seq. No.

% identity

1033 6.R1011 Contig ID

5'-most EST LIB3180-002-P1-M1-D8

BLASTX Method NCBI GI q2493131 BLAST score 452 E value 8.0e-45 Match length 94 % identity 96

VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B NCBI Description

SUBUNIT) >gi 167108 (L11862) vacuolar ATPase B subunit

[Hordeum vulgare]

Seq. No. 260074

1033 9.R1011 Contig ID mwy700439691.h1 5'-most EST

Seq. No. 260075

1034 1.R1011 Contig ID tfd700575256.h1 5'-most EST

Method BLASTX q3367519 NCBI GI BLAST score 294 2.0e-26 E value

Match length 141 59 % identity

(AC004392) Contains similarity to gb_U51898 NCBI Description

Ca2+-independent phospholipase A2 from Rattus norvegicus.

[Arabidopsis thaliana]

260076 Seq. No.

1038 1.R1011 Contig ID

5'-most EST LIB3075-023-Q1-K1-E8

260077 Seq. No.

1040 1.R1011 Contig ID

5'-most EST LIB3075-026-Q1-K1-C4

Method BLASTX NCBI GI q4514716 231 BLAST score



4.0e-19 E value 99 Match length % identity 43 (AB017533) EPc [Nicotiana tabacum] NCBI Description 260078 Seq. No. 1041 1.R1011 Contig ID 5'-most EST uC-zmflmo17242f01b1 Method BLASTX NCBI GI g1184776 BLAST score 1653 E value 0.0e + 00Match length 337 96 % identity (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase NCBI Description GAPC4 [Zea mays] 260079 Seq. No. Contig ID 1041 2.R1011

5'-most EST LIB143-041-Q1-E1-G9 Method BLASTX NCBI GI g2668744 BLAST score 807 E value 3.0e-86 Match length 148

100

(AF034946) ubiquitin conjugating enzyme [Zea mays] NCBI Description

260080 Seq. No. Contig ID 1041 3.R1011 rvt700548484.h1 5'-most EST BLASTX Method NCBI GI g2668744 BLAST score 327 2.0e-30 E value

Match length 61 97 % identity

% identity

NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]

260081 Seq. No. 1041 4.R1011 Contig ID 5'-most EST uC-zmflmo17066a07b1 Method BLASTX

NCBI GI q2668744 546 BLAST score E value 5.0e-56 Match length 101 % identity

NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]

260082 Seq. No. Contig ID 1041 5.R1011

5'-most EST LIB143-043-Q1-E1-A10

Method BLASTX NCBI GI q1184774 BLAST score 1202 E value 1.0e-132



Match length 254 % identity 94

NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]

Seq. No. 260083 Contig ID 1041 9.R1011

5'-most EST uC-zmflb731216a04a1

Method BLASTX
NCBI GI g1184774
BLAST score 172
E value 4.0e-12
Match length 31
% identity 100

NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]

Seq. No. 260084

Contig ID 1041_11.R1011 5'-most EST uC-zmflb73015c04b1

Method BLASTX
NCBI GI g1184776
BLAST score 273
E value 9.0e-36
Match length 90
% identity 90

% identity 90 NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC4 [Zea mays]

Seq. No. 260085

Contig ID 1041 12.R1011

5'-most EST LIB3180-043-P2-M2-C12

Method BLASTX
NCBI GI g1184774
BLAST score 518
E value 9.0e-53
Match length 149
% identity 89

NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]

Seq. No. 260086

Contig ID 1041 15.R1011

5'-most EST LIB3150-118-P2-K1-G3

Method BLASTX
NCBI GI g1184776
BLAST score 162
E value 6.0e-11
Match length 35
% identity 89

NCBI Description (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC4 [Zea mays]

Seq. No. 260087

Contig ID 1041 16.R1011

5'-most EST LIB3150-081-P2-N2-D9

Method BLASTN



NCBI GI g1184773 BLAST score 166 E value 3.0e-88 Match length 174 99 % identity

NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC3

(gpc3) mRNA, complete cds

Seq. No. 260088

Contig ID 1043 1.R1011

5'-most EST uC-zmflm017211b12b1

Seq. No. Contig ID 260089

260090

1045 1.R1011 5'-most EST

LIB3062-025-Q1-K1-F4

Method BLASTX g4455287 NCBI GI BLAST score 414 E value 5.0e-42Match length 179 % identity 54

NCBI Description (AL035527) putative protein [Arabidopsis thaliana]

Seq. No.

Contig ID 1045 2.R1011 5'-most EST wyr700235314.h1

Method BLASTX NCBI GI q4455287 BLAST score 406 E value 2.0e-39 131 Match length 62 % identity

NCBI Description (AL035527) putative protein [Arabidopsis thaliana]

Seq. No.

260091

1045 4.R1011 Contig ID

5'-most EST LIB3075-046-Q1-K1-D2

Seq. No. 260092

1047 1.R1011 Contig ID

LIB3156-021-Q1-K1-H4 5'-most EST

 ${\tt BLASTX}$ Method NCBI GI g3386611 BLAST score 376 E value 3.0e - 36Match length 116 55 % identity

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 260093

1049 1.R1011 Contig ID

5'-most EST LIB3075-046-Q1-K1-D6

Seq. No. 260094

Contiq ID 1050 1.R1011

5'-most EST LIB3150-056-Q1-N1-C5

Method BLASTX



g417745 NCBI GI BLAST score 2200 0.0e + 00E value 481 Match length 87 % identity

ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE NCBI Description

HYDROLASE) (ADOHCYASE) >gi 170773 (L11872)

S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]

260095 Seq. No.

1050 2.R1011 Contig ID 5'-most EST uC-zmflb73207c06b1

BLASTX Method g577301 NCBI GI 730 BLAST score 9.0e-77 E value 593 Match length

32 % identity (D42044) The ha3523 gene product is related to S.cerevisiae NCBI Description

gene product located in chromosome III. [Homo sapiens]

260096 Seq. No.

1050 3.R1011 Contig ID 5'-most EST xsy700217412.h1

Method BLASTX NCBI GI g464734 BLAST score 502 8.0e-51 E value Match length 109 87 % identity

ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE NCBI Description

HYDROLASE) (ADOHCYASE) >gi_481237_pir__S38379 adenosylhomocysteinase (EC 3.3.1.1) - Madagascar periwinkle >gi_407412_emb_CAA81527_ (Z26881) S-adenosyl-L-homocysteine

hydrolase [Catharanthus roseus]

Seq. No. 260097

1050 4.R1011 Contig ID 5'-most EST rv1700457294.h1

Method BLASTX NCBI GI q417745 BLAST score 487 E value 3.0e-49Match length 104 % identity 88

NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE

HYDROLASE) (ADOHCYASE) >gi 170773 (L11872)

S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]

Seq. No. 260098

1050 5.R1011 Contig ID

5'-most EST uC-zmflb73136f11a1

260099 Seq. No.

1050 6.R1011 Contig ID

5'-most EST LIB3059-032-Q1-K1-A8

BLASTX Method



NCBI GI g1724102 BLAST score 458 E value 2.0e-45 Match length 156 % identity 62

NCBI Description (U79766) S-adenosyl-L-homocystein hydrolase; SAH

[Mesembryanthemum crystallinum]

Seq. No. 260100

Contig ID 1050_8.R1011

5'-most EST uC-zmflb73019b05b1

Seq. No. 260101

Contig ID 1051_1.R1011

5'-most EST uC-zmflMo17007a07b1

Method BLASTX
NCBI GI g2497542
BLAST score 1029
E value 0.0e+00
Match length 489
% identity 80

NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR

>gi_629696_pir__S44287 pyruvate kinase, plastid - common
tobacco >gi_482938_emb_CAA82223_ (Z28374) Pyruvate kinase;

plastid isozyme [Nicotiana tabacum]

Seq. No. 260102 Contig ID 1051 2.R1011

5'-most EST gwl700616432.h1

Method BLASTX
NCBI GI g2497542
BLAST score 336
E value 5.0e-31
Match length 169
% identity 49

NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR

>gi_629696_pir__S44287 pyruvate kinase, plastid - common
tobacco >gi_482938_emb_CAA82223_ (Z28374) Pyruvate kinase;

plastid isozyme [Nicotiana tabacum]

Seq. No. 260103

Contig ID 1056 1.R1011

5'-most EST uC-zmroteosinte059a05b1

Method BLASTX
NCBI GI g1657619
BLAST score 209
E value 3.0e-16
Match length 121
% identity 37

NCBI Description (U72504) G5p [Arabidopsis thaliana] >gi_3068710 (AF049236) putative transmembrane protein G5p [Arabidopsis thaliana]

Seq. No. 260104

Contig ID 1056 2.R1011

5'-most EST LIB3075-046-Q1-K1-B11

Method BLASTX NCBI GI g1657619



BLAST score 374 EE value 6.0e-36 Match length 123 % identity 57

NCBI Description (U72504) G5p [Arabidopsis thaliana] >gi_3068710 (AF049236) putative transmembrane protein G5p [Arabidopsis thaliana]

Seq. No. 260105 Contig ID 1058 1.R1011

5'-most EST uC-zmflb73214f01b1

Method BLASTX
NCBI GI g1167953
BLAST score 194
E value 2.0e-14
Match length 152
% identity 51

NCBI Description (U43496) putative 32.6 kDa jasmonate-induced protein

[Hordeum vulgare] >gi 2465426 (AF021256) 32 kDa protein

[Hordeum vulgare]

Seq. No. 260106

Contig ID 1067_1.R1011

5'-most EST LIB3075-046-Q1-K1-C12

Seq. No. 260107

Contig ID 1067_2.R1011 5'-most EST dyk700102182.h1

Seq. No. 260108

Contig ID 1068_1.R1011

5'-most EST LIB3075-046-Q1-K1-A8

Method BLASTX
NCBI GI g401238
BLAST score 1097
E value 1.0e-120
Match length 249

% identity 82

NCBI Description UBIQUITIN-ACTIVATING ENZYME E1 3 >gi_170686 (M90664) ubiquitin activating enzyme [Triticum aestivum]

Seq. No. 260109 Contig ID 1070 1.R1011

5'-most EST LIB3075-017-Q1-K1-B5

Seq. No. 260110

Contig ID 1073_1.R1011

5'-most EST LIB3075-042-Q1-K1-C11

Seq. No. 260111

Contig ID 1074_1.R1011 5'-most EST LIB148-018-Q1-E1-H10

Seq. No. 260112 Contig ID 1076 1.R1011

5'-most EST uC-zmflb73280b07b2

Method BLASTX NCBI GI g3319340



BLAST score 651 E value 8.0e-68 Match length 189 % identity 64

NCBI Description (AF077407) contains similarity to E. coli cation transport

protein ChaC (GB:D90756) [Arabidopsis thaliana]

Seq. No. 260113 Contig ID 1076_2.R1011

5'-most EST uC-zmroteosinte091e12b2

Seq. No. 260114

Contig ID 1076_3.R1011 5'-most EST ntr700074015.h1

Method BLASTX
NCBI GI g2827524
BLAST score 239
E value 1.0e-19
Match length 164
% identity 36

NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]

Seq. No. 260115 Contig ID 1076 4.R1011

5'-most EST uC-zmflmo17069d06b1

Method BLASTX
NCBI GI g3319340
BLAST score 383
E value 2.0e-36
Match length 213

% identity 44

NCBI Description (AF077407) contains similarity to E. coli cation transport

protein ChaC (GB:D90756) [Arabidopsis thaliana]

Seq. No. 260116

Contig ID 1080_1.R1011

5'-most EST LIB143-013-Q1-E1-A1

Method BLASTX
NCBI GI 94507873
BLAST score 400
E value 2.0e-38
Match length 180
% identity 45

NCBI Description von Hippel-Lindau binding protein 1

>gi_3212112_emb_CAA76761 (Y17394) prefoldin subunit 3

[Homo sapiens]

Seq. No. 260117

Contig ID 1081_1.R1011 5'-most EST pmx700088133.h1

Method BLASTX
NCBI GI g2494144
BLAST score 1046
E value 1.0e-114
Match length 330
% identity 62

NCBI Description (AC002329) predicted leucine-rich protein [Arabidopsis



thaliana]

```
260118
Seq. No.
                  1082 1.R1011
Contig ID
                  LIB3180-001-P1-M1-F5
5'-most EST
                  BLASTX
Method
                  g4580389
NCBI GI
                  511
BLAST score
                  5.0e-71
E value
                  253
Match length
                  59
% identity
                  (AC007171) unknown protein [Arabidopsis thaliana]
NCBI Description
                  260119
Seq. No.
                  1082 2.R1011
Contig ID
5'-most EST
                  LIB3059-060-Q1-K1-C6
                  BLASTX
Method
                  g4580389
NCBI GI
                  456
BLAST score
                  2.0e-45
E value
Match length
                  135
                  70
% identity
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]
                  260120
Seq. No.
                  1082 3.R1011
Contig ID
5'-most EST
                  uC-zmflb73237e06b2
Method
                  BLASTX
                  q4580389
NCBI GI
                  285
BLAST score
E value
                  1.0e-25
Match length
                  101
                   53
% identity
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]
                   260121
Seq. No.
Contig ID
                   1082 4.R1011
                   LIB3075-046-Q1-K1-A5
5'-most EST
                  BLASTX
Method
                   q4580389
NCBI GI
                   144
BLAST score
E value
                   5.0e-09
Match length
                   93
% identity
NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]
Seq. No.
                   260122
Contig ID
                   1083 1.R1011
5'-most EST
                   LIB3150-041-Q1-N1-E4
                   BLASTX
Method
NCBI GI
                   g4337210
BLAST score
                   798
                   7.0e-85
E value
                   392
Match length
                   41
% identity
```

NCBI Description (AC006403) hypothetical protein [Arabidopsis thaliana]



260123 Seq. No.

1083 2.R1011 Contig ID

uC-zmflmo17128d10b1 5'-most EST

260124 Seq. No.

1084 1.R1011 Contig ID

uC-zmroteosinte087d12b2 5'-most EST

BLASTX Method g3522929 NCBI GI 1339 BLAST score 1.0e-148 E value Match length 273 90 % identity

(AC002535) putative dTDP-glucose 4-6-dehydratase NCBI Description

[Arabidopsis thaliana] >gi 3738279 (AC005309) putative

dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No. 260125

1084 2.R1011 Contig ID

LIB3067-033-Q1-K1-D11 5'-most EST

BLASTX Method NCBI GI g1370603 BLAST score 1079 1.0e-118 E value 213 Match length 100 % identity

(X98245) annexin p35 [Zea mays] NCBI Description

260126 Seq. No.

1084 3.R1011 Contig ID

 $uC-z\overline{m}flmo17065d06a1$ 5'-most EST

BLASTX Method g3522929 NCBI GI BLAST score 529 E value 1.0e-53 169 Match length

63 % identity

(AC002535) putative dTDP-glucose 4-6-dehydratase NCBI Description

[Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-qlucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No. 260127

1084 4.R1011 Contig ID wyr700243072.h1 5'-most EST

BLASTX Method NCBI GI q1370603 BLAST score 700 E value 6.0e-74Match length 138 % identity

(X98245) annexin p35 [Zea mays] NCBI Description

Seq. No. 260128

Contig ID 1085 1.R1011

LIB3075-045-Q1-K1-F10 5'-most EST

Method BLASTX NCBI GI g4467147



BLAST score 463 4.0e-85 E value 233 Match length % identity 68

(AL035540) putative protein [Arabidopsis thaliana] NCBI Description

260129 Seq. No. 1085 2.R1011 Contig ID tfd700571674.hl 5'-most EST

Method BLASTX q4467147 NCBI GI BLAST score 399 6.0e-39 E value Match length 122 % identity 63

(AL035540) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 260130 1088 1.R1011 Contig ID

LIB3075-045-Q1-K1-F5 5'-most EST

BLASTX Method g3150406 NCBI GI BLAST score 220 6.0e-18E value 90 Match length 53 % identity

(AC004165) putative indole-3-acetate NCBI Description

beta-glucosyltransferase [Arabidopsis thaliana]

260131 Seq. No.

1089 1.R1011 Contig ID

5'-most EST LIB143-013-Q1-E1-F12

Method BLASTX g114420 NCBI GI 2419 BLAST score 0.0e + 00E value Match length 516

% identity 93

ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR NCBI Description

>gi_100882_pir__S11491 H+-transporting ATP synthase (EC

3.6.1.34) beta chain, mitochondrial - maize

>gi_22173_emb_CAA38140_ (X54233) ATPase F1 subunit protein [Zea mays] >gi 897618 (M36087) F-1-ATPase subunit 2 [Zea

mays]

260132 Seq. No.

Contig ID 1089 2.R1011

5'-most EST uC-zmroteosinte067h04b1

Method BLASTX q114420 NCBI GI 548 BLAST score 7.0e-56 E value Match length 140 81 % identity

NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR

100882 pir S11491 H+-transporting ATP synthase (EC

3.6.1.34) beta chain, mitochondrial - maize



>gi_22173_emb_CAA38140_ (X54233) ATPase F1 subunit protein
[Zea mays] >gi_897618 (M36087) F-1-ATPase subunit 2 [Zea
mays]

Seq. No. 260133

Contig ID 1089 3.R1011

5'-most EST uC-zmroteosinte105b05b1

Method BLASTX
NCBI GI g114420
BLAST score 534
E value 2.0e-54
Match length 122
% identity 87

NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR

>gi_100882_pir__S11491 H+-transporting ATP synthase (EC

3.6.1.34) beta chain, mitochondrial - maize

>gi_22173_emb_CAA38140_ (X54233) ATPase F1 subunit protein
[Zea mays] >gi 897618 (M36087) F-1-ATPase subunit 2 [Zea

mays]

Seq. No. 260134

Contig ID 1089 4.R1011

5'-most EST uC-zmflb73077f12a1

Method BLASTN
NCBI GI g22172
BLAST score 193
E value 1.0e-104

Match length 391 % identity 89

NCBI Description Maize ATP2 mRNA for mitochondrial ATP synthase beta subunit

Seq. No. 260135

Contig ID 1089 5.R1011

5'-most EST LIB3\overline{150}-022-\overline{Q1}-N1-F2

Method BLASTN
NCBI GI g342631
BLAST score 68
E value 9.0e-30
Match length 68
% identity 100

NCBI Description Maize mitochondrial F-1-ATPase subunit-2 mRNA, complete cds

Seq. No. 260136

Contig ID 1089 7.R1011

5'-most EST uC-zmflb73049c01b1

Method BLASTN
NCBI GI g22172
BLAST score 64
E value 2.0e-27
Match length 123
% identity 90

NCBI Description Maize ATP2 mRNA for mitochondrial ATP synthase beta subunit

Seq. No. 260137

Contig ID 1090_1.R1011

5'-most EST LIB1 $\overline{4}$ 3-050-Q1-E1-E5

Method BLASTX

```
g1575128
NCBI GI
BLAST score
                   2919
                   0.0e + 00
E value
                   644
Match length
                   91
% identity
                   (U58208) lumenal binding protein cBiPe2 [Zea mays]
NCBI Description
                   260138
Seq. No.
                   1090 3.R1011
Contig ID
5'-most EST
                   uwc700150445.hl
                   BLASTX
Method
                   g2267006
NCBI GI
BLAST score
                   505
                   3.0e-51
E value
                   100
Match length
                   100
% identity
                   (AF006825) endosperm lumenal binding protein [Oryza sativa]
NCBI Description
                   260139
Seq. No.
                   1090 8.R1011
Contig ID
5'-most EST
                   wyr700240820.h1
Method
                   BLASTX
                   g729617
NCBI GI
                   299
BLAST score
                   4.0e-27
E value
Match length
                   63
                   97
% identity
                   78 KD GLUCOSE REGULATED PROTEIN HOMOLOG 1 (GRP 78-1)
NCBI Description
                   (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG 1) (BIP
                   1) >gi_100337_pir__S21877 heat shock protein BiP homolog
                   blp1 - common tobacco (fragment) >gi_19805_emb_CAA42662_ (X60060) luminal binding protein (BiP) [Nicotiana tabacum]
                   260140
Seq. No.
                   1095 1.R1011
Contig ID
5'-most EST
                   LIB3059-044-Q1-K1-F8
Method
                   BLASTX
NCBI GI
                   q3738297
                   160
BLAST score
                    1.0e-10
E value
                    38
Match length
% identity
                    66
                   (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                    260141
Seq. No.
                    1096 1.R1011
Contig ID
5'-most EST
                    LIB3066-001-Q1-K1-F12
Seq. No.
                    260142
                    1098 1.R1011
Contig ID
                    LIB3075-045-Q1-K1-G5
5'-most EST
Method
                    BLASTX
```

Method BLASTX
NCBI GI g2498608
BLAST score 174
E value 3.0e-12
Match length 98
% identity 42





```
NCBI Description L-ASPARTATE OXIDASE (QUINOLINATE SYNTHETASE B) >gi 608530
                   (U17232) L-aspartate oxidase [Pseudomonas aeruginosa]
                  260143
Seq. No.
                  1099 1.R1011
Contig ID
                  LIB3066-025-Q1-K1-G10
5'-most EST
                  260144
Seq. No.
                  1099 2.R1011
Contig ID
                  LIB3069-043-Q1-K1-G9
5'-most EST
                  BLASTX
Method
                  g1431629
NCBI GI
BLAST score
                  485
                  1.0e-48
E value
Match length
                  137
% identity
                  63
NCBI Description (X99348) pectinacetylesterase precursor [Vigna radiata]
                  260145
Seq. No.
                  1102 1.R1011
Contig ID
                  uC-zmflb73085b11b2
5'-most EST
                  BLASTX
Method
                  g4490737
NCBI GI
                  579
BLAST score
                   3.0e-59
E value
Match length
                  286
                   48
% identity
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                  260146
                  1112 1.R1011
Contig ID
5'-most EST
                  LIB3\overline{1}37-017-Q1-K1-B2
                  BLASTX
Method
                   g2984709
NCBI GI
BLAST score
                  1861
                   0.0e + 00
E value
Match length
                   415
% identity
                   87
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                   260147
Seq. No.
Contig ID
                   1112 2.R1011
                   uC-zmflb73032c02b1
5'-most EST
Method
                   BLASTX
                   q2984709
NCBI GI
BLAST score
                   625
E value
                   5.0e-65
Match length
                   120
% identity
                   97
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
```

260148 Seq. No.

1112 3.R1011 Contig ID

5'-most EST uC-zmflb73040d03b1

Method BLASTX NCBI GI g2984709 BLAST score 759

E value 1.0e-80

Match length 188
% identity 80

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 260149

Contig ID 1112_4.R1011
5'-most EST uC-zmflb73283f12a1

5'-most EST uC-zmflb'
Method BLASTX
NCBI GI g1197168
BLAST score 183
E value 6.0e-13
Match length 339
% identity 23

NCBI Description (D45163) embryonic muscle myosin heavy chain [Halocynthia

roretzi]

 Seq. No.
 260150

 Contig ID
 1112_8.R1011

 5'-most EST
 xyt700344443.h1

 Method
 BLASTX

 NCBI GI
 q2984709

NCBI GI g2984709
BLAST score 304
E value . 2.0e-27
Match length 71
% identity 87

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 260151

Contig ID 1112_10.R1011 5'-most EST uC-zmflb73197b09b1

Method BLASTX
NCBI GI g2984709
BLAST score 397
E value 4.0e-38
Match length 125
% identity 93

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 260152

Contig ID 1112_11.R1011 5'-most EST uC-zmflb73135d05b2

Method BLASTX
NCBI GI g2984709
BLAST score 417
E value 6.0e-41
Match length 134
% identity 65

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 260153 Contig ID 1113_2.R1011

5'-most EST LIB3062-046-Q1-K1-A4

Seq. No. 260154

Contig ID 1118_1.R1011

5'-most EST LIB3060-001-Q1-K2-B10



Method BLASTX
NCBI GI 9746510
BLAST score 447
E value 7.0e-44
Match length 136
% identity 58

NCBI Description (U23517) similar to ubiquitin conjugating enzyme

[Caenorhabditis elegans]

Seq. No. 260155 Contig ID 1118_2.R1011

5'-most EST LIB3062-032-Q1-K1-E9

Method BLASTX
NCBI GI g746510
BLAST score 253
E value 1.0e-21
Match length 78
% identity 56

NCBI Description (U23517) similar to ubiquitin conjugating enzyme

[Caenorhabditis elegans]

 Seq. No.
 260156

 Contig ID
 1118_3.R1011

 5'-most EST
 nwy700446670.h1

Seq. No. 260157

Contig ID 1120 1.R1011

5'-most EST LIB3078-053-Q1-K1-C1

Seq. No. 260158

Contig ID 1121_1.R1011

5'-most EST uC-zmflMo17012b12b1

Seq. No. 260159

Contig ID 1122_1.R1011

5'-most EST uC-zmflmo17340h09a1

Seq. No. 260160

Contig ID 1122_2.R1011 5'-most EST dyk700103740.h1

Method BLASTX
NCBI GI g3309086
BLAST score 333
E value 1.0e-38

Match length 131 % identity 63

NCBI Description (AF076253) calcineurin B-like protein 3 [Arabidopsis

thaliana]

Seq. No. 260161

Contig ID 1124 1.R1011 5'-most EST fwa700098915.h1

Method BLASTX
NCBI GI g3560264
BLAST score 352
E value 1.0e-32
Match length 236



% identity (AL031535) soll family protein [Schizosaccharomyces pombe] NCBI Description 260162 Seq. No. 1124 2.R1011 Contig ID LIB3069-009-Q1-K1-B7 5'-most EST BLASTX Method g3860020 NCBI GI 231 BLAST score 7.0e-19 E value 108 Match length 42 % identity (AF091091) unknown [Homo sapiens] NCBI Description 260163 Seq. No. 1124 4.R1011 Contig ID yyf700351094.h1 5'-most EST 260164 Seq. No. 1126 1.R1011 Contig ID rvt700553326.hl 5'-most EST 260165 Seq. No. 1126 2.R1011 Contig ID LIB3067-023-Q1-K1-D5 5'-most EST BLASTN Method NCBI GI g2062705 36 BLAST score 1.0e-10 E value 36 Match length 100 % identity NCBI Description Human butyrophilin (BTF5) mRNA, complete cds 260166 Seq. No. Contig ID 1127_1.R1011 5'-most EST uC-zmflmo17215f03b1 Method BLASTX NCBI GI q3617837 2447 BLAST score 0.0e + 00E value Match length 520 % identity 54 (AF035820) gibberellin action negative regulator SPY NCBI Description [Hordeum vulgare] 260167 Seq. No. Contig ID 1128 1.R1011 ypc700803702.h1 5'-most EST Method BLASTX NCBI GI q4263790 BLAST score 2089 E value 0.0e + 00Match length 686

Seq. No. 260168

65

% identity

NCBI Description (AC006068) putative ch-TOG protein [Arabidopsis thaliana]



```
1130 1.R1011
Contig ID
                  ntr700072903.hl
5'-most EST
                  BLASTX
Method
                  q2317908
NCBI GI
                  379
BLAST score
                  1.0e-35
E value
                  338
Match length
% identity
                  30
                 (U89959) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  260169
Seq. No.
                  1130 2.R1011
Contig ID
                  uC-zmflb73361h07a2
5'-most EST
                  260170
Seq. No.
                  1130 3.R1011
Contig ID
                  uwc700150193.hl
5'-most EST
Seq. No.
                  260171
                  1130 5.R1011
Contig ID
                  LIB143-043-Q1-E1-D3
5'-most EST
                   260172
Seq. No.
                   1131 1.R1011
Contig ID
                   LIB3075-045-Q1-K1-C5
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1764100
BLAST score
                   447
                   6.0e-47
E value
Match length
                   124
                   74
% identity
                  (U81805) GDP-D-mannose-4,6-dehydratase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   260173
                   1134 1.R1011
Contig ID
                   uC-zmflb73278f04b1
5'-most EST
                   BLASTX
Method
                   q4582465
NCBI GI
BLAST score
                   491
                   3.0e-49
E value
                   142
Match length
% identity
                   61
NCBI Description (AC007071) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   260174
                   1134 2.R1011
Contig ID
5'-most EST
                   uC-zmromo17113h07a1
```

Seq. No. 260175

Contig ID 1134_3.R1011 5'-most EST wty700168951.h1 Method BLASTX

Method BLASTX
NCBL GI g4582465
BLAST score 302
E value 1.0e-27
Match length 84



% identity 65

NCBI Description (AC007071) hypothetical protein [Arabidopsis thaliana]

Seq. No. 260176

Contig ID 1135_1.R1011

5'-most EST uC-zmflmo17163d10b1

Method BLASTX
NCBI GI g2462825
BLAST score 545
E value 4.0e-55
Match length 209
% identity 59

NCBI Description (AF000657) contains Procite 'RNP1' putative RNA-binding

region [Arabidopsis thaliana]

Seq. No. 260177

Contig ID 1135 2.R1011

5'-most EST LIB3059-009-Q1-K1-G11

Method BLASTX
NCBI GI g3122572
BLAST score 2979
E value 0.0e+00
Match length 685
% identity 82

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR

(COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial

complex I subunit [Solanum tuberosum]

Seq. No. 260178

Contig ID 1135_3.R1011

5'-most EST uC-zmflmo17288g03b1

Seq. No. 260179

Contig ID 1135 4.R1011

5'-most EST LIB3078-037-Q1-K1-G4

Method BLASTX
NCBI GI g3122572
BLAST score 182
E value 3.0e-13
Match length 51
% identity 71

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR

(COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi 758340 emb CAA59818_ (X85808) 76 kDa mitochondrial

complex I subunit [Solanum tuberosum]

Seq. No. 260180

Contig ID 1135_7.R1011 5'-most EST ntr700075419.h1

Seq. No. 260181

Contig ID 1135 9.R1011



5'-most EST wyr700241570.h1

Method BLASTX
NCBI GI g3122572
BLAST score 353
E value 8.0e-34
Match length 81
% identity 85

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR

(COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir__ S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial

complex I subunit [Solanum tuberosum]

Seq. No. 260182

Contig ID 1136_1.R1011

5'-most EST uC-zmflMo17018c01b1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 2.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 260183

Contig ID 1137_1.R1011 5'-most EST fdz701163477.h1

Method BLASTN
NCBI GI g4220643
BLAST score 41
E value 2.0e-13
Match length 161

E value 2.0e-Match length 161 % identity 81

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MWD22, complete sequence [Arabidopsis thaliana]

Seq. No. 260184

Contig ID 1137_2.R1011

5'-most EST LIB3075-044-Q1-K1-H12

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 2.0e-10
Match length 48
% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 260185

Contig ID 1137_3.R1011 5'-most EST hbs701183577.h1

Seq. No. 260186

Contig ID 1138_1.R1011 5'-most EST cjh700196142.h1

Seq. No. 260187



```
Contig ID
                   1139 1.R1011
5'-most EST
                  LIB148-060-Q1-E1-G11
Seq. No.
                   260188
Contig ID
                   1142 1.R1011
5'-most EST
                  LIB148-049-Q1-E1-G12
                   260189
Seq. No.
Contig ID
                   1143 1.R1011
5'-most EST
                  LIB3066-051-Q1-K1-A9
                   260190
Seq. No.
Contig ID
                  1145 1.R1011
5'-most EST
                  yyf700350060.h1
Method
                  BLASTX
NCBI GI
                   q2341061
BLAST score
                   2115
E value
                   0.0e + 00
Match length
                   414
% identity
                  100
NCBI Description (U73459) translational initiation factor eIF-4A [Zea mays]
Seq. No.
                  260191
Contig ID
                   1145 2.R1011
5'-most EST
                  LIB3078-018-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                   q2500522
BLAST score
                   758
E value
                   1.0e-80
Match length
                   151
% identity
                   97
                  EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) >gi 603190
NCBI Description
                   (U17979) translation initiation factor eIF-4A [Zea mays]
Seq. No.
                   260192
Contig ID
                  1145 4.R1011
5'-most EST
                  uC-zmflmo17158f06b1
Method
                  BLASTX
                  g2500522
NCBI GI
BLAST score
                   655
E value
                   1.0e-68
Match length
                   127
                   100
% identity
                  EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) >gi_603190
NCBI Description
                   (U17979) translation initiation factor eIF-4A [Zea mays]
                   260193
Seq. No.
                  1145 5.R1011
Contig ID
                  LIB3069-037-Q1-K1-F10
5'-most EST
```

Method BLASTX
NCBI GI g4454799
BLAST score 218
E value 2.0e-17
Match length 48
% identity 94

NCBI Description (AF079782) translation initiation factor 4A2 [Zea mays]



```
260194
Seq. No.
                  1145 6.R1011
Contig ID
                  uC\text{-}zmflb73086g05b2
5'-most EST
Method
                  BLASTX
                  g2341061
NCBI GI
                  314
BLAST score
E value
                  8.0e-50
Match length
                  104
% identity
                  99
                  (U73459) translational initiation factor eIF-4A [Zea mays]
NCBI Description
Seq. No.
                  260195
                  1150 1.R1011
Contig ID
                  uC-zmflmo17c12b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3281853
BLAST score
                  1005
E value
                  1.0e-109
Match length
                  259
                  78
% identity
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  260196
                  1150 2.R1011
Contig ID
                  LIB3066-055-Q1-K1-D3
5'-most EST
Method
                  BLASTX
                  g3281853
NCBI GI
BLAST score
                   301
E value
                  5.0e-27
Match length
                  112
                   68
% identity
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                  260197
Seq. No.
                  1150 3.R1011
Contig ID
                  LIB3076-006-Q1-K1-C3
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3281853
                   338
BLAST score
E value
                   2.0e-31
                   80
Match length
                   78
% identity
NCBI Description
                  (AL031004) putative protein [Arabidopsis thaliana]
                   260198
Seq. No.
                   1150_4.R1011
Contig ID
5'-most EST
                  LIB3279-055-P1-K1-E10
                   260199
Seq. No.
Contig ID
                   1150 5.R1011
                   uC-zmflmo17201f03b1
5'-most EST
```

Seq. No. 260200 Contig ID 1155 1.R1011

5'-most EST LIB3066-023-Q1-K1-F9

Seq. No. 260201



```
1160 1.R1011
Contig ID
5'-most EST
                  LIB3062-013-Q1-K1-F8
                  BLASTX
Method
                  g2832672
NCBI GI
BLAST score
                  562
                  1.0e-57
E value
                  138
Match length
                  78
% identity
                  (AL021712) nifU-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  260202
                  1161 1.R1011
Contig ID
5'-most EST
                  tzu700206143.h1
                  260203
Seq. No.
                  1163 1.R1011
Contig ID
5'-most EST
                  zuv700356152.h1
                  260204
Seq. No.
                  1167 1.R1011
Contig ID
5'-most EST
                  LIB189-026-Q1-E1-F12
Method
                  BLASTX
NCBI GI
                  g417154
BLAST score
                  1469
E value
                  0.0e+00
Match length
                  508
% identity
                  76
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
```

HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

260205 Seq. No. 1167_2.R1011 Contig ID 5'-most EST uC-zmflb73055f10b1

Method BLASTX NCBI GI q417154 BLAST score 1903 0.0e+00 E value Match length 436 86 % identity

NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 260206

Contig ID 1167 3.R1011 5'-most EST wty700169781.h1

BLASTX Method NCBI GI q417154 BLAST score 1108 E value 1.0e-121 Match length 276 % identity 82

NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock

protein 82 - rice (strain Taichung Native One)



>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

 Seq. No.
 260207

 Contig ID
 1167_4.R1011

 5'-most EST
 LIB3059-047-Q1-K1-C5

 Method
 BLASTX

Method BLASIX
NCBI GI g417154
BLAST score 2863
E value 0.0e+00
Match length 699
% identity 83

NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 260208

Contig ID 1167_5.R1011 5'-most EST ymt700224320.h1

Method BLASTX
NCBI GI g417154
BLAST score 2983
E value 0.0e+00
Match length 697
% identity 86

NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi 20256_emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 260209

Contig ID 1167 6.R1011

5'-most EST uC-zmflb73188e02a1

Method BLASTX
NCBI GI g3327957
BLAST score 219
E value 4.0e-17
Match length 195
% identity 29

NCBI Description (AF060490) TLS-associated protein TASR-2 [Mus musculus]

>gi_3327976 (AF067730) TLS-associated protein TASR-2 [Homo

sapiens]

Seq. No. 260210

Contig ID 1167 7.R1011

5'-most EST uC-zmflb73140b04b1

Method BLASTX
NCBI GI g2943792
BLAST score 2138
E value 0.0e+00
Match length 489
% identity 76

NCBI Description (AB006809) PV72 [Cucurbita sp.]

Seq. No. 260211 Contig ID 1167 8.R1011





```
5'-most EST
                     uC-zmflmo17125e11a1
 Method
                     BLASTX
  NCBI GI
                     g2443857
 BLAST score
                     300
 E value
                     5.0e-27
 Match length
                     85
  % identity
                     68
 NCBI Description
                     (U79961) vacuolar sorting receptor homolog [Zea mays]
 Seq. No.
                     260212
 Contig ID
                     1167 9.R1011
  5'-most EST
                     wty700170834.h1
 Method
                     BLASTX
 NCBI GI
                     g2495365
 BLAST score
                     319
 E value
                     4.0e-29
 Match length
                     119
 % identity
                     86
 NCBI Description
                     HEAT SHOCK PROTEIN 81-2 (HSP81-2) >qi 445127 prf 1908431B
                     heat shock protein HSP81-2 [Arabidopsis thaliana]
 Seq. No.
                     260213
 Contig ID
                     1167 12.R1011
 5'-most EST
                     uC-zmflmo17067a07b1
 Method
                     BLASTN
 NCBI GI
                     g20257
 BLAST score
                     34
 E value
                     1.0e-09
 Match length
                     50
                     92
 % identity
 NCBI Description O.sativa hsp82 gene for heat shock protein
 Seq. No.
                     260214
 Contig ID
                     1167_14.R1011
 5'-most EST
                     uC-zmflmo17297h04b1
 Method
                     BLASTX
 NCBI GI
                     g1765899
 BLAST score
                     957
                     1.0e-110
 E value
 Match length
                     233
 % identity
                     78
 NCBI Description
                     (Y07917) Spot 3 protein [Arabidopsis thaliana] >gi 1839244
                     (U86700) EGF receptor like protein [Arabidopsis thaliana]
 Seq. No.
                     260215
 Contig ID
                     1167 15.R1011
 5'-most EST
                     uC-zmflmo17280c04b1
 Method
                     BLASTX
 NCBI GI
                     g417154
 BLAST score
                     600
 E value
                     3.0e-62
 Match length
                     188
 % identity
                     86
NCBI Description
                    HEAT SHOCK PROTEIN 82 >gi_100685_pir__ S25541 heat shock
protein 82 - rice (strain Taichung Native One)
```

35996

(HSP82) [Oryza sativa]

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82



```
260216
Seq. No.
Contig ID
                  1167 16.R1011
                  LIB3136-023-Q1-K1-D5
5'-most EST
                  260217
Seq. No.
Contig ID
                  1167 17.R1011
                  uC-zmflmo17161e08b1
5'-most EST
Method
                  BLASTX
                  g477226
NCBI GI
BLAST score
                   671
                   2.0e-70
E value
                   157
Match length
                   86
% identity
                  heat shock protein HSP82 - maize >gi_300083_bbs_130886
NCBI Description
                   (S59780) HSP82=82 kda heat shock protein [Zea mays,
                   seedling, leaves, Peptide, 715 aa] [Zea mays]
                   260218
Seq. No.
                   1167 24.R1011
Contig ID
                   LIB3069-043-Q1-K1-D11
5'-most EST
Method
                   BLASTN
NCBI GI
                   g20255
BLAST score
                   91
                   2.0e-43
E value
                   256
Match length
% identity
                   86
NCBI Description O.sativa gene for heat shock protein 82 HSP82
                   260219
Seq. No.
                   1168 1.R1011
Contig ID
5'-most EST
                   LIB3151-042-Q1-K1-F10
                   BLASTX
Method
NCBI GI
                   g534982
                   436
BLAST score
                   1.0e-42
E value
Match length
                   257
% identity
                   41
                  (X75898) phosphoglucomutase [Spinacia oleracea]
NCBI Description
                   260220
Seq. No.
Contig ID
                   1168 2.R1011
                   nwy7\overline{0}0446984.h1
5'-most EST
                   BLASTX
Method
                   q4337025
NCBI GI
                   2252
BLAST score
E value
                   0.0e+00
Match length
                   640
% identity
                   66
                  (AF123253) AIM1 protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 260221

Contig ID 1168_3.R1011

5'-most EST LIB3068-008-Q1-K1-G9

MethodBLASTNNCBI GIg11957BLAST score356



E value 0.0e + 00376 Match length 49 % identity

NCBI Description Rice complete chloroplast genome

260222 Seq. No.

1168 4.R1011 Contig ID

LIB3067-037-Q1-K1-A7 5'-most EST

BLASTN Method g11957 NCBI GI BLAST score 164 5.0e-87 E value Match length 164 50 % identity

NCBI Description Rice complete chloroplast genome

Seq. No. 260223

1168 6.R1011 Contig ID

LIB83-002-Q1-E1-B10 5'-most EST

BLASTX Method q4337025 NCBI GI BLAST score 390 2.0e-37 E value Match length 143 54 % identity

NCBI Description (AF123253) AIM1 protein [Arabidopsis thaliana]

260224 Seq. No.

1168 7.R1011 Contig ID

uC-zmflMo17082f10b1 5'-most EST

BLASTX Method g4337027 NCBI GI 304 BLAST score 1.0e-27 E value 125 Match length

46 % identity

(AF123254) MFP2 [Arabidopsis thaliana] NCBI Description

260225 Seq. No.

1171 1.R1011 Contig ID nbm700475623.h1 5'-most EST

BLASTX Method NCBI GI q3878494 389 BLAST score 5.0e-37 E value 334 Match length 32 % identity

(Z79602) predicted using Genefinder; Similarity to Yeast NCBI Description

hypothetical protein YAE2 (SW:YAE2_YEAST); cDNA EST EMBL:T01631 comes from this gene; CDNA EST EMBL:M88949

comes from this gene [Caenorhabditis elegans]

260226 Seq. No.

1171 2.R1011 Contig ID

uC-zmflb73245d07b2 5'-most EST

260227 Seq. No.



Contig ID

1171 3.R1011

```
uC-zmflmo17070a10b1
5'-most EST
                   260228
Seq. No.
                   1171 4.R1011
Contig ID
                  nbm700465357.h1
5'-most EST
                   BLASTX
Method
                   g1351651
NCBI GI
BLAST score
                   151
                   1.0e-09
E value
                   88
Match length
                   34
% identity
                   HYPOTHETICAL 43.7 KD PROTEIN C24B11.08C IN CHROMOSOME I
NCBI Description
                   >gi_2130353_pir__S62553 hypothetical protein SPAC24B11.08c
                   - fission yeast (Schizosaccharomyces pombe)
                   >gi 1061296 emb CAA91773 (Z67757) unknown
                   [Schizosaccharomyces pombe]
                   260229
Seq. No.
                   1171 7.R1011
Contig ID
                   ceu7\overline{0}0433559.h1
5'-most EST
                   BLASTN
Method
                   g3925238
NCBI GI
                   35
BLAST score
                   2.0e-10
E value
                   62
Match length
% identity
                   90
                   Zea mays 6-phosphogluconate dehydrogenase isoenzyme A gene,
NCBI Description
                   partial cds
                   260230
Seq. No.
                   1171 8.R1011
Contig ID
                   xdb700339801.hl
5'-most EST
                   260231
Seq. No.
Contig ID
                   1171 9.R1011
5'-most EST
                   nbm700469174.h1
                   260232
Seq. No.
                   1173 1.R1011
Contig ID
                   wty700167053.h1
5'-most EST
Method
                   BLASTX
                   g3850129
NCBI GI
BLAST score
                   328
                   3.0e - 30
E value
Match length
                   164
% identity
                   43
                   (AL033391) conserved hypothetical protein [Candida
NCBI Description
                   albicans]
                   260233
Seq. No.
                   1174 1.R1011
Contig ID
                   uC-zmflmo17125c04a1
5'-most EST
                   260234
Seq. No.
```

1179 1.R1011

nbm700466467.h1

Contig ID

5'-most EST





BLASTX Method q2342682 NCBI GI 452 BLAST score 1.0e-44 E value Match length 132 66 % identity (AC000106) Contains similarity to Rattus AMP-activated NCBI Description protein kinase (gb_X95577). [Arabidopsis thaliana] 260235 Seq. No. 1183_1.R1011 Contig ID LIB3075-044-Q1-K1-E1 5'-most EST BLASTX Method q1174162 NCBI GI 435 BLAST score E value 3.0e-43113 Match length % identity (U44976) ubiquitin-conjugating enzyme [Arabidopsis NCBI Description thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana] 260236 Seq. No. 1186_1.R1011 Contig ID 5'-most EST LIB148-032-Q1-E1-B1 BLASTX Method g3236246 NCBI GI 778 BLAST score 1.0e-82 E value 234 Match length 59 % identity NCBI Description (AC004684) putative expansin protein [Arabidopsis thaliana] 260237 Seq. No. 1186 2.R1011 Contig ID 5'-most EST LIB148-008-Q1-E1-G8 Method BLASTX g3236246 NCBI GI 647 BLAST score 4.0e-71 E value 227 Match length % identity NCBI Description (AC004684) putative expansin protein [Arabidopsis thaliana] 260238 Seq. No. 1186 3.R1011 Contig ID 5'-most EST LIB148-030-Q1-E1-C11 Seq. No. 260239 1188 1.R1011 Contig ID 5'-most EST LIB148-018-Q1-E1-D12 260240 Seq. No.

Contig ID 1191_1.R1011 5'-most EST LIB3066-054-Q1-K1-B3 Method BLASTX NCBI GI g2270994



```
BLAST score
                   319
E value
                   2.0e-36
Match length
                   164
% identity
                   52
NCBI Description (AF004809) Ca+2-binding EF hand protein [Glycine max]
Seq. No.
                   260241
Contig ID
                   1192 1.R1011
5'-most EST
                   LIB189-025-Q1-E1-C6
Seq. No.
                   260242
                   1195_1.R1011
Contig ID
5'-most EST
                   LIB3075-044-Q1-K1-A7
Method
                   BLASTX
NCBI GI
                   g1370180
BLAST score
                   390
E value
                   1.0e-37
Match length
                   103
% identity
                   75
NCBI Description (Z73939) RAB5B [Lotus japonicus]
Seq. No.
                   260243
Contig ID
                   1196 1.R1011
5'-most EST
                   xmt7\overline{0}0267630.h1
                   BLASTX
Method
NCBI GI
                   g3108075
BLAST score
                   313
E value
                   1.0e-28
Match length
                   140
% identity
                   49
NCBI Description
                  (AF060797) putative beta-ureidopropionase [Manduca sexta]
Seq. No.
                   260244
Contig ID
                   1198_1.R1011
5'-most EST
                   wen7\overline{0}0335652.h1
Method
                   BLASTX
NCBI GI
                   g3213227
BLAST score
                   289
E value
                   2.0e-25
Match length
                   197
% identity
                   31
                  (AF035209) putative v-SNARE Vtila [Mus musculus]
NCBI Description
                   >gi_3421062 (AF035823) 29-kDa Golgi SNARE [Mus musculus]
Seq. No.
                   260245
Contig ID
                   1198 2.R1011
5'-most EST
                   LIB3069-021-Q1-K1-B8
Method
                   BLASTX
NCBI GI
                   g3213227
BLAST score
                   224
E value
                   6.0e-18
Match length
                   173
```

Match length 173 % identity 28 NCBI Description (AF03

NCBI Description (AF035209) putative v-SNARE Vtila [Mus musculus]

>gi_3421062 (AF035823) 29-kDa Golgi SNARE [Mus musculus]

Seq. No. 260246

% identity

19



```
Contig ID
                   1198 4.R1011
5'-most EST
                   uC-zmflmo17269a11a1
Seq. No.
                   260247
Contig ID
                   1198_6.R1011
5'-most EST
                  dyk700105231.h1
Seq. No.
                   260248
Contig ID
                  1199 1.R1011
5'-most EST
                  yyf700351942.h1
Method
                  BLASTX
NCBI GI
                   g3249105
BLAST score
                   1217
E value
                   1.0e-134
Match length
                   351
% identity
                   68
NCBI Description (AC003114) Contains similarity to protein phosphatase 2C
                   (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                   260249
Contig ID
                  1201 1.R1011
5'-most EST
                  LIB3059-005-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g2104959
BLAST score
                  511
E value
                  1.0e-51
Match length
                  112
% identity
                  81
NCBI Description (U96925) immunophilin [Vicia faba]
Seq. No.
                  260250
Contig ID
                  1204 1.R1011
5'-most EST
                  LIB3075-044-Q1-K1-B8
Seq. No.
                  260251
Contig ID
                  1209 1.R1011
5'-most EST
                  uC-zmflmo17030f06b1
Method
                  BLASTX
NCBI GI
                  q320608
BLAST score
                  725
                  9.0e-77
E value
Match length
                  145
% identity
                  28
NCBI Description ubiquitin precursor - wild oat >gi_15989 emb CAA49200
                   (X69422) tetraubiquitin [Avena fatua] >gi 777758 (L41658)
                  polyubiquitin [Saccharum sp.]
Seq. No.
                  260252
Contig ID
                  1209 2.R1011
5'-most EST
                  LIB3116-017-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g481477
BLAST score
                  768
E value
                  9.0e-82
Match length
                  165
```

36002

NCBI Description ubiquitin precursor - rice >gi_416038 emb CAA53665



(X76064) polyubiquitin [Oryza sativa] >gi_1574944 (U37687) polyubiquitin [Oryza sativa]

Seq. No. 260253 Contig ID 1209 3.R1011 LIB3062-052-Q1-K1-B12 5'-most EST Method BLASTX NCBI GI q902586 BLAST score 876 E value 2.0e-94 Match length 176 % identity 26 NCBI Description (U29162) ubiquitin [Zea mays] Seq. No. 260254 Contig ID 1209 4.R1011

5'-most EST LIB3150-088-P2-K1-D1 Method BLASTX NCBI GI q899608 BLAST score 344

E value 2.0e-32 Match length 70 % identity 20

NCBI Description (U29158) polyubiquitin [Zea mays]

Seq. No. 260255 Contig ID 1209 5.R1011

5'-most EST LIB3078-035-Q1-K1-G3

Method BLASTN NCBI GI q902583 BLAST score 157 E value 8.0e-83 Match length 248

% identity 95

NCBI Description Zea mays clone MubG1 ubiquitin gene, complete cds

Seq. No. 260256 1209 6.R1011 Contiq ID 5'-most EST vux700157060.h1

Method BLASTX g100812 NCBI GI BLAST score 300 E value 3.0e-27 Match length 61 98 % identity

NCBI Description ubiquitin precursor - wheat (fragment)

>gi_21816_emb_CAA40138_ (X56803) ubiquitin [Triticum
aestivum] >gi_21900_emb_CAA39938_ (X56601) ubiquitin

[Triticum aestivum]

Seq. No. 260257

Contig ID 1209 8.R1011 5'-most EST tfd700576177.h1

Method BLASTN NCBI GI g1220422 BLAST score 227 E value 1.0e-124



```
Match length
                   235
                   99
% identity
NCBI Description Zea mays ubiquitin (MUB14) mRNA, 3' end
                   260258
Seq. No.
                  1209 9.R1011
Contig ID
5'-most EST
                  LIB3059-009-Q1-K1-D5
                  {\tt BLASTX}
Method
NCBI GI
                   g100934
BLAST score
                   200
                   6.0e-30
E value
                   75
Match length
                   15
% identity
NCBI Description
                  ubiquitin precursor Ubi-1 - maize >gi 422037 pir S20926
                   ubiquitin precursor Ubi-2 - maize >gi 248337 bbs 94465
                   (S94464) polyubiquitin(ubiquitin) [maize, Peptide, 533 aa]
                   [Zea mays] >gi 248339 bbs 94467 (S94466)
                   polyubiquitin(ubiquitin) [maize, Peptide, 533 aa] [Zea
                   mays]
                   260259
Seq. No.
Contig ID
                  1209 10.R1011
5'-most EST
                  LIB189-018-Q1-E1-H12
Method
                  BLASTN
NCBI GI
                  g902585
                   292
BLAST score
E value
                   1.0e-163
Match length
                  296
                   67
% identity
NCBI Description Zea mays clone MubG9 ubiquitin gene, complete cds
                   260260
Seq. No.
                  1209 19.R1011
Contig ID
5'-most EST
                  nbm7\overline{0}0475688.h1
Method
                  BLASTN
NCBI GI
                  g1220422
BLAST score
                   69
E value
                   1.0e-30
Match length
                   214
                   96
% identity
NCBI Description
                  Zea mays ubiquitin (MUB14) mRNA, 3' end
Seq. No.
                   260261
Contig ID
                   1211 1.R1011
5'-most EST
                  ymt700221194.h1
                   260262
Contig ID
                   1211 2.R1011
5'-most EST
                  LIB3066-029-Q1-K1-D8
```

Seq. No.

260263 Seq. No. Contig ID 1214 1.R1011

5'-most EST LIB3153-006-Q1-K1-G5

Seq. No. 260264 Contig ID 1218 1.R1011

5'-most EST LIB3075-054-Q1-K1-G1

% identity

NCBI Description

79

[Medicago sativa]



```
260265
Seq. No.
                  1224 1.R1011
Contig ID
                  uC-zmflb73185a04b1
5'-most EST
Method
                  BLASTX
                  g3096935
NCBI GI
BLAST score
                  1004
                   1.0e-111
E value
Match length
                   367
                   61
% identity
                  (AL023094) putative protein [Arabidopsis thaliana]
NCBI Description
                  260266
Seq. No.
                  1224 3.R1011
Contig ID
                  LIB3075-043-Q1-K1-E9
5'-most EST
                  BLASTX
Method
                  g4539321
NCBI GI
BLAST score
                   237
                   1.0e-19
E value
                  72
Match length
                   58
% identity
                  (AL035679) putative protein [Arabidopsis thaliana]
NCBI Description
                   260267
Seq. No.
                   1224 5.R1011
Contig ID
                  LIB3180-012-P2-M1-H10
5'-most EST
Method
                   BLASTX
                   g3096935
NCBI GI
BLAST score
                   256
                   2.0e-22
E value
                   67
Match length
                   81
% identity
                  (AL023094) putative protein [Arabidopsis thaliana]
NCBI Description
                   260268
Seq. No.
Contig ID
                   1228_1.R1011
5'-most EST
                   uwc700151117.h1
Method
                   BLASTX
NCBI GI
                   q2435511
                   512
BLAST score
E value
                   2.0e-51
Match length
                   184
% identity
                   55
                  (AF024504) contains similarity to prolyl 4-hydroxylase
NCBI Description
                   alpha subunit [Arabidopsis thaliana]
Seq. No.
                   260269
Contig ID
                   1235 1.R1011
5'-most EST
                   xjt700094561.h1
Method
                   BLASTX
NCBI GI
                   a3334756
BLAST score
                   479
E value
                   1.0e-47
Match length
                   114
```

36005

(Y16672) putative arginine/serine-rich splicing factor



260270 Seq. No. Contig ID 1235 2.R1011 5'-most EST LIB3067-026-Q1-K1-C10 260271 Seq. No. 1235 4.R1011 Contig ID LIB143-064-Q1-E1-G12 5'-most EST Method BLASTX NCBI GI g3334756 BLAST score 328 E value 1.0e-30 Match length 106 % identity 63 NCBI Description (Y16672) putative arginine/serine-rich splicing factor [Medicago sativa] 260272 Seq. No. 1237 1.R1011 Contig ID 5'-most EST LIB3150-068-P1-N1-A5 Method BLASTX NCBI GI g1172836 BLAST score 1004 E value 1.0e-109 Match length 193 96 % identity NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi 496272 (L16787) small ras-related protein [Nicotiana tabacum] 260273 Seq. No. Contig ID 1237 2.R1011 5'-most EST LIB3088-003-Q1-K1-A9 Method BLASTX NCBI GI q4336905 BLAST score 227 E value 2.0e-18 Match length 46 % identity NCBI Description (AF112244) Ran-related GTP binding protein [Zea mays] Seq. No. 260274 1237 3.R1011 Contig ID 5'-most EST xyt700343776.h1 Method BLASTX NCBI GI g2149051 BLAST score 737 E value 1.0e-100 Match length 233 % identity 81 NCBI Description (U73810) small Ras-like GTP-binding protein [Arabidopsis

thaliana]

Seq. No. 260275

1237 4.R1011 Contig ID

5'-most EST LIB189-028-Q1-E1-B2

Method BLASTX NCBI GI g4336905



```
BLAST score
                  533
                  3.0e-54
E value
Match length
                  103
                  97
% identity
                  (AF112244) Ran-related GTP binding protein [Zea mays]
NCBI Description
                  260276
Seq. No.
                  1237 5.R1011
Contig ID
5'-most EST
                  LIB3069-027-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  g1172836
BLAST score
                  996
                  1.0e-108
E value
Match length
                  194
                  94
% identity
NCBI Description
                  GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi 496272 (L16787)
                  small ras-related protein [Nicotiana tabacum]
Seq. No.
                  260277
Contig ID
                  1237 6.R1011
5'-most EST
                  uC-zmflb73181c03b2
Method
                  BLASTX
NCBI GI
                  g4336905
BLAST score
                  157
E value
                  3.0e-10
Match length
                  33
% identity
                  91
                  (AF112244) Ran-related GTP binding protein [Zea mays]
NCBI Description
                  260278
Seq. No.
Contig ID
                  1237 7.R1011
5'-most EST
                  uer700579760.h1
                  260279
Seq. No.
                  1237 8.R1011
Contig ID
5'-most EST
                  LIB3068-009-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  q495731
BLAST score
                  413
E value
                  2.0e-40
Match length
                  88
% identity
NCBI Description (L16790) small ras-related protein [Arabidopsis thaliana]
Seq. No.
                  260280
Contig ID
                  1237 10.R1011
5'-most EST
                  fdz701165701.h1
Method
                  BLASTX
NCBI GI
                  g4336905
BLAST score
                  456
E value
                  3.0e-45
                  88
Match length
% identity
NCBI Description
                  (AF112244) Ran-related GTP binding protein [Zea mays]
```

36007

260281

1237 12.R1011

Seq. No.

Contig ID

NCBI Description

thaliana]



```
pwr700449772.h2
5'-most EST
                   260282
Seq. No.
                   1238 1.R1011
Contig ID
5'-most EST
                  LIB3150-048-Q1-N1-E6
                   BLASTX
Method
                   g2459420
NCBI GI
BLAST score
                   714
E value
                   2.0e-75
Match length
                   140
                   97
% identity
NCBI Description
                  (AC002332) putative ribosomal protein L17 [Arabidopsis
                   thaliana]
                   260283
Seq. No.
                   1238 2.R1011
Contig ID
                   nbm7\overline{0}0471476.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1174613
BLAST score
                   2046
                   0.0e+00
E value
                   416
Match length
                   97
% identity
                   26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
NCBI Description
                   PROTEIN HOMOLOG 1) (TBP-1) >gi_556560_dbj_BAA04614_
                   (D17788) rice homologue of Tat binding protein [Oryza
                   sativa]
                   260284
Seq. No.
Contig ID
                   1238 3.R1011
5'-most EST
                   LIB3061-057-Q1-K1-H1
                   260285
Seq. No.
Contig ID
                   1238 4.R1011
                   wyr700235948.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1174613
BLAST score
                   289
                   4.0e-28
E value
Match length
                   95
                   76
% identity
                   26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
NCBI Description
                   PROTEIN HOMOLOG 1) (TBP-1) >gi_556560_dbj_BAA04614_
                   (D17788) rice homologue of Tat binding protein [Oryza
                   sativa]
Seq. No.
                   260286
Contig ID
                   1238 5.R1011
5'-most EST
                   uC-zmroteosinte035b11b2
Method
                   BLASTX
NCBI GI
                   g2459420
BLAST score
                   714
                   2.0e-75
E value
Match length
                   140
% identity
                   97
```

(AC002332) putative ribosomal protein L17 [Arabidopsis

E value

Match length

NCBI Description

% identity

1.0e-151

338 77



```
260287
Seq. No.
Contig ID
                   1238 6.R1011
                   uwc700152967.hl
5'-most EST
                   BLASTX
Method
                   q3096910
NCBI GI
BLAST score
                   1055
                   1.0e-115
E value
Match length
                   249
% identity
                   80
                   (AJ005813) neoxanthin cleavage enzyme [Arabidopsis
NCBI Description
                   thaliana]
                   260288
Seq. No.
Contig ID
                   1238 7.R1011
5'-most EST
                  LIB3060-043-Q1-K1-B11
Seq. No.
                   260289
                   1238 8.R1011
Contig ID
                   uC-zmflmo17222d06b1
5'-most EST
                   BLASTX
Method
                   g3236247
NCBI GI
BLAST score
                   738
                   8.0e-78
E value
                   230
Match length
% identity
                   60
                  (AC004684) SCARECROW-like protein [Arabidopsis thaliana]
NCBI Description
                   260290
Seq. No.
                   1238 9.R1011
Contig ID
                   uC-zmflb73286e05b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2341028
BLAST score
                   251
                   3.0e-21
E value
Match length
                   73
                   75
% identity
NCBI Description
                   (AC000104) Strong similarity to 60S ribosomal protein L17
                   (gb_X01694). EST gb_AA042332 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   260291
                   1238 10.R1011
Contig ID
5'-most EST
                   uC-zmrob73079d10b1
                   260292
Seq. No.
Contig ID
                   1238_11.R1011
5'-most EST
                   uC-zmrob73036g10b1
Method
                   BLASTX
NCBI GI
                   q3096910
BLAST score
                   1243
```

(AJ005813) neoxanthin cleavage enzyme [Arabidopsis thaliana]



Seq. No. 260293

Contig ID 1238_12.R1011 5'-most EST pmx700091679.h1

Method BLASTX
NCBI GI g1174613
BLAST score 295
E value 1.0e-26
Match length 92
% identity 68

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING

PROTEIN HOMOLOG 1) (TBP-1) >gi_556560_dbj_BAA04614_ (D17788) rice homologue of Tat binding protein [Oryza

sativa]

Seq. No. 260294

Contig ID 1238_13.R1011

5'-most EST LIB3137-049-Q1-K1-H12

Seq. No. 260295

Contig ID 1238_14.R1011 5'-most EST uC-zmflb73279g11a2

Seq. No. 260296

Contig ID 1238_15.R1011 5'-most EST uC-zmflb73047a08b1

Seq. No. 260297

Contig ID 1238 17.R1011

5'-most EST LIB3180-013-P2-M1-F11

Seq. No. 260298

Contig ID 1241 1.R1011

5'-most EST LIB3062-048-Q1-K1-F11

Method BLASTX
NCBI GI g3757521
BLAST score 708
E value 2.0e-74
Match length 227
% identity 57

NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 260299

Contig ID 1242 1.R1011

5'-most EST LIB3069-029-Q1-K1-E1

Seq. No. 260300

Contig ID 1243 1.R1011

5'-most EST LIB143-036-Q1-E1-D11

Method BLASTX
NCBI GI g3660469
BLAST score 671
E value 3.0e-70
Match length 144
% identity 93

NCBI Description (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis

thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569)

succinyl-CoA ligase beta subunit [Arabidopsis thaliana]

Match length

136



```
260301
Seq. No.
                  1243 2.R1011
Contig ID
                  tzu700206564.h1
5'-most EST
                  BLASTX
Method
                  q3660469
NCBI GI
                  1298
BLAST score
                  1.0e-144
E value
                   301
Match length
                   82
% identity
                   (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis
NCBI Description
                   thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569)
                  succinyl-CoA ligase beta subunit [Arabidopsis thaliana]
                   260302
Seq. No.
                   1243 3.R1011
Contig ID
                  uC-zmflb73247e01a2
5'-most EST
                  BLASTX
Method
                   g3212855
NCBI GI
BLAST score
                   626
E value
                   1.0e-64
                   330
Match length
                   41
% identity
                  (AC004005) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   260303
Contig ID
                   1243 4.R1011
5'-most EST
                   uC-zmflb73196b07b1
                   BLASTX
Method
                   g3660469
NCBI GI
BLAST score
                   145
E value
                   9.0e-09
                   39
Match length
                   77
% identity
                   (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis
NCBI Description
                   thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569)
                   succinyl-CoA ligase beta subunit [Arabidopsis thaliana]
                   260304
Seq. No.
Contig ID
                   1243 5.R1011
5'-most EST
                   LIB3279-060-P1-K1-E6
                   260305
Seq. No.
Contig ID
                   1245 1.R1011
5'-most EST
                   LIB3075-043-Q1-K1-E4
Seq. No.
                   260306
Contig ID
                   1246 1.R1011
                   wyr700242564.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3668097
BLAST score
                   560
                   3.0e-57
E value
```



Seq. No. 260307

Contig ID 1246 2.R1011

5'-most EST LIB3151-026-Q1-K1-D5

Method BLASTX
NCBI GI g3668097
BLAST score 352
E value 2.0e-33
Match length 85
% identity 82

NCBI Description (AC004667) putative glycine cleavage system protein H

precursor [Arabidopsis thaliana]

Seq. No. 260308

Contig ID 1246 3.R1011

5'-most EST LIB3069-009-Q1-K1-C1

Method BLASTX
NCBI GI g3668097
BLAST score 233
E value 2.0e-19
Match length 66
% identity 70

NCBI Description (AC004667) putative glycine cleavage system protein H

precursor [Arabidopsis thaliana]

Seq. No. 260309

Contig ID 1246_4.R1011 5'-most EST uwc700153157.h1

Method BLASTX
NCBI GI g3668097
BLAST score 150
E value 1.0e-09
Match length 43
% identity 67

NCBI Description (AC004667) putative glycine cleavage system protein H

precursor [Arabidopsis thaliana]

Seq. No. 260310

Contig ID 1246_5.R1011

5'-most EST uC-zmroteosinte043h03b2

Method BLASTX
NCBI GI g3668097
BLAST score 231
E value 9.0e-22
Match length 114
% identity 53

NCBI Description (AC004667) putative glycine cleavage system protein H

precursor [Arabidopsis thaliana]

Seq. No. 260311

Contig ID 1246_6.R1011 5'-most EST hbs701185611.h1

Seq. No. 260312

Contig ID 1249_1.R1011

5'-most EST uC-zmroteosinte096c07b2

Method BLASTX



NCBI GI g116054 BLAST score 415 E value 4.0e-40 Match length 189 % identity 44

NCBI Description CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK)

>gi_280393_pir__A43713 calcium-dependent protein kinase (EC
2.7.1.-) - soybean >gi_169931 (M64987) Glycine max calcium

dependent protein kinase mRNA. [Glycine max]

Seq. No. 260313

Contig ID 1250_1.R1011 5'-most EST afb700380915.h1

Method BLASTX
NCBI GI g3641837
BLAST score 2521
E value 0.0e+00
Match length 741
% identity 70

NCBI Description (AL023094) Nonclathrin coat protein gamma - like protein

[Arabidopsis thaliana]

Seq. No. 260314

Contig ID 1251_1.R1011 5'-most EST pmx700086817.h1

Method BLASTX
NCBI GI g3372671
BLAST score 386
E value 5.0e-37
Match length 120
% identity 59

NCBI Description (AF061286) gamma-adaptin 1 [Arabidopsis thaliana]

Seq. No. 260315

Contig ID 1251_2.R1011

5'-most EST uC-zmflmo17060h06b1

Method BLASTX
NCBI GI g3372671
BLAST score 194
E value 2.0e-14
Match length 60
% identity 60

NCBI Description (AF061286) gamma-adaptin 1 [Arabidopsis thaliana]

Seq. No. 260316

Contig ID 1253_2.R1011

5'-most EST LIB3060-016-Q1-K1-A4

Method BLASTX
NCBI GI g4454484
BLAST score 621
E value 4.0e-69
Match length 192
% identity 71

NCBI Description (AC006234) putative diacylglycerol kinase [Arabidopsis

thaliana]

Seq. No. 260317



```
1259 1.R1011
Contig ID
                  LIB3075-043-Q1-K1-B7
5'-most EST
Seq. No.
                  260318
                  1260 1.R1011
Contig ID
                  ymt700220438.h1
5'-most EST
Method
                  BLASTX
                  g4455223
NCBI GI
                  740
BLAST score
                   4.0e-78
E value
                  219
Match length
% identity
                   66
                   (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  260319
                  1260 2.R1011
Contig ID
5'-most EST
                  uC-zmflb73253a11b1
Method
                  BLASTX
                  g4455223
NCBI GI
BLAST score
                  166
                   5.0e-12
E value
Match length
                   61
% identity
                   62
                  (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  260320
Contig ID
                  1261 1.R1011
                  LIB36-012-Q1-E1-H4
5'-most EST
                  BLASTX
Method
                  g4586049
NCBI GI
BLAST score
                   602
                   4.0e-62
E value
                   279
Match length
% identity
                   42
NCBI Description
                  (AC007020) hypothetical protein [Arabidopsis thaliana]
                   260321
Seq. No.
Contig ID
                   1263 1.R1011
5'-most EST
                   LIB3075-043-Q1-K1-A8
Method
                   BLASTX
                   g2262105
NCBI GI
BLAST score
                   520
E value
                   2.0e-52
Match length
                   344
                   34
% identity
NCBI Description
                  (AC002343) unknown protein [Arabidopsis thaliana]
Seq. No.
                   260322
                   1268 1.R1011
Contig ID
5'-most EST
                   yyf700350395.h1
Method
                   BLASTX
NCBI GI
                   q3643603
BLAST score
                   289
```

36014

2.0e-47

442

E value Match length



% identity

NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

260323 Seq. No.

Contig ID 1269 1.R1011

5'-most EST uC-zmflm017093q09b1

Method BLASTX NCBI GI q3914431 BLAST score 1089 E value 1.0e-119 Match length 229 % identity 88

NCBI Description PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8)

(MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8)

>gi_2285802_dbj_BAA21651 (D78173) 26S proteasome alpha

subunit [Spinacia oleracea]

260324 Seq. No.

Contig ID 1269 2.R1011 5'-most EST rvt700551861.h1

Method BLASTX NCBI GI g3914431 BLAST score 574 E value 4.0e-59 Match length 126 % identity 88

NCBI Description PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8)

(MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8)

>gi_2285802_dbj_BAA21651 (D78173) 26S proteasome alpha

subunit [Spinacia oleracea]

260325 Seq. No.

Contig ID 1269 3.R1011

5'-most EST LIB3088-001-Q1-K1-E10

Method BLASTX NCBI GI q3914431 BLAST score 261 E value 3.0e-22 Match length 56 % identity

NCBI Description PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8)

(MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8)

>gi 2285802 dbj BAA21651 (D78173) 26S proteasome alpha

subunit [Spinacia oleracea]

Seq. No. 260326

Contig ID 1270 1.R1011

5'-most EST uC-zmflmo17217g09b1

Seq. No. 260327

Contig ID 1270 2.R1011

5'-most EST LIB36-019-Q1-E1-D3

260328 Seq. No.

Contig ID 1270 3.R1011

5'-most EST LIB3136-001-P1-K1-F5

Method BLASTX

NCBI Description



```
NCBI GI
                   g2588895
BLAST score
                  150
                   2.0e-09
E value
Match length
                   143
% identity
                   29
NCBI Description
                  (AB008515) RanBPM [Homo sapiens]
                  260329
Seq. No.
                  1271 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17342h07a1
Method
                  BLASTX
NCBI GI
                  g3551247
BLAST score
                  339
E value
                  1.0e-31
Match length
                   69
                   94
% identity
NCBI Description
                  (AB012703) 181 [Daucus carota]
                   260330
Seq. No.
                  1271 2.R1011
Contig ID
5'-most EST
                  LIB3075-043-Q1-K1-B5
Method
                   BLASTX
NCBI GI
                   g3551247
BLAST score
                   968
E value
                   1.0e-105
Match length
                   190
% identity
                   96
                  (AB012703) 181 [Daucus carota]
NCBI Description
                   260331
Seq. No.
                   1272 1.R1011
Contig ID
5'-most EST
                  xmt700258684.h1
                   260332
Seq. No.
Contig ID
                   1273 1.R1011
5'-most EST
                   uC-zmflmo17265f06b1
Method
                   BLASTX
NCBI GI
                   g1203832
BLAST score
                   2768
                   0.0e + 00
E value
Match length
                   622
% identity
                   84
NCBI Description
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
                   [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan
                   exohydrolase [Hordeum vulgare]
Seq. No.
                   260333
Contig ID
                   1273 3.R1011
5'-most EST
                   xjt700093504.h1
Method
                   BLASTX
NCBI GI
                   q1203832
BLAST score
                   446
E value
                   3.0e-44
                 124
Match length
% identity
                   71
```

(U46003) beta-D-glucan exohydrolase, isoenzyme ExoII [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan



exohydrolase [Hordeum vulgare]

```
Seq. No.
                  260334
Contig ID
                  1273 6.R1011
5'-most EST
                  LIB3066-040-Q1-K1-B5
                  BLASTX
Method
                  a3201554
NCBI GI
BLAST score
                  300
                  2.0e-27
E value
                  61
Match length
                  89
% identity
                  (AJ006501) beta-D-glucosidase [Tropaeolum majus]
NCBI Description
Seq. No.
                  260335
                  1275 1.R1011
Contig ID
                  LIB3075-011-Q1-K1-H3
5'-most EST
Method
                  BLASTX
                  g1203832
NCBI GI
BLAST score
                  573
                  4.0e-59
E value
                  175
Match length
                  65
% identity
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
NCBI Description
                  [Hordeum vulgare] >gi 1588407 prf 2208395A beta-D-glucan
                  exohydrolase [Hordeum vulgare]
                  260336
Seq. No.
Contig ID
                  1280 1.R1011
5'-most EST
                  uC-zmflmo17030g08b1
Method
                  BLASTX
NCBI GI
                  q4220474
BLAST score
                  1399
                  1.0e-155
E value
Match length
                  470
% identity
                  66
                  (AC006069) putative myosin heavy chain [Arabidopsis
NCBI Description
                  thaliana]
                  260337
Seq. No.
Contig ID
                  1280 2.R1011
5'-most EST
                  xsy700208501.h1
                  BLASTX
Method
NCBI GI
                  q4220474
BLAST score
                  434
E value
                  5.0e-44
Match length
                  160
                  60
% identity
                  (AC006069) putative myosin heavy chain [Arabidopsis
NCBI Description
                  thaliana]
                  260338
Seq. No.
                  1283 1.R1011
Contig ID
                  LIB3181-007-P1-K2-D10
5'-most EST
Method
                  BLASTX
                  g3044218
NCBI GI
BLAST score
                  708
```

1.0e-74

E value



```
167
Match length
% identity
                   77
                  (AF057144) signal peptidase [Arabidopsis thaliana]
NCBI Description
                  260339
Seq. No.
                  1283 2.R1011
Contig ID
                  uC-zmflb73233h07b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3044218
BLAST score
                  543
E value
                  2.0e-55
Match length
                  124
                   79
% identity
                  (AF057144) signal peptidase [Arabidopsis thaliana]
NCBI Description
                  260340
Seq. No.
                  1286 1.R1011
Contig ID
5'-most EST
                  LIB3066-048-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g2924512
BLAST score
                  516
                   2.0e-52
E value
                  172
Match length
                   55
% identity
NCBI Description
                  (AL022023) beta-galactosidase - like protein [Arabidopsis
                  thaliana]
                   260341
Seq. No.
                  1289 1.R1011
Contig ID
5'-most EST
                  LIB3159-013-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                   g4539420
BLAST score
                   154
                   4.0e-10
E value
Match length
                   54
% identity
                   57
NCBI Description
                  (AL049171) putative protein (fragment) [Arabidopsis
                   thaliana]
                   260342
Seq. No.
Contig ID
                   1289 3.R1011
5'-most EST
                   nwy700445592.h1
Seq. No.
                   260343
Contig ID
                   1292 1.R1011
5'-most EST
                   LIB3075-042-Q1-K1-E11
Method
                   BLASTX
NCBI GI
                   g3420299
BLAST score
                   502
E value
                   1.0e-50
Match length
                   111
% identity
                  (AF072849) jab1 protein [Oryza sativa subsp. indica]
NCBI Description
```

Seq. No. 260344 1295 1.R1011 Contig ID

5'-most EST uC-zmflMo17064h05b1



Method BLASTX
NCBI GI g3738333
BLAST score 402
E value 4.0e-39
Match length 143
% identity 59

NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 260345

Contig ID 1295 2.R1011

5'-most EST LIB3075-042-Q1-K1-E3

Method BLASTX
NCBI GI g3738333
BLAST score 285
E value 2.0e-25
Match length 139
% identity 47

NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 260346

Contig ID 1296_1.R1011 5'-most EST uwc700156331.h1

Method BLASTX
NCBI GI g2832628
BLAST score 615
E value 2.0e-63
Match length 275
% identity 51

NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

 Seq. No.
 260347

 Contig ID
 1296_2.R1011

5'-most EST uC-zmflb73067f07b1

Seq. No. 260348

Contig ID 1296 3.R1011

5'-most EST LIB3067-019-Q1-K1-H10

Seq. No. 260349

Contig ID 1296_4.R1011

5'-most EST LIB3059-025-Q1-K1-A2

Seq. No. 260350

Contig ID 1297 1.R1011

5'-most EST uC-zmflmo17283a12b1

Method BLASTX
NCBI GI g3386596
BLAST score 442
E value 9.0e-44
Match length 110
% identity 75

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

>gi_3702346 (AC005397) unknown protein [Arabidopsis

thaliana]

Seq. No. 260351

Contig ID 1298_1.R1011



79

thaliana]

% identity

NCBI Description

```
5'-most EST
                  LIB3061-034-Q1-K1-E1
                   260352
Seq. No.
                   1298 2.R1011
Contig ID
                   LIB3075-042-Q1-K1-E7
5'-most EST
                   260353
Seq. No.
                   1299 1.R1011
Contig ID
                  LIB3075-042-Q1-K1-E8
5'-most EST
                   260354
Seq. No.
Contig ID
                   1299 3.R1011
                   wyr700238930.hl
5'-most EST
                   260355
Seq. No.
                   1299 4.R1011
Contig ID
5'-most EST
                   uwc700151623.hl
                   260356
Seq. No.
                   1304 1.R1011
Contig ID
                   uC-z\overline{m}flb73047d11b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2462925
BLAST score
                   1167
                   1.0e-128
E value
Match length
                   268
                   83
% identity
NCBI Description
                   (AJ000053) GTP cyclohydrolase II /
                   3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis
                   thaliana]
                   260357
Seq. No.
                   1304 2.R1011
Contig ID
                   uC-zmflb73260b03b2
5'-most EST
                   BLASTX
Method
                   g2462925
NCBI GI
BLAST score
                   1112
E value
                   1.0e-122
                   262
Match length
                   82
% identity
                   (AJ000053) GTP cyclohydrolase II /
NCBI Description
                   3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis
                   thaliana]
                   260358
Seq. No.
                   1304_3.R1011
Contig ID
                   uC-zmflb73093f10b2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2462925
BLAST score
                   629
                   3.0e-65
E value
Match length
                   191
```

3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis

(AJ000053) GTP cyclohydrolase II /



Seq. No. 260359 Contig ID 1304_5.R1011 5'-most EST ntr700074925.h1

Seq. No. 260360

Contig ID 1304_6.R1011

5'-most EST uC-zmromo17028b06a1

Seq. No. 260361

Contig ID 1305_1.R1011 5'-most EST pmx700083315.h1

Seq. No. 260362

Contig ID 1307_1.R1011

5'-most EST LIB3060-021-Q1-K1-D10

Method BLASTN
NCBI GI g2274991
BLAST score 42
E value 7.0e-14
Match length 86
% identity 87

NCBI Description Hordeum vulgare mRNA for expressed sequence tag

Seq. No. 260363

Contig ID 1307_3.R1011 5'-most EST tfd700575789.h1

Seq. No. 260364

Contig ID 1314_1.R1011

5'-most EST LIB148-046-Q1-E1-D4

Seq. No. 260365

Contig ID 1314_2.R1011

5'-most EST LIB148-058-Q1-E1-G2

Seq. No. 260366

Contig ID 1315_1.R1011

5'-most EST uC-zmflb73349f05a2

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 2.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 260367

Contig ID 1315_2.R1011 5'-most EST wty700164525.h1

Method BLASTX
NCBI GI g2275635
BLAST score 166
E value 5.0e-11
Match length 194
% identity 28

NCBI Description (AF014940) similar to the EMP24/GP25L family of membrane

proteins [Caenorhabditis elegans]



```
Seq. No.
                  260368
Contig ID
                  1315 5.R1011
5'-most EST
                  LIB143-064-Q1-E1-G1
                  260369
Seq. No.
Contig ID
                  1321 1.R1011
5'-most EST
                  uC-zmflb73051h05b1
                  260370
Seq. No.
                  1322 1.R1011
Contig ID
5'-most EST
                  LIB3066-032-Q1-K1-E12
Method
                  BLASTX
                  q2739370
NCBI GI
                  990
BLAST score
                  1.0e-111
E value
Match length
                  420
% identity
                  50
NCBI Description
                  (AC002505) putative pectinesterase [Arabidopsis thaliana]
                  260371
Seq. No.
                  1323 1.R1011
Contig ID
                  uC-zmflb73298c11b1
5'-most EST
                  BLASTX
Method
                  q1419090
NCBI GI
                  1174
BLAST score
                  1.0e-129
E value
                  272
Match length
% identity
                  79
NCBI Description
                  (X94968) 37kDa chloroplast inner envelope membrane
                  polypeptide precursor [Nicotiana tabacum]
Seq. No.
                   260372
Contig ID
                  1324 1.R1011
5'-most EST
                  uC-zmflmo17108e05b1
Method
                  BLASTX
                   q3947690
NCBI GI
BLAST score
                   917
E value
                   1.0e-98
Match length
                   584
% identity
                   38
NCBI Description (AJ131245) Sec24B protein [Homo sapiens]
                   260373
Seq. No.
                   1330 1.R1011
Contig ID
                   uC-zmrob73050d03b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g799177
BLAST score
                   828
                   3.0e-88
E value
                   674
Match length
% identity
                   24
```

NCBI Description (U22055) 100 kDa coactivator [Homo sapiens]

Seq. No. 260374 Contig ID 1330 2.R1011

5'-most EST LIB3069-025-Q1-K1-C2



```
Seq. No.
                  260375
Contig ID
                  1330 3.R1011
5'-most EST
                  ypc700800359.h1
                  260376
Seq. No.
                  1330 5.R1011
Contig ID
5'-most EST
                  LIB3059-036-Q1-K1-C7
                  260377
Seq. No.
                  1330 6.R1011
Contig ID
                  ypc700801796.h1
5'-most EST
                  BLASTX
Method
                  g141613
NCBI GI
BLAST score
                  145
                  2.0e-09
E value
Match length
                  33
                  88
% identity
NCBI Description
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
                  >qi 72305 pir ZIZM21 22K zein precursor (clone pZ22.1) -
                  maize >gi_22532_emb_CAA24725_ (V01478) zein [Zea mays]
                  260378
Seq. No.
                  1330 7.R1011
Contig ID
                  rvt700552891.hl
5'-most EST
                  260379
Seq. No.
                  1333 1.R1011
Contig ID
5'-most EST
                  LIB3075-042-Q1-K1-B10
Seq. No.
                  260380
                  1341 1.R1011
Contig ID
5'-most EST
                  LIB143-064-Q1-E1-A6
                  260381
Seq. No.
Contig ID
                  1342 1.R1011
                  LIB3075-041-Q1-K1-F9
5'-most EST
Method
                  BLASTX
NCBI GI
                   q4006932
BLAST score
                   170
E value
                   1.0e-11
Match length
                   107
                   41
% identity
                  (AJ011400) NADH: ubiquinone oxidoreductase b17.2 subunit
NCBI Description
                   [Bos taurus]
                   260382
Seq. No.
                   1342 2.R1011
Contig ID
5'-most EST
                   uC-zmflMo17016b11b1
Method
                   BLASTX
                   g4006932
NCBI GI
```

Method BLASTX
NCBI GI 94006932
BLAST score 154
E value 4.0e-10
Match length 74

% identity 47

NCBI Description (AJ011400) NADH: ubiquinone oxidoreductase b17.2 subunit

[Bos taurus]



 Seq. No.
 260383

 Contig ID
 1343_1.R1011

 5'-most EST
 ymt700219804.h1

 Method
 BLASTX

 NCBI GI
 g4538929

NCBI GI g4538929
BLAST score 943
E value 1.0e-102
Match length 412
% identity 49

NCBI Description (AL049483) putative nucleic acid binding protein

[Arabidopsis thaliana]

Seq. No. 260384

Contig ID 1343_2.R1011

5'-most EST uC-zmflmo17267f04b1

Method BLASTX
NCBI GI 94538929
BLAST score 311
E value 2.0e-28
Match length 88
% identity 60

NCBI Description (AL049483) putative nucleic acid binding protein

[Arabidopsis thaliana]

Seq. No. 260385

Contig ID 1345_1.R1011 5'-most EST clt700044841.f1

Method BLASTX
NCBI GI g3287695
BLAST score 399
E value 2.0e-38
Match length 150
% identity 51

NCBI Description (AC003979) Similar to hypothetical protein C34B7.2

gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis

thaliana]

Seq. No. 260386 Contig ID 1351_1.R1011

5'-most EST uC-zmflb73267h06a1

Method BLASTX
NCBI GI g1279358
BLAST score 154
E value 1.0e-09
Match length 166
% identity 31

NCBI Description (X97159) aquaporin [Cicadella viridis]

 Seq. No.
 260387

 Contig ID
 1353_1.R1011

 5'-most EST
 zuv700353065.h1

Method BLASTX
NCBI GI g137460
BLAST score 3024
E value 0.0e+00
Match length 619



% identity VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD NCBI Description SUBUNIT) >gi 67952 pir PXPZV9 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 69K chain - carrot >gi_167560 (J03769) vacular H+-ATPase [Daucus carota] 260388 Seq. No. 1353 2.R1011 Contig ID LIB3115-036-P1-K2-G2 5'-most EST BLASTX Method NCBI GI g2326947 BLAST score 1411 1.0e-157 E value Match length 281 % identity 96 (Z50801) Chlorophyll a/b-binding protein CP29 precursor NCBI Description [Zea mays] 260389 Seq. No. 1353 3.R1011 Contig ID 5'-most EST LIB148-020-Q1-E1-E3 Method BLASTX g629839 NCBI GI BLAST score 2189 E value 0.0e + 00Match length 426 % identity 97 NCBI Description beta-6 tubulin - maize >gi 416147 (L10633) beta-6 tubulin [Zea mays] Seq. No. 260390 Contig ID 1353 4.R1011 fdz701163423.hl 5'-most EST Method BLASTX NCBI GI q398849 BLAST score 2165 0.0e+00E value Match length 422 ... % identity 97 (X74656) beta-5 tubulin [Zea mays] NCBI Description Seq. No. 260391 1353 5.R1011 Contig ID 5'-most EST ceu700432894.h1 BLASTX Method NCBI GI q629840 BLAST score 2183 E value 0.0e + 00Match length 426 % identity tubulin beta-7 chain - maize >gi 416149 (L10634) beta-7 NCBI Description tubulin [Zea mays]

Seq. No. 260392 Contig ID 1353 6.R1011 5'-most EST uC-zmflb73195g09b1

Method BLASTX

```
NCBI GI
                  q4415992
BLAST score
                  2145
                  0.0e + 00
E value
Match length
                  420
% identity
                  96
                 (AF059288) beta-tubulin 2 [Eleusine indica]
NCBI Description
Seg. No.
                  260393
                  1353 7.R1011
Contig ID
                  wyr700243089.h1
5'-most EST
                  BLASTX
Method
                  g1352830
NCBI GI
BLAST score
                  470
                  6.0e-47
E value
                  91
Match length
                  97
% identity
NCBI Description
                  VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
                  SUBUNIT) >gi 1049253 (U36436) vacuolar ATPase 69 kDa
                  subunit [Zea mays]
Seq. No.
                  260394
                  1353 8.R1011
Contig ID
                  rv1700455962.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q629838
                  2214
BLAST score
                  0.0e + 00
E value
                  432
Match length
% identity
                  97
NCBI Description tubulin beta-4 chain - maize >gi 416145 (L10635) beta-4
                  tubulin [Zea mays]
                  260395
Seq. No.
Contig ID
                  1353 9.R1011
5'-most EST
                  LIB3067-049-Q1-K1-D3
Method
                  BLASTX
NCBI GI
                  g629840
BLAST score
                  1029
E value
                  1.0e-112
Match length
                  199
                  98
```

% identity

NCBI Description tubulin beta-7 chain - maize >gi 416149 (L10634) beta-7

tubulin [Zea mays]

260396 Seq. No.

1353 11.R1011 Contig ID 5'-most EST wyr700243681.h1

BLASTX Method NCBI GI g398849 BLAST score 1896 E value 0.0e+00Match length 374 % identity 96

NCBI Description (X74656) beta-5 tubulin [Zea mays]

260397 Seq. No.

1353 12.R1011 Contig ID



```
5'-most EST
                  xsy700212269.h1
Method
                  BLASTX
NCBI GI
                  q398849
BLAST score
                   2176
                  0.0e+00
E value
Match length
                  430
% identity
                   95
                  (X74656) beta-5 tubulin [Zea mays]
NCBI Description
Seq. No.
                  260398
                  1353 13.R1011
Contig ID
5'-most EST
                  wyr700237849.h1
Method
                  BLASTN
NCBI GI
                  g416146
BLAST score
                  52
E value
                   2.0e-20
Match length
                   68
% identity
                   94
                  Zea mays beta-6 tubulin (tub6) gene and mRNA, complete cds
NCBI Description
                   260399
Seq. No.
Contig ID
                   1353 14.R1011
5'-most EST
                  xsy700217357.hl
Method
                  BLASTX
NCBI GI
                   g2326947
BLAST score
                   500
                   1.0e-50
E value
Match length
                  122
% identity
                   83
                  (Z50801) Chlorophyll a/b-binding protein CP29 precursor
NCBI Description
                   [Zea mays]
                   260400
Seq. No.
                   1353 15.R1011
Contig ID
5'-most EST
                   LIB3078-038-Q1-K1-B4
                   BLASTX
Method
NCBI GI
                   g398845
BLAST score
                   274
                   4.0e-24
E value
Match length
                   62
% identity
                   85
NCBI Description
                  (X74654) beta3 tubulin [Zea mays]
Seq. No.
                   260401
                   1353 16.R1011
Contig ID
5'-most EST
                   wen700333832.h1
                   BLASTX
Method
NCBI GI
                   g4415994
BLAST score
                   694
E value
                   3.0e-73
Match length
                   128
% identity
                  (AF059289) beta-tubulin 3 [Eleusine indica]
```

NCBI Description

260402 Seq. No.

Contig ID 1353 17.R1011 5'-most EST LIB36-015-Q1-E1-G9



BLASTX Method g2326947 NCBI GI BLAST score 301 2.0e-27 E value Match length 59 98 % identity (Z50801) Chlorophyll a/b-binding protein CP29 precursor NCBI Description [Zea mays] 260403 Seq. No. 1353 18.R1011 Contig ID 5'-most EST uC-zmflmo17174a04a1 Method BLASTX q1162986 NCBI GI BLAST score 180 E value 3.0e-13Match length 34 % identity 97 (M32430) beta-2 tubulin [Lytechinus pictus] NCBI Description 260404 Seq. No. 1353 19.R1011 Contig ID 5'-most EST LIB83-016-Q1-E1-D11 Method BLASTX q135449 NCBI GI BLAST score 341 1.0e-31 E value Match length 81 % identity 84 TUBULIN BETA-1 CHAIN >gi_100932_pir__S14701 tubulin beta-1 NCBI Description chain - maize >gi 295851 emb CAA37060 (X52878) beta 1 tubulin [Zea mays] Seq. No. 260405 1353 20.R1011 Contig ID LIB148-025-Q1-E1-F11 5'-most EST Method BLASTX NCBI GI g4098323 BLAST score 1214 E value 1.0e-134 233 Match length % identity NCBI Description (U76746) beta-tubulin 3 [Triticum aestivum] Seq. No. 260406 Contig ID 1353 21.R1011 5'-most EST uC-zmroteosinte101c01b2 Method BLASTX NCBI GI g1352830

Method BLASTX
NCBI GI g135283
BLAST score 567
E value 2.0e-58
Match length 142
% identity 81

NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD

SUBUNIT) >gi_1049253 (U36436) vacuolar ATPase 69 kDa

subunit [Zea mays]



```
Seq. No.
                   260407
                   1353 22.R1011
Contig ID
5'-most EST
                  uC-zmrob73075h06b1
Method
                  BLASTN
NCBI GI
                  q416150
                  235
BLAST score
E value
                   1.0e-129
                  251
Match length
                   99
% identity
                  Zea mays beta-8 tubulin (tub8) mRNA, complete cds
NCBI Description
Seq. No.
                   260408
                   1353 23.R1011
Contig ID
5'-most EST
                  LIB3150-066-P2-K1-A10
Method
                  BLASTX
NCBI GI
                   g1805274
BLAST score
                   188
E value
                   4.0e-14
                   37
Match length
% identity
                   92
                  (U83110) beta-tubulin [Homo sapiens]
NCBI Description
Seq. No.
                   260409
Contig ID
                   1353 29.R1011
5'-most EST
                  LIB3059-009-Q1-K1-A8
Method
                   BLASTX
NCBI GI
                   g4098329
BLAST score
                   391
E value
                   1.0e-37
Match length
                   75
                   99
% identity
NCBI Description
                  (U76895) beta-tubulin 4 [Triticum aestivum]
                   260410
Seq. No.
                   1353 30.R1011
Contig ID
5'-most EST
                   yyf700350642.h1
Method
                   BLASTX
NCBI GI
                   q629840
                   319
BLAST score
E value
                   3.0e-29
Match length
                   65
                   95
% identity
NCBI Description
                  tubulin beta-7 chain - maize >gi 416149 (L10634) beta-7
                   tubulin [Zea mays]
                   260411
Seq. No.
Contig ID
                   1353 31.R1011
5'-most EST
                   uC-zmflb73208b06b1
Method
                   BLASTX
                   g135460
NCBI GI
BLAST score
                   691
E value
                   4.0e-73
```

Match length 135 % identity 98

TUBULIN BETA-2 CHAIN >gi_100933_pir__S14702 tubulin beta-2 NCBI Description chain - maize >gi_22184_emb_CAA $\overline{37061}$ _(X52879) beta 2 tubulin (AA 1-444) [Zea mays]



```
Seq. No.
                    260412
 Contig ID
                    1353 36.R1011
 5'-most EST
                   xsy700211027.h1
 Method
                    BLASTX
 NCBI GI
                    q267079
 BLAST score
                    354
                    7.0e-59
 E value
 Match length
                    140
                    83
 % identity
                   TUBULIN BETA-6 CHAIN >gi 320187 pir JQ1590 tubulin beta-6
 NCBI Description
                    chain - Arabidopsis thaliana >gi 166904 (M84703) beta-6
                    tubulin [Arabidopsis thaliana]
 Seq. No.
                    260413
 Contig ID
                    1353 44.R1011
 5'-most EST
                    clt700041807.f1
                    BLASTX
 Method
 NCBI GI
                    q2326947
 BLAST score
                    229
                    3.0e-19
 E value
                    66
 Match length
                    71
 % identity
 NCBI Description
                    (Z50801) Chlorophyll a/b-binding protein CP29 precursor
                    [Zea mays]
 Seq. No.
                    260414
 Contig ID
                    1353 48.R1011
 5'-most EST
                    uC-zmflmo17181b10b1
 Method
                    BLASTX
                    q629839
 NCBI GI
 BLAST score
                    171
                    3.0e-12
 E value
 Match length
                    40
                    78
 % identity
CB Description
                   beta-6 tubulin - maize >gi 416147 (L10633) beta-6 tubulin
                    [Zea mays]
                    260415
 Seq. No.
                    1355 1.R1011
 Contig ID
                   LIB3066-040-Q1-K1-B9
 5'-most EST
 Method
                   BLASTX
 NCBI GI
                    q4538993
 BLAST score
                    302
                    3.0e-27
 E value
 Match length
                    131
                    50
 % identity
 NCBI Description
                   (AL049481) putative host response protein [Arabidopsis
                    thaliana]
                    260416
 Seq. No.
                    1356 2.R1011
 Contig ID
 5'-most EST
                   uC-zmflb73026e03b1
 Seq. No.
                    260417
```

36030

1356 3.R1011

mwy700440517.hl

Contig ID 5'-most EST



```
Seq. No.
                  260418
Contig ID
                  1357 1.R1011
5'-most EST
                  fwa700099366.hl
Method
                  BLASTX
                  q2983997
NCBI GI
BLAST score
                  388
E value
                   5.0e-37
                  159
Match length
% identity
                  47
                  (AE000749) hypothetical protein [Aquifex aeolicus]
NCBI Description
Seq. No.
                  260419
                  1357 2.R1011
Contig ID
                  ntr700077254.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3861068
BLAST score
                  144
E value
                  6.0e-09
                  58
Match length
                  47
% identity
                 (AJ235272) unknown [Rickettsia prowazekii]
NCBI Description
Seq. No.
                  260420
                  1360 1.R1011
Contig ID
5'-most EST
                  wyr700240794.h1
                  BLASTX
Method
                  q3643607
NCBI GI
BLAST score
                   1154
E value
                  1.0e-126
Match length
                  267
% identity
NCBI Description
                 (AC005395) unknown protein [Arabidopsis thaliana]
                  260421
Seq. No.
Contig ID
                  1360 2.R1011
                  LIB3069-003-Q1-K1-G7
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3643607
BLAST score
                  774
E value
                  4.0e-92
Match length
                  216
                  73
% identity
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
                  260422
Seq. No.
                  1360 3.R1011
Contig ID
5'-most EST
                  LIB36-022-Q1-E1-C10
Method
                  BLASTX
NCBI GI
                  g3643607
BLAST score
                  540
                  4.0e-55
E value
                  133
Match length
% identity
                  72
NCBI Description
                  (AC005395) unknown protein [Arabidopsis thaliana]
```

36031

260423

Seq. No.



```
1360 4.R1011
Contig ID
                  xjt700093221.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3643607
BLAST score
                  196
                  2.0e-25
E value
                  89
Match length
% identity
                  69
                  (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
                  260424
Seq. No.
                  1360 7.R1011
Contig ID
5'-most EST
                  tfd700573750.h1
                  BLASTX
Method
                  q3643607
NCBI GI
BLAST score
                  232
E value
                   3.0e-19
Match length
                  51
% identity
                  84
                  (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
                   260425
Seq. No.
                   1366 1.R1011
Contig ID
5'-most EST
                   uC-zmroteosinte032a11b1
                   BLASTX
Method
                   q134889
NCBI GI
                   200
BLAST score
                   3.0e-18
E value
Match length
                   241
% identity
                   29
                   SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68)
NCBI Description
                   >gi_108065_pir__S12981 68K protein - gray wolf
                   >gi_227342_prf__1702226A SRP68 protein [Canis familiaris]
                   260426
Seq. No.
                   1366 2.R1011
Contig ID
                   vux700157958.h1
5'-most EST
                   260427
Seq. No.
                   1368 1.R1011
Contig ID
                   uC-z\overline{m}flmo17176a05b1
5'-most EST
                   260428
Seq. No.
                   1369 1.R1011
Contig ID
                   LIB3067-009-Q1-K1-G7
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1261917
BLAST score
                   358
                   1.0e-33
E value
Match length
                   120
                   56
% identity
NCBI Description (X96979) lipid transfer protein 7a2b [Hordeum vulgare]
```

 Seq. No.
 260429

 Contig ID
 1369_2.R1011

 5'-most EST
 LIB3075-041-Q1-K1-E9

Method BLASTN



```
NCBI GI
                  q600117
BLAST score
                  72
                  4.0e-32
E value
Match length
                  112
% identity
                  91
                  Z.mays (B73) gene for extensin-like protein
NCBI Description
Seq. No.
                  260430
                  1369 3.R1011
Contig ID
5'-most EST
                  LIB3066-025-Q1-K1-H10
                  BLASTX
Method
NCBI GI
                  g1261917
BLAST score
                  220
                  1.0e-17
E value
Match length
                  87
                   48
% identity
                  (X96979) lipid transfer protein 7a2b [Hordeum vulgare]
NCBI Description
Seq. No.
                  260431
                  1373 1.R1011
Contig ID
5'-most EST
                  LIB143-012-Q1-E1-D3
                  BLASTX
Method
NCBI GI
                  q4512667
BLAST score
                   1598
                   1.0e-179
E value
Match length
                   403
                   73
% identity
NCBI Description
                  (AC006931) putative MAP kinase [Arabidopsis thaliana]
                   260432
Seq. No.
                   1374 1.R1011
Contig ID
                  LIB3075-041-Q1-K1-B12
5'-most EST
                   BLASTX
Method
                   g4580461
NCBI GI
                   257
BLAST score
                   3.0e-22
E value
                   136
Match length
                   43
% identity
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                   260433
Seq. No.
                   1375 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73027f10b1
Method
                   BLASTX
                   g3290022
NCBI GI
                   1264
BLAST score
                   1.0e-139
E value
Match length
                   333
                   73
% identity
NCBI Description
                  (AF044173) cysteine synthase; CS-B; O-acetylserine (thiol)
                   lyase; plastidic isoform [Solanum tuberosum]
Seq. No.
                   260434
                   1375 2.R1011
```

Contig ID

5'-most EST LIB3150-007-Q1-N1-B1

Seq. No. 260435



Contig ID 1378_1.R1011 5'-most EST uC-zmflb73196c02b1 Method BLASTX NCBI GI q3193303

NCBI GI g3193303
BLAST score 306
E value 2.0e-27
Match length 96
% identity 61

NCBI Description (AF069298) similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem

repeat protein (GB:U27807); partial CDS [Arabidopsis

thaliana]

Seq. No. 260436

Contig ID 1378_2.R1011 5'-most EST xyt700342223.h1

Method BLASTX
NCBI GI g3193303
BLAST score 308
E value 6.0e-28
Match length 96
% identity 61

NCBI Description (AF069298) similar to several proteins containing a tandem

repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis

thaliana]

Seq. No. 260437

Contig ID 1380_1.R1011 5'-most EST ntr700073011.h1

Seq. No. 260438

Contig ID 1380_2.R1011

5'-most EST uC-zmflmo17314f03a1

Seq. No. 260439

Contig ID 1385 1.R1011

5'-most EST LIB3159-021-Q1-K1-F1

Method BLASTX
NCBI GI g126722
BLAST score 166
E value 3.0e-11
Match length 158
% identity 29

NCBI Description ALPHA-MANNOSIDASE II (MANNOSYL-OLIGOSACCHARIDE

1,3-1,6-ALPHA-MANNOSIDASE) (MAN II) (GOLGI ALPHA-MANNOSIDASE II) >gi_110673_pir__A41641

mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase (EC 3.2.1.114) - mouse >gi_49944 emb_CAA43480_ (X61172) mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase [Mus

musculus]

Seq. No. 260440

Contig ID 1386_1.R1011 5'-most EST xsy700209125.h1

Method BLASTX NCBI GI g3914425



BLAST score 349 E value 1.0e-32 Match length 113 % identity 65

NCBI Description PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON

CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)

>gi_2511596_emb_CAA74029.1_ (Y13695) multicatalytic

endopeptidase complex, proteasome precursor, beta subunit

[Arabidopsis thaliana] >gi_3421117 (AF043536) 20S proteasome beta subunit PBE1 [Arabidopsis thaliana]

Seq. No. 260441

Contig ID 1386_2.R1011

5'-most EST uC-zmflb73095f12b1

Method BLASTX
NCBI GI g3914425
BLAST score 1053
E value 1.0e-115
Match length 273
% identity 74

NCBI Description PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON

CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)

>gi 2511596 emb CAA74029.1 (Y13695) multicatalytic

endopeptidase complex, proteasome precursor, beta subunit

[Arabidopsis thaliana] >gi_3421117 (AF043536) 20S proteasome beta subunit PBE1 [Arabidopsis thaliana]

Seq. No. 260442

Contig ID 1387_1.R1011 5'-most EST nbm700470960.h1

Method BLASTX
NCBI GI g2129568
BLAST score 334
E value 2.0e-30
Match length 100
% identity 64

NCBI Description cytosolic cyclophilin ROC2 - Arabidopsis thaliana

>qi 1305457 (U40400) cytosolic cyclophilin [Arabidopsis

thaliana]

Seq. No. 260443 Contig ID 1387_2.R1011

5'-most EST LIB3136-017-Q1-K1-G3

Method BLASTX
NCBI GI g3599491
BLAST score 1770
E value 0.0e+00
Match length 454
% identity 71

NCBI Description (AF085149) putative aminotransferase [Capsicum chinense]

Seq. No. 260444 Contig ID 1387 3

Contig ID 1387_3.R1011 5'-most EST xdb700339502.h1

Seq. No. 260445 Contig ID 1387 4.R1011



```
5'-most EST
                  pmx700089687.h1
                  260446
Seq. No.
Contig ID
                  1387 5.R1011
5'-most EST
                  xsy700211558.hl
                  BLASTX
Method
NCBI GI
                  q3599491
BLAST score
                  160
                  1.0e-10
E value
                  67
Match length
                  45
% identity
                  (AF085149) putative aminotransferase [Capsicum chinense]
NCBI Description
Seq. No.
                  260447
                  1387 6.R1011
Contig ID
5'-most EST
                  LIB3076-044-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g2498465
BLAST score
                  177
                  2.0e-12
E value
                  139
Match length
                  40
% identity
                  28 KD HEAT- AND ACID-STABLE PHOSPHOPROTEIN (HASPP28) (PDGF
NCBI Description
                  ASSOCIATED PROTEIN) >gi 2143777 pir S62782 heat and
                  acid-stable phosphoprotein, 28K - rat >gi_847785 (U26541)
                  HASPP28 [Rattus norvegicus] >gi 1588241 prf__2208261A
                  casein kinase II substrate [Rattus norvegicus]
Seq. No.
                  260448
                  1387 7.R1011
Contig ID
                  wty700167074.h1
5'-most EST
                  260449
Seq. No.
Contig ID
                   1387 8.R1011
                  uC-zmflmo17116d04b1
5'-most EST
                   260450
Seq. No.
                   1387 9.R1011
Contig ID
                   xdb700339534.h1
5'-most EST
                   260451
Seq. No.
                   1387 10.R1011
Contig ID
                   pmx700085673.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2244792
BLAST score
                   1710
                   0.0e+00
E value
Match length
                   442
% identity
                   71
                  (Z97336) ankyrin homolog [Arabidopsis thaliana]
NCBI Description
                   260452
Seq. No.
                   1387 11.R1011
Contig ID
                   xsy700208748.hl
5'-most EST
Method
                   BLASTX
```

g3914014

180

NCBI GI BLAST score



5.0e-25E value Match length 144 47 % identity

TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF) NCBI Description

>qi 3261715 emb CAB06859 (Z92539) mfd [Mycobacterium

tuberculosis]

Seq. No.

260453 1387 13.R1011 Contig ID fdz701160334.h1 5'-most EST

260454 Seq. No.

1387 14.R1011 Contig ID tfd700571974.h1 5'-most EST

Method BLASTX NCBI GI q2498465 180 BLAST score 8.0e-13 E value 139 Match length 40 % identity

28 KD HEAT- AND ACID-STABLE PHOSPHOPROTEIN (HASPP28) (PDGF NCBI Description

ASSOCIATED PROTEIN) >gi_2143777_pir__S62782 heat and acid-stable phosphoprotein, 28K - rat >gi_847785 (U26541) HASPP28 [Rattus norvegicus] >gi 1588241_prf 2208261A

casein kinase II substrate [Rattus norvegicus]

260455 Seq. No.

Contig ID 1387 15.R1011 uC-zmflmo17066g12b1 5'-most EST

260456 Seq. No.

1387 16.R1011 Contig ID

LIB3158-003-Q1-K1-B4 5'-most EST

260457 Seq. No.

- 1387 17.R1011 Contig ID 5'-most EST uC-zmflb73359a01a2

Method BLASTX NCBI GI q3953478 BLAST score 285 E value 3.0e-25 Match length 70 % identity 81

NCBI Description (AC002328) F2202.23 [Arabidopsis thaliana]

260458 Seq. No.

Contig ID 1387 18.R1011 5'-most EST uC-zmflb73238f03b2

260459 Seq. No.

Contig ID 1387 31.R1011 5'-most EST gwl700613841.hl

260460 Seq. No. Contig ID 1389 1.R1011

5'-most EST LIB3062-057-Q1-K1-D9



```
Seq. No.
                  260461
                  1395 1.R1011
Contig ID
5'-most EST
                  LIB3066-014-Q1-K1-A3
Seq. No.
                  260462
                  1395 2.R1011
Contig ID
5'-most EST
                  uwc700151372.h1
                   260463
Seq. No.
                   1395 3.R1011
Contig ID
                   xmt700262280.h1
5'-most EST
                   260464
Seq. No.
                   1403 1.R1011
Contig ID
                   uC-zmflb73261g06b3
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4204300
BLAST score
                   414
E value
                   4.0e-40
                   149
Match length
                   60
% identity
                  (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   260465
                   1403 2.R1011
Contig ID
5'-most EST
                   LIB3156-009-Q1-K1-B2
                   BLASTX
Method
NCBI GI
                   g4204300
BLAST score
                   219
                   1.0e-17
E value
                   77
Match length
                   61
% identity
                  (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   260466
Seq. No.
                   1403 5.R1011
Contig ID
                   cat700018088.rl
5'-most EST
                   260467
Seq. No.
                   1403 6.R1011
Contig ID
                   xsy700212857.hl
5'-most EST
                   260468
Seq. No.
                   1404 1.R1011
Contig ID
                   uC-z\overline{m}flmo17126a04b1
5'-most EST
                   BLASTX
Method
                   g4406759
NCBI GI
BLAST score
                   225
                   4.0e-18
E value
Match length
                   179
% identity
```

260469 Seq. No. 1404 2.R1011 Contig ID uC-zmflb73122d05b2

5'-most EST

BLASTX Method

NCBI Description (AC006836) hypothetical protein [Arabidopsis thaliana]

BLAST score

E value Match length 607 8.0e-63

141



```
g4406759
NCBI GI
BLAST score
                   386
                   6.0e-37
E value
Match length
                   247
                   40
% identity
                  (AC006836) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   260470
                   1404 3.R1011
Contig ID
5'-most EST
                  uC-zmflb73401b04a1
                   260471
Seq. No.
Contig ID
                   1404 4.R1011
                   uC-z\overline{m}flb73216b09b2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4406759
BLAST score
                   208
                   2.0e-16
E value
Match length
                   74
% identity
                   55
                  (AC006836) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   260472
Seq. No.
                   1409 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17185d02b1
                   260473
Seq. No.
                   1410_1.R1011
Contig ID
5'-most EST
                   uC-zmroteosinte059a02b1
Method
                   BLASTN
NCBI GI
                   q459268
BLAST score
                   89
E value
                   3.0e-42
Match length
                   125
% identity
                   93
NCBI Description Z.mays mRNA Transcribed Sequence
Seq. No.
                   260474
Contig ID
                   1410 2.R1011
5'-most EST
                   LIB3180-005-P2-M1-F11
Method
                   BLASTX
                   g542190
NCBI GI
                   612
BLAST score
                   2.0e-63
E value
                   225
Match length
% identity
NCBI Description hypothetical protein 1087 - maize >gi_459269_emb_CAA54960_
                   (X78029) transcribed sequence 1087 [Zea mays]
                   260475
Seq. No.
Contig ID
                   1411_1.R1011
                   LIB143-004-Q1-E1-B11
5'-most EST
Method
                   BLASTX
NCBI GI
                   g123553
```



% identity 86

NCBI Description 17.8 KD CLASS II HEAT SHOCK PROTEIN >gi_100884_pir__S14997

heat shock protein, 18K - maize >gi_22337_emb_CAA38012_

(X54075) 18kDa heat shock protein [Zea mays]

Seq. No. 260476

Contig ID 1411_2.R1011 5'-most EST wty700163850.h1

Method BLASTX
NCBI GI g123549
BLAST score 583
E value 5.0e-60
Match length 142
% identity 83

NCBI Description 17.5 KD CLASS II HEAT SHOCK PROTEIN >gi_100885_pir__S14998

heat shock protein, 18K - maize >gi_22339_emb_CAA38013_

(X54076) 18kDa heat shock protein [Zea mays]

Seq. No. 260477

Contig ID 1411 3.R1011

5'-most EST LIB143-060-Q1-E1-F8

Method BLASTX
NCBI GI g729762
BLAST score 649
E value 8.0e-68
Match length 131
% identity 97

NCBI Description 17.0 KD CLASS II HEAT SHOCK PROTEIN (HSP 18)

>gi_477225_pir__A48425 heat shock protein HSP18 - maize
>gi_300079_bbs_130952 (S59777) HSP18=18 kda heat shock
protein [Zea mays, Oh43, clone cMHSP18-1, Peptide, 154 aa]

[Zea mays]

Seq. No. 260478

Contig ID 1411 6.R1011

5'-most EST LIB143-055-Q1-E1-C10

Method BLASTX
NCBI GI g729762
BLAST score 364
E value 7.0e-35
Match length 95
% identity 82

NCBI Description 17.0 KD CLASS II HEAT SHOCK PROTEIN (HSP 18)

>gi_477225_pir__A48425 heat shock protein HSP18 - maize
>gi_300079_bbs_130952 (S59777) HSP18=18 kda heat shock
protein [Zea mays, Oh43, clone cMHSP18-1, Peptide, 154 aa]

[Zea mays]

Seq. No. 260479 Contig ID 1412_1.R1011

5'-most EST LIB3079-026-Q1-K1-F3

Method BLASTX
NCBI GI g1346121
BLAST score 1649
E value 0.0e+00
Match length 367
% identity 84



NCBI Description AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T PROTEIN) >gi_542104_pir__S40217 T protein - Flaveria

pringlei >gi_1362139_pir__S56660 glycine decarboxylase T

protein precursor - Flaveria pringlei

>gi_438005_emb_CAA81077_ (Z25858) T protein [Flaveria

pringlei]

Seq. No. 260480

Contig ID 1414 1.R1011

5'-most EST LIB3115-017-P1-K1-C6

Method BLASTX
NCBI GI g132918
BLAST score 160
E value 1.0e-10
Match length 40
% identity 82

NCBI Description 50S RIBOSOMAL PROTEIN L35, CHLOROPLAST PRECURSOR (CL35)

>gi_81486_pir_A36107 ribosomal protein L35 precursor,

chloroplast - spinach >gi 170139 (M60449) ribosomal protein

L35 [Spinacia oleracea]

Seq. No. 260482

Contig ID 1414 3.R1011

5'-most EST LIB3076-024-Q1-K1-D4

Seq. No. 260483

Contig ID 1415 1.R1011

5'-most EST uC-zmflmo17267g10b1

Method BLASTX
NCBI GI g2746787
BLAST score 286
E value 3.0e-25
Match length 120
% identity 47

NCBI Description (AF040642) contains similarity to RNA recognition motifs

(RNP) [Caenorhabditis elegans]

Seq. No. 260484

Contig ID 1415_2.R1011

5'-most EST LIB143-014-Q1-E1-B6

Method BLASTX
NCBI GI g2746787
BLAST score 277
E value 2.0e-24
Match length 110
% identity 48

NCBI Description (AF040642) contains similarity to RNA recognition motifs

(RNP) [Caenorhabditis elegans]

Seq. No. 260485 Contig ID 1417 1.R1011

5'-most EST uC-zmroteosinte043e06b2

Method BLASTX



NCBI GI g3786016
BLAST score 958
E value 1.0e-103
Match length 367
% identity 54

NCBI Description (AC005499) putative elongation factor [Arabidopsis

thaliana]

Seq. No. 260486

Contig ID 1417 2.R1011

5'-most EST LIB3151-011-Q1-K1-B8

Method BLASTX
NCBI GI g3786016
BLAST score 185
E value 9.0e-14

Match length 89 % identity 43

NCBI Description (AC005499) putative elongation factor [Arabidopsis

thaliana]

Seq. No. 260487

Contig ID 1419 1.R1011 5'-most EST nwy700446195.h1

Seq. No. 260488 Contig ID 1422 1.R1011

5'-most EST uC-zmflmo17023a12b1

Method BLASTX
NCBI GI g3929545
BLAST score 1438
E value 1.0e-160
Match length 384
% identity 72

NCBI Description (AF067194) S-adenosylmethionine decarboxylase [Oryza

sativa]

Seq. No. 260489

Contig ID 1422_2.R1011

5'-most EST LIB3\overline{1}36-020-Q1-K1-E2

Method BLASTX
NCBI GI g1421751
BLAST score 160
E value 1.0e-10
Match length 35
% identity 94

NCBI Description (U60592) putative ORF; conserved in 5' leaders of plant

SAMdC [Pisum sativum]

Seq. No. 260490 Contig ID 1422_3.R1011

5'-most EST LIB3060-028-Q1-K1-C9

Seq. No. 260491 Contig ID 1423 1.R1011

5'-most EST LIB3066-035-Q1-K1-H8

Method BLASTN NCBI GI g3821780

```
BLAST score
                   36
E value
                   1.0e-10
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  260492
Seq. No.
Contig ID
                  1432_1.R1011
5'-most EST
                  uC-zmroteosinte044e02b2
Method
                  BLASTX
NCBI GI
                  g4582787
BLAST score
                  1718
E value
                  0.0e + 00
Match length
                  331
% identity
                  100
NCBI Description (AJ012281) adenosine kinase [Zea mays]
Seq. No.
                  260493
Contig ID
                  1432 2.R1011
5'-most EST
                  LIB3059-025-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  g4582787
                  775
BLAST score
E value
                  1.0e-82
Match length
                  155
% identity
                  97
NCBI Description
                 (AJ012281) adenosine kinase [Zea mays]
                  260494
                  1432 4.R1011
                  ntr700076826.h1
                  BLASTX
                  g4582787
```

Seq. No. Contig ID 5'-most EST Method NCBI GI BLAST score 374 8.0e-36

E value Match length 80 % identity 93

NCBI Description (AJ012281) adenosine kinase [Zea mays]

Seq. No. 260495 Contig ID 1432 7.R1011 ceu700426364.h1 5'-most EST Method BLASTN

NCBI GI g4582786 BLAST score 91 E value 8.0e-44Match length 146 91 % identity

NCBI Description Zea mays mRNA for adenosine kinase, putative

Seq. No. 260496 1434 1.R1011 Contig ID

5'-most EST LIB3158-016-Q1-K1-G3

Seq. No. 260497

Contig ID 1434 2.R1011 5'-most EST uwc700152971.h1



Method BLASTX
NCBI GI g3758859
BLAST score 196
E value 1.0e-14
Match length 114
% identity 32

NCBI Description (Z98551) predicted using hexExon; MAL3P6.7 (PFC0730w), Hypothetical protein, len: 222 aa [Plasmodium falciparum]

Seq. No. 260498

Contig ID 1434_3.R1011

5'-most EST LIB148-024-Q1-E1-G3

Seq. No. 260499

Contig ID 1434_4.R1011

5'-most EST uC-zmflb73028d12b1

Seq. No. 260500

Contig ID 1434 5.R1011

5'-most EST LIB148-032-Q1-E1-B6

Method BLASTX
NCBI GI g3758859
BLAST score 192
E value 3.0e-14

Match length 107 % identity 35

NCBI Description (Z98551) predicted using hexExon; MAL3P6.7 (PFC0730w),

Hypothetical protein, len: 222 aa [Plasmodium falciparum]

Seq. No. 260501

Contig ID 1434 7.R1011

5'-most EST uC-zmflmo17187h04b1

Seq. No. 260502

Contig ID 1434 10.R1011

5'-most EST uC-zmroteosinte093a01b2

Seq. No. 260503

Contig ID 1438 1.R1011

5'-most EST uC-zmflmo17270e09b1

Method BLASTX
NCBI GI g4539423
BLAST score 679
E value 7.0e-72
Match length 183
% identity 75

NCBI Description (AL049171) pyrophosphate-dependent phosphofructo-1-kinase

[Arabidopsis thaliana]

Seq. No. 260504

Contig ID 1444_1.R1011

5'-most EST LIB3075-008-Q1-K1-E4

 Seq. No.
 260505

 Contig ID
 1445_1.R1011

 5'-most EST
 nbm700470620.h1

Method BLASTX



```
NCBI GI
                    g2980767
BLAST score
                     226
E value
                     4.0e-18
Match length
                    146
% identity
                    36
NCBI Description
                    (AL022198) putative protein [Arabidopsis thaliana]
Seq. No.
                    260506
                    1452 1.R1011
Contig ID
5'-most EST
                    LIB3078-046-Q1-K1-E5
Method
                    BLASTX
NCBI GI
                    g2130089
BLAST score
                    1275
E value
                    1.0e-141
Match length
                    285
% identity
                    87
                    2-oxoglutarate/malate translocator (clone OMT103),
NCBI Description
                    mitochondrial membrane - proso millet
>gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate
                    translocator [Panicum miliaceum]
Seq. No.
                    260507
Contig ID
                    1452 2.R1011
5'-most EST
                    uC-zmflmo17263a11b1
Method
                    BLASTX
NCBI GI
                    g2130089
BLAST score
                    413
E value
                    3.0e-40
Match length
                    101
                    80
% identity
NCBI Description
                    2-oxoglutarate/malate translocator (clone OMT103),
                    mitochondrial membrane - proso millet
>gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate
                    translocator [Panicum miliaceum]
                    260508
Seq. No.
Contig ID
                    1452 3.R1011
5'-most EST
                    LIB3067-058-Q1-K1-C7
Method
                    BLASTX
NCBI GI
                    g2130089
BLAST score
                    449
E value
                    1.0e-44
Match length
                    102
                    88
% identity
NCBI Description
                    2-oxoglutarate/malate translocator (clone OMT103),
                    mitochondrial membrane - proso millet
>gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate
                    translocator [Panicum miliaceum]
Seq. No.
                    260509
Contig ID
                    1455 1.R1011
5'-most EST
                    uC-zmflb73017q05a2
Method
                    BLASTX
NCBI GI
```

36045

q1174162

4.0e-71

677

136

BLAST score

Match length

E value



% identity NCBI Description (U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi 3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana] 260510 Seq. No. 1461 1.R1011 Contig ID 5'-most EST nwy700445390.h1 BLASTX Method NCBI GI q3319340 BLAST score 427 1.0e-41 E value Match length 179 % identity 46 NCBI Description (AF077407) contains similarity to E. coli cation transport protein ChaC (GB:D90756) [Arabidopsis thaliana] 260511 Seq. No. Contig ID 1464 1.R1011 5'-most EST LIB3066-044-Q1-K1-A7 BLASTX Method NCBI GI g2239262 BLAST score 1131 E value 1.0e-124 330 Match length % identity 62 (Y13285) pectin methylesterase-like protein [Zea mays] NCBI Description Seq. No. 260512 Contig ID 1465 1.R1011 5'-most EST xyt700343230.h1 Method BLASTX NCBI GI q4588003 BLAST score 1177 E value 1.0e-129 Match length 333 % identity 71 (AF085279) hypothetical EIF-2-Alpha [Arabidopsis thaliana] NCBI Description Seq. No. 260513 1468 1.R1011 Contig ID 5'-most EST LIB3066-005-Q1-K1-A10 BLASTX Method NCBI GI g3415117 BLAST score 1160 1.0e-127 E value 454 Match length % identity 34 NCBI Description (AF081203) villin 3 [Arabidopsis thaliana]

Seq. No. 260514 Contig ID 1468_2.R1011

5'-most EST LIB3066-048-Q1-K1-C3

Method BLASTX
NCBI GI g3415117
BLAST score 357
E value 1.0e-33



Match length 218 % identity 40

NCBI Description (AF081203) villin 3 [Arabidopsis thaliana]

Seq. No. 260515

Contig ID 1470_1.R1011

5'-most EST LIB3075-035-Q1-K1-B6

Method BLASTX
NCBI GI g1723566
BLAST score 183
E value 2.0e-13
Match length 129
% identity 34

NCBI Description PUTATIVE GLUCOSYLTRANSFERASE C17C9.07

>gi_1314159_emb_CAA97353_ (Z73099) SPAC17C9.07, putative
glucosyl transferase len: 501, similar to SW:ALG8_YEAST
P40351 glucosyltransferase ALG8 (35.0% identity in 509 aa

overlap) [Schizosaccharomyces pombe]

Seq. No. 260516

Contig ID 1472 1.R1011

5'-most EST uC-zmflmo17031c08b1

Method BLASTX
NCBI GI g2463567
BLAST score 607
E value 4.0e-63
Match length 117
% identity 98

NCBI Description (AB007502) squalene synthase [Zea mays]

Seq. No. 260517

Contig ID 1472_2.R1011

5'-most EST uC-zmflmo17160b03b1

Method BLASTX
NCBI GI g2463567
BLAST score 660
E value 2.0e-69
Match length 134
% identity 96

NCBI Description (AB007502) squalene synthase [Zea mays]

Seq. No. 260518

Contig ID 1474 1.R1011 5'-most EST xjt700092132.h1

Method BLASTX
NCBI GI g1718097
BLAST score 1101
E value 1.0e-120
Match length 342
% identity 58

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)

(41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016

lysosomal membrane protein DVA41 - slime mold

(Dictyostelium discoideum) >gi_532733 (U13150) vacuolar

ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No. 260519



Contig ID 1474 3.R1011

5'-most EST uC-zmflmo17269a05a1

Seq. No. 260520

Contig ID 1475 1.R1011

5'-most EST uC-zmflmo17293d05b1

Seq. No. 260521

1475 2.R1011 Contig ID

5'-most EST uC-zmflmo17129e08b1

260522 Seq. No.

Contig ID 1477 1.R1011

5'-most EST LIB3136-028-Q1-K1-B3

260523 Seq. No.

Contig ID 1479 1.R1011 5'-most EST ymt700218535.h1

Seq. No. 260524

1479 2.R1011 Contig ID 5'-most EST xsy700208031.hl

Seq. No. 260525

Contig ID 1482 1.R1011

5'-most EST LIB3075-035-Q1-K1-A10

Method BLASTX NCBI GI g3142292 BLAST score 690 E value 1.0e-72Match length 193 70 % identity

(AC002411) Contains similarity to tetratricopeptide repeat NCBI Description

protein qb U46571 from home sapiens. EST qb Z47802 and gb Z48402 come from this gene. [Arabidopsis thaliana]

Seq. No. 260526

Contig ID 1485 1.R1011

5'-most EST uC-zmroteosinte011g10b1

Method BLASTX NCBI GI q466160 BLAST score 357 1.0e-33 E value Match length 81 % identity 84

HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III NCBI Description

>gi 630771 pir S44903 ZK652.3 protein - Caenorhabditis elegans >gi 289769 (L14429) putative [Caenorhabditis

elegans]

Seq. No. 260527

Contig ID 1485 2.R1011

5'-most EST uC-zmflb73195e05b1

BLASTX Method NCBI GI q466160 267 BLAST score 3.0e-23 E value



Match length 62 % identity 81

NCBI Description HYP

HYPOTHETICAL 9.8 KD PROTEIN ZK652.3 IN CHROMOSOME III >gi_630771_pir__S44903 ZK652.3 protein - Caenorhabditis elegans >gi_289769 (L14429) putative [Caenorhabditis

elegans]

Seq. No. 260528

Contig ID 1485_4.R1011 5'-most EST wyr700236990.h1

Method BLASTX
NCBI GI g2224846
BLAST score 308
E value 2.0e-28
Match length 59
% identity 93

NCBI Description (Y13905) anionic peroxidase [Zea mays]

Seq. No. 260529

Contig ID 1487_1.R1011 5'-most EST fdz701161172.h1

Method BLASTX
NCBI GI g1154954
BLAST score 381
E value 2.0e-36
Match length 95

% identity 81

NCBI Description (X94693) histone H2A [Triticum aestivum]

Seq. No. 260530

Contig ID 1487_2.R1011 5'-most EST wty700172473.h1

Method BLASTX
NCBI GI g2257756
BLAST score 957
E value 1.0e-103

Match length 297 % identity 68

NCBI Description (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays]

>gi 3650466 (AF026917) histone deacetylase HD2-p39 [Zea

mays]

Seq. No. 260531

Contig ID 1487_3.R1011

5'-most EST LIB3116-001-Q1-K1-G11

Method BLASTN
NCBI GI g2257755
BLAST score 494
E value 0.0e+00
Match length 567
% identity 97

NCBI Description Zea mays nucleolar histone deacetylase HD2-p39 mRNA,

complete cds

Seq. No. 260532

Contig ID 1487_6.R1011 5'-most EST nbm700477250.h1



Method BLASTN
NCBI GI g2257755
BLAST score 218
E value 1.0e-119
Match length 358
% identity 95

NCBI Description Zea mays nucleolar histone deacetylase HD2-p39 mRNA,

complete cds

Seq. No. 260533

Contig ID 1491_1.R1011 5'-most EST ceu700433529.h1

Seq. No. 260534

Contig ID 1492 1.R1011

5'-most EST LIB3136-022-Q1-K1-D3

Seq. No. 260535

Contig ID 1493 1.R1011

5'-most EST uC-zmflmo17077g03b1

Method BLASTX
NCBI GI g4008156
BLAST score 3480
E value 0.0e+00
Match length 761

% identity 87

NCBI Description (AB008845) NADH dependent Glutamate Synthase [Oryza sativa]

Seq. No. 260536

Contig ID 1493 2.R1011

5'-most EST uC-zmflmo17177h11a1

Method BLASTX
NCBI GI g3142300
BLAST score 850
E value 7.0e-91
Match length 347
% identity 52

NCBI Description (AC002411) Contains similarity to pre-mRNA processing

protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908

and gb T88158, gb N38703 and gb AA651043 come from this

gene. [Arabidopsis thaliana]

Seq. No. 260537

Contig ID 1493 3.R1011

5'-most EST uC-zmflb73284b10b1

Method BLASTX
NCBI GI g3142300
BLAST score 1305
E value 1.0e-144
Match length 448
% identity 57

NCBI Description (AC002411) Contains similarity to pre-mRNA processing

protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb T88158, gb N38703 and gb AA651043 come from this

gene. [Arabidopsis thaliana]

Seq. No. 260538



Contig ID 1493_4.R1011 5'-most EST LIB3\overline{150}-018-Q1-N1-F8 Method BLASTX

NCBI GI g4406775 BLAST score 214 E value 2.0e-16 Match length 238 % identity 41

NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]

Seq. No. 260539

Contig ID 1493 5.R1011

5'-most EST fC-zmle700445521g2

Seq. No. 260540

Contig ID 1493_8.R1011 5'-most EST rv1700454230.h1

Method BLASTX
NCBI GI 94406775
BLAST score 144
E value 6.0e-09
Match length 109
% identity 36

NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]

Seq. No. 260541

Contig ID 1493_9.R1011

5'-most EST LIB3150-102-P2-K1-H1

Seq. No. 260542

Contig ID 1493_13.R1011 5'-most EST rvt700551812.h1

Method BLASTX
NCBI GI g3142300
BLAST score 208
E value 9.0e-17
Match length 70
% identity 67

NCBI Description (AC002411) Contains similarity to pre-mRNA processing

protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb N38703 and gb AA651043 come from this

gene. [Arabidopsis thaliana]

Seq. No. 260543 Contig ID 1494 1.R1011

5'-most EST uC-zmroteosinte094g03b2

Method BLASTX
NCBI GI g4454452
BLAST score 1311
E value 1.0e-145
Match length 409
% identity 63

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 260544 Contig ID 1494 2.R1011

5'-most EST LIB3 $\overline{1}$ 50-043-Q1-N1-C5



Method BLASTX
NCBI GI 94454452
BLAST score 175
E value 7.0e-22
Match length 88
% identity 56

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 260545 Contig ID 1494 3.R1011

5'-most EST LIB3180-040-P2-M2-C8

Method BLASTX
NCBI GI g4454452
BLAST score 696
E value 3.0e-73
Match length 210
% identity 65

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 260546

Contig ID 1494_5.R1011

5'-most EST uC-zmflm017016e07b1

Method BLASTX
NCBI GI 94454452
BLAST score 242
E value 2.0e-20
Match length 120
% identity 44

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 260547

Contig ID 1495 1.R1011

5'-most EST LIB3075-034-Q1-K1-A6

Seq. No. 260548

Contig ID 1496_1.R1011

5'-most EST uC-zmflb73060c01b1

Seq. No. 260549

Contig ID 1502_1.R1011 5'-most EST vux700159350.h1

Method BLASTX
NCBI GI g4150963
BLAST score 451
E value 2.0e-44
Match length 171
% identity 55

NCBI Description (Y18620) DsPTP1 protein [Arabidopsis thaliana]

 Seq. No.
 260550

 Contig ID
 1502_4.R1011

5'-most EST zuv700355861.h1

Method BLASTX
NCBI GI g4150963
BLAST score 270
E value 7.0e-24
Match length 113



% identity 57

NCBI Description (Y18620) DsPTP1 protein [Arabidopsis thaliana]

Seq. No. 260551

Contig ID 1503 1.R1011

5'-most EST LIB3075-009-Q1-K1-E10

Seq. No. 260552

Contig ID 1504 1.R1011

5'-most EST uC-zmroteosinte004h12b1

Method BLASTX
NCBI GI g2347098
BLAST score 1120
E value 1.0e-123
Match length 362

% identity 76

NCBI Description (U76845) ubiquitin-specific protease [Arabidopsis thaliana]

>gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific

protease (AtUBP3) [Arabidopsis thaliana]

Seq. No. 260553

Contig ID 1505 1.R1011

5'-most EST LIB3\overline{1}36-058-Q1-K1-B3

Seq. No. 260554

Contig ID 1508_1.R1011 5'-most EST mwy700441010.h1

Seq. No. 260555

Contig ID 1508 2.R1011

5'-most EST LIB3\overline{1}36-022-Q1-K1-F5

Seq. No. 260556

Contig ID 1508_3.R1011 5'-most EST gwl700613333.h1

Seq. No. 260557

Contig ID 1508_5.R1011 5'-most EST wyr700240416.h1

Seq. No. 260558

Contig ID 1514 1.R1011

5'-most EST uC-zmflb73032g06b1

Method BLASTX
NCBI GI g2315363
BLAST score 328
E value 3.0e-30
Match length 250
% identity 36

NCBI Description (AF016441) No definition line found [Caenorhabditis

elegans]

Seq. No. 260559 Contig ID 1515 1.R1011

5'-most EST uC-zmflb73186b01b1

Method BLASTX NCBI GI 94586674



BLAST score 527 E value 2.0e-53 Match length 175 % identity 59

NCBI Description (AB022714) signal peptidase 21kDa subunit [Rattus

norvegicus]

Seq. No. 260560

Contig ID 1516 1.R1011

5'-most EST uC-zmflb73239f10b2

Method BLASTX
NCBI GI g2511574
BLAST score 1078
E value 1.0e-118
Match length 235
% identity 91

NCBI Description (Y13176) multicatalytic endopeptidase [Arabidopsis

thaliana] >gi 3421075 (AF043520) 20S proteasome subunit

PAB1 [Arabidopsis thaliana]

Seq. No. 260561 Contig ID 1516_2.R1011

5'-most EST uC-zmflb73057b03b1

Method BLASTX
NCBI GI g2511574
BLAST score 371
E value 2.0e-35
Match length 79
% identity 96

NCBI Description (Y13176) multicatalytic endopeptidase [Arabidopsis

thaliana] >gi 3421075 (AF043520) 20S proteasome subunit

PAB1 [Arabidopsis thaliana]

Seq. No. 260562

Contig ID 1516 3.R1011

5'-most EST uC-zmflmo17310b06b1

Method BLASTX
NCBI GI g3915186
BLAST score 339
E value 4.0e-31
Match length 147
% identity 47

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-21 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) (PEROXIN-4) >gi_3128447 (AF061604) ubiquitin-conjugating enzyme homolog peroxin 4

[Pichia angusta]

Seq. No. 260563

Contig ID 1516 4.R1011

5'-most EST LIB3150-001-Q1-N1-H4

Method BLASTX
NCBI GI g3915186
BLAST score 316
E value 1.0e-28
Match length 147
% identity 44

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-21 KD (UBIQUITIN-PROTEIN



LIGASE) (UBIQUITIN CARRIER PROTEIN) (PEROXIN-4) >gi_3128447 (AF061604) ubiquitin-conjugating enzyme homolog peroxin 4 [Pichia angusta]

 Seq. No.
 260564

 Contig ID
 1516_5.R1011

 5'-most EST
 uwc700152427

Seq. No. 260565

Contig ID 1516_6.R1011 5'-most EST xyt700343071.h1

Seq. No. 260566

Contig ID 1516_10.R1011

5'-most EST LIB3075-022-Q1-K1-C11

Method BLASTN
NCBI GI g3406034
BLAST score 44
E value 2.0e-15
Match length 196

Match length 196 % identity 82

NCBI Description BAC F18A17 from chromosome V containing TINY at 60.5 cM,

complete sequence [Arabidopsis thaliana]

Seq. No. 260567 Contig ID 1520 1.R1011

5'-most EST LIB3060-025-Q1-K1-G11

Seq. No. 260568 Contig ID 1521 1.R1011

5'-most EST LIB3075-009-Q1-K1-G7

Method BLASTX
NCBI GI g541951
BLAST score 810
E value 1.0e-86
Match length 218
% identity 72

NCBI Description SPCP2 protein - soybean >gi_310578 (L12258) nodulin-26

[Glycine max]

Seq. No. 260569

Contig ID 1529_1.R1011 5'-most EST nbm700472244.h1

Method BLASTX
NCBI GI g3033400
BLAST score 343
E value 1.0e-32
Match length 98
% identity 66

NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 260570

Contig ID 1534 1.R1011 5'-most EST gwl700615558.h1

Method BLASTX NCBI GI g606811



```
BLAST score
                   975
                   1.0e-105
E value
Match length
                   301
% identity
                   48
                  (U08401) carbonic anhydrase [Zea mays]
NCBI Description
Seq. No.
                   260571
                  1534 2.R1011
Contig ID
                   clt700042847.f1
5'-most EST
Method
                  BLASTX
                   g606811
NCBI GI
BLAST score
                   2057
                   0.0e+00
E value
Match length
                   408
% identity
                   96
NCBI Description
                  (U08401) carbonic anhydrase [Zea mays]
Seq. No.
                   260572
                   1534 3.R1011
Contig ID
5'-most EST
                  nwy700445473.h1
Method
                  BLASTX
NCBI GI
                   g606811
BLAST score
                   273
E value
                   6.0e-24
Match length
                   75
% identity
                   40
NCBI Description
                  (U08401) carbonic anhydrase [Zea mays]
                   260573
Seq. No.
                  1534 4.R1011
Contig ID
                  LIB3116-004-Q1-K2-H2
5'-most EST
Method
                  BLASTX
NCBI GI
                   g168562
                   209
BLAST score
E value
                   2.0e-16
Match length
                   43
                   88
% identity
NCBI Description
                  (M95073) putative. silimar to carbonic anhydrases [Zea
Seq. No.
                   260574
                   1534 7.R1011
Contig ID
5'-most EST
                   wyr700240888.h1
Method
                   BLASTX
NCBI GI
                   q606815
BLAST score
                   891
                   4.0e-96
E value
Match length
                   223
% identity
                   28
                  (U08403) carbonic anhydrase [Zea mays]
```

NCBI Description

260575 Seq. No. Contig ID 1534 9.R1011

clt700043008.f1 5'-most EST

Method BLASTX g606811 NCBI GI BLAST score 327



```
E value
                  3.0e-30
Match length
                  74
% identity
                  43
NCBI Description
                  (U08401) carbonic anhydrase [Zea mays]
                  260576
Seq. No.
Contig ID
                  1534 11.R1011
5'-most EST
                  LIB3078-026-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  g606815
BLAST score
                  526
E value
                  1.0e-53
Match length
                  115
% identity
NCBI Description
                  (U08403) carbonic anhydrase [Zea mays]
Seq. No.
                  260577
Contig ID
                  1536 1.R1011
5'-most EST
                  LIB3069-041-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  q3928084
BLAST score
                  225
E value
                  3.0e-18
Match length
                  147
                  37
% identity
                  (AC005770) retrotransposon-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  260578
Contig ID
                  1537 1.R1011
5'-most EST
                  LIB3067-033-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                  q3341679
BLAST score
                  1677
E value
                  0.0e+00
Match length
                  490
% identity
                  65
NCBI Description
                  (AC003672) dynamin-like protein phragmoplastin 12
                  [Arabidopsis thaliana]
                  260579
Seq. No.
                  1537 3.R1011
Contig ID
5'-most EST
                  LIB3067-033-Q1-K1-D2
Method
                  BLASTX
NCBI GI
                  q3341679
BLAST score
                  320
E value
                  8.0e-53
Match length
                  146
% identity
                  74
                  (AC003672) dynamin-like protein phragmoplastin 12
NCBI Description
                  [Arabidopsis thaliana]
                  260580
Seq. No.
Contig ID
                  1541 1.R1011
```

5'-most EST uC-zmflb73162b12b2 Method BLASTX NCBI GI g3643611



```
BLAST score
                  1127
E value
                  1.0e-123
Match length
                  257
% identity
                  79
NCBI Description
                 (AC005395) putative casein kinase [Arabidopsis thaliana]
Seq. No.
                  260581
Contig ID
                  1542 1.R1011
5'-most EST
                  LIB148-066-Q2-E1-A5
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  3.0e-10
Match length
                  48
                  67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  260582
Seq. No.
Contig ID
                  1543 1.R1011
5'-most EST
                  LIB3075-011-Q1-K1-B6
Method
                  BLASTX
NCBI GI
                  g4567311
BLAST score
                  375
E value
                  2.0e-35
Match length
                  95
% identity
                  66
NCBI Description
                 (AC005956) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  260583
Contig ID
                  1544 1.R1011
5'-most EST
                  LIB148-004-Q1-E1-B6
Method
                  BLASTX
NCBI GI
                  q4218011
BLAST score
                  892
E value
                  1.0e-109
Match length
                  279
% identity
                  74
NCBI Description
                  (AC006135) putative protein kinase [Arabidopsis thaliana]
                  >gi_4309721_gb_AAD15491_ (AC006439) putative
                  serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.
                  260584
Contig ID
                  1546 1.R1011
5'-most EST
                  LIB3180-008-P2-M1-B4
Method
                  BLASTX
NCBI GI
                  q2808638
BLAST score
                  798
E value
                  4.0e-85
```

Match length 201 % identity 80

NCBI Description (AJ001367) small GTP-binding protein [Daucus carota]

Seq. No. 260585 Contig ID 1546 2.R1011 5'-most EST uC-zmflb73013d12b1 Method BLASTX NCBI GI g1654144



BLAST score 344 E value 3.0e-32 Match length 89 % identity 79

NCBI Description (U38471) small GTP-binding protein rab [Brassica rapa]

Seq. No. 260586

Contig ID 1546_3.R1011 5'-most EST xjt700093402.h1

Method BLASTX
NCBI GI g1654144
BLAST score 186
E value 4.0e-14
Match length 39
% identity 97

NCBI Description (U38471) small GTP-binding protein rab [Brassica rapa]

Seq. No. 260587

Contig ID 1546_4.R1011 5'-most EST dyk700103144.h1

Method BLASTX
NCBI GI g2808638
BLAST score 167
E value 9.0e-12
Match length 55
% identity 64

NCBI Description (AJ001367) small GTP-binding protein [Daucus carota]

Seq. No. 260588

Contig ID 1549 1.R1011

5'-most EST LIB3066-054-Q1-K1-C5

Seq. No. 260589

Contig ID 1549_4.R1011

5'-most EST LIB3075-007-Q1-K1-H11

Method BLASTX
NCBI GI 94218991
BLAST score 257
E value 5.0e-22
Match length 125
% identity 43

NCBI Description (AF098632) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 260590

Contig ID 1552_1.R1011 5'-most EST bdu700382138.h1

Method BLASTX
NCBI GI g1542941
BLAST score 1310
E value 1.0e-145
Match length 393
% identity 67

NCBI Description (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No. 260591

Contig ID 1552 2.R1011

5'-most EST uC-zmflb73298e02b1



```
BLASTX
Method
                  g1542941
NCBI GI
BLAST score
                  436
                  4.0e-43
E value
                  118
Match length
                  75
% identity
                  (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
NCBI Description
                  260592
Seq. No.
                  1552 3.R1011
Contig ID
                  LIB143-023-Q1-E1-H8
5'-most EST
                  BLASTX
Method
                  g1542941
NCBI GI
                  684
BLAST score
                  8.0e-72
E value
                  179
Match length
                  74
% identity
                  (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
NCBI Description
                  260593
Seq. No.
                  1552 4.R1011
Contig ID
                  tzu700202142.h1
5'-most EST
                  BLASTX
Method
                  g323018
NCBI GI
                  179
BLAST score
                  8.0e-13
E value
                  77
Match length
                  51
% identity
                  acetoacetyl-CoA thiolase (EC 2.3.1.9) - imperfect fungus
NCBI Description
                   (Candida tropicalis) >gi 218366 dbj BAA02715 (D13470)
                   acetoacetyl-CoA thiolase A [Candida tropicalis]
                   260594
Seq. No.
                   1552 5.R1011
Contig ID
5'-most EST
                   uC-zmflb73270d11b1
Method
                   BLASTX
                   q1542941
NCBI GI
BLAST score
                   257
                   3.0e-22
È value
Match length
                   78
                   69
% identity
NCBI Description (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
                   260595
Seq. No.
Contig ID
                   1553 1.R1011
5'-most EST
                   LIB3068-038-Q1-K1-B7
Method
                   BLASTX
NCBI GI
                   g4160402
BLAST score
                   2007
E value
                   0.0e + 00
Match length
                   442
                   90
% identity
                   (AJ132240) eukaryotic translation initiation factor 5 [Zea
NCBI Description
                   mays]
```

36060

260596

1553 2.R1011

Seq. No.

Contig ID



5'-most EST uC-zmflb73175e06b1

Method BLASTX
NCBI GI g2494320
BLAST score 174
E value 3.0e-12
Match length 38
% identity 87

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5)

>gi_1806575_emb_CAA67868_ (X99517) Eukaryotic initiation

factor-5 [Zea mays]

Seq. No. 260597

Contig ID 1553 3.R1011

5'-most EST uC-zmflmo17092a07a1

Method BLASTN
NCBI GI g4160401
BLAST score 101
E value 2.0e-49
Match length 193
% identity 88

NCBI Description Zea mays eIF-5 gene, exons 1-2

Seq. No. 260598

Contig ID 1553 5.R1011

5'-most EST uĆ-zmrob73044f12a1

Method BLASTX
NCBI GI g2494320
BLAST score 164
E value 2.0e-11
Match length 31
% identity 100

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5)

>gi_1806575_emb_CAA67868_ (X99517) Eukaryotic initiation

factor-5 [Zea mays]

Method BLASTX
NCBI GI - g3851001
BLAST score 1195
E value 1.0e-132
Match length 236
% identity 100

NCBI Description (AF069909) pyruvate dehydrogenase E1 beta subunit isoform 2

[Zea mays]

Seq. No. 260600

Contig ID 1555_2.R1011 5'-most EST uC-zmflB73045g04b1

Method BLASTX
NCBI GI g3851001
BLAST score 461
E value 5.0e-46
Match length 101
% identity 92

NCBI Description (AF069909) pyruvate dehydrogenase E1 beta subunit isoform 2

BLAST score

Match length

E value

267

72

1.0e-23



[Zea mays]

```
Seq. No.
                  260601
                  1555 3.R1011
Contig ID
5'-most EST
                  LIB3136-018-Q1-K1-B12
Method
                  BLASTX
NCBI GI
                  q3851003
BLAST score
                   1845
E value
                  0.0e + 00
Match length
                   367
% identity
                  100
NCBI Description
                   (AF069910) pyruvate dehydrogenase E1 beta subunit isoform 3
                   [Zea mays]
Seq. No.
                  260602
Contig ID
                   1555 5.R1011
5'-most EST
                   fC-zmf1700552621a1
Method
                  BLASTN
NCBI GI
                  q3851000
BLAST score
                   67
E value
                   4.0e-29
Match length
                  136
% identity
                  99
NCBI Description
                  Zea mays pyruvate dehydrogenase E1 beta subunit isoform 2
                  mRNA, nuclear gene encoding mitochondrial protein, complete
                  cds
Seq. No.
                  260603
Contig ID
                  1562 1.R1011
5'-most EST
                  LIB3075-033-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  q4091080
BLAST score
                   791
                  2.0e-84
E value
                  234
Match length
% identity
                   65
NCBI Description
                  (AF045571) nucleic acid binding protein [Oryza sativa]
                  260604
Seq. No.
Contig ID
                  1562 2.R1011
5'-most EST
                  uC-zmflb73054b01b1
Method
                  BLASTX
NCBI GI
                  q4091117
BLAST score
                  469
E value
                  5.0e-47
Match length
                  125
                  70
% identity
NCBI Description
                  (AF047428) nucleic acid binding protein [Oryza sativa]
                  260605
Seq. No.
Contig ID
                  1562 3.R1011
5'-most EST
                  xmt700267866.h1
Method
                  BLASTX
NCBI GI
                  g4091080
```



% identity NCBI Description (AF045571) nucleic acid binding protein [Oryza sativa] 260606 Seq. No. Contig ID 1563 1.R1011 uC-zmflB73107f03b2 5'-most EST Method BLASTX NCBI GI a2708624 BLAST score 3064 0.0e + 00E value 691 Match length 80 % identity NCBI Description (AF036618) acetyl-CoA synthetase [Arabidopsis thaliana] 260607 Seq. No. 1563 4.R1011 Contig ID 5'-most EST ceu700428687.h1 Method BLASTX q4107276 NCBI GI BLAST score 395 1.0e-38 E value 86 Match length 92 % identity NCBI Description (X98506) acetyl-CoA synthetase [Solanum tuberosum] 260608 Seq. No. 1564 1.R1011 Contig ID 5'-most EST uC-zmrob73050e01b1 Seq. No. 260609 Contiq ID 1568 1.R1011 5'-most EST LIB3075-033-Q1-K1-D11 Seq. No. 260610 1569 1.R1011 Contig ID $xmt7\overline{0}0261412.h1$ 5'-most EST Method BLASTX q514324 NCBI GI BLAST score 400 E value 6.0e-39 Match length 136 % identity 63 (L34773) RNA polymerase subunit [Arabidopsis thaliana] NCBI Description >gi 2462755 (AC002292) RNA polymerase subunit (isoform B) [Arabidopsis thaliana] >gi 1586550 prf 2204246B RNA polymerase [Arabidopsis thaliana] 260611 Seq. No. Contig ID 1573 1.R1011 5'-most EST LIB3150-013-Q1-N1-E9

Seq. No. 260612 Contig ID 1581 1.R1011

5'-most EST LIB3075-033-Q1-K1-B12

Method BLASTX NCBI GI g4218122 BLAST score 169



E value 1.0e-11 Match length 131 % identity 33

NCBI Description (AL035353) putative protein [Arabidopsis thaliana]

 Seq. No.
 260613

 Contig ID
 1581_2.R1011

 5'-most EST
 xjt700092613.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 2.0e-10
Match length 36

% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 260614

Contig ID 1582_1.R1011

5'-most EST LIB3150-094-P1-N1-H8

Method BLASTX
NCBI GI g3426036
BLAST score 233
E value 5.0e-19
Match length 184
% identity 346

NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 260615

Contig ID 1585 2.R1011

5'-most EST LIB3076-033-Q1-K1-G4

Seq. No. 260616

Contig ID 1587 1.R1011

5'-most EST LIB3060-019-Q1-K1-F7

Method BLASTX
NCBI GI g2895866
BLAST score 2220
E value 0.0e+00
Match length 534
% identity 82

NCBI Description (AF045770) methylmalonate semi-aldehyde dehydrogenase

[Oryza sativa]

Seq. No. 260617 Contig ID 1591 1.R1011

5'-most EST LIB3066-010-Q1-K1-B3

Seq. No. 260618 Contig ID 1595_1.R1011

5'-most EST LIB189-010-Q1-E1-D7

Method BLASTX
NCBI GI g3860277
BLAST score 881
E value 7.0e-95
Match length 215
% identity 80

NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis



thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 260619

Contig ID 1595 2.R1011

5'-most EST LIB3088-021-Q1-K1-G2

Method BLASTX
NCBI GI g3860277
BLAST score 520
E value 8.0e-53
Match length 114
% identity 87

NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis

thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative

ribosomal protein L10A [Ārabidopsīs thaliana]

Seq. No. 260620 Contig ID 1595_3.R1011

5'-most EST uC-zmflb73262e03a2

Method BLASTX
NCBI GI g3860277
BLAST score 373
E value 9.0e-36
Match length 81
% identity 89

NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis

thaliana] >gi_4314394_gb_AAD15604 (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 260621

Contig ID 1595_5.R1011 5'-most EST nwy700445941.h1

Method BLASTX
NCBI GI g1709970
BLAST score 204
E value 5.0e-16
Match length 66
% identity 64

NCBI Description 60S RIBOSOMAL PROTEIN L10A

Seq. No. 260622

Contig ID 1595_7.R1011 5'-most EST wty700173014.h1

Seq. No. 260623

Contig ID 1595 8.R1011

5'-most EST LIB3151-023-Q1-K1-E9

Method BLASTX
NCBI GI g3860277
BLAST score 382
E value 5.0e-53
Match length 198
% identity 62

NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis

thaliana] >gi 4314394 gb AAD15604 (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]



```
Seq. No.
                  260624
Contig ID
                  1596 1.R1011
5'-most EST
                  uC-zmflb73189a06b1
                  BLASTX
Method
NCBI GI
                  g731529
BLAST score
                  314
E value
                  3.0e-28
Match length
                  381
% identity
                  30
                  HYPOTHETICAL 92.5 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION
NCBI Description
                  >qi 1077719 pir S50660 hypothetical protein YER157w -
                  yeast (Saccharomyces cerevisiae) >gi 603397 (U18917)
                  Yer157wp [Saccharomyces cerevisiae]
Seq. No.
                  260625
Contig ID
                  1596 2.R1011
5'-most EST
                  LIB36-017-Q1-E1-F9
Seq. No.
                  260626
                  1597 1.R1011
Contig ID
5'-most EST
                  pmx700088839.h1
                  BLASTX
Method
NCBI GI
                  q1175426
BLAST score
                   458
                   3.0e-61
E value
Match length
                   382
                   37
% identity
NCBI Description
                  PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06
                  >gi 984214 emb CAA90819 (Z54140) probable ATP-dependent
                  RNA helicase [Schizosaccharomyces pombe]
                   260627
Seq. No.
                  1600 1.R1011
Contig ID
5'-most EST
                  wty700171589.h1
Method
                  BLASTX
NCBI GI
                  g3342821
BLAST score
                   1195
E value
                   1.0e-131
Match length
                   218
% identity
                   100
                 (AF076954) eukaryotic translation initiation factor small
NCBI Description
                  subunit [Zea mays]
Seq. No.
                   260628
Contig ID
                   1600 2.R1011
5'-most EST
                  LIB3069-034-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                   g4588906
BLAST score
                   908
E value
                   5.0e-98
```

Match length 192 % identity

NCBI Description (AF118149) ribosomal protein S7 [Secale cereale]

260629 Seq. No. 1600 3.R1011 Contig ID 5'-most EST LIB3059-019-Q1-K1-A7



Method BLASTX NCBI GI q4588906 BLAST score 392 E value 1.0e-37 Match length 87 % identity 86 NCBI Description (AF118149) ribosomal protein S7 [Secale cereale] Seq. No. 260630 Contig ID 1600 4.R1011 5'-most EST uC-zmflb73267c02a1 Method BLASTX NCBI GI q3342821 BLAST score 162 6.0e-12 E value 50 Match length % identity 75 (AF076954) eukaryotic translation initiation factor small NCBI Description subunit [Zea mays] Seq. No. 260631 Contig ID 1600 5.R1011 LIB3070-015-Q1-N1-C8 5'-most EST Method BLASTX NCBI GI q4588906 BLAST score 398 1.0e-38 E value Match length 90 % identity 88 NCBI Description (AF118149) ribosomal protein S7 [Secale cereale] Seq. No. 260632 Contig ID 1600 9.R1011 5'-most EST uC-zmroteosinte022c12b1 Method BLASTX NCBI GI g4588906 BLAST score 534 2.0e-54 E value Match length 128 % identity 84 (AF118149) ribosomal protein S7 [Secale cereale] NCBI Description 260633 Seq. No. Contig ID 1601 1.R1011 5'-most EST LIB3075-032-Q1-K1-D12 260634 Seq. No. 1604 1.R1011 Contig ID LIB3075-032-Q1-K1-D6 5'-most EST 260635 Seq. No. Contig ID 1606 1.R1011

5'-most EST uC-zmrob73033h01b1

Method BLASTX
NCBI GI g2511535
BLAST score 2086
E value 0.0e+00



```
428
Match length
                   93
% identity
                  (AF008122) alpha-tubulin 3 [Eleusine indica]
NCBI Description
Seq. No.
                   260636
Contig ID
                   1606 2.R1011
5'-most EST
                   uC-zmflb73119a07b1
Method
                   BLASTX
NCBI GI
                   g401161
BLAST score
                   659
                   6.0e-79
E value
Match length
                   147
% identity
                   90
                   TUBULIN ALPHA-5 CHAIN >gi_322879_pir__S28982 tubulin
NCBI Description
                   alpha-5 chain - maize >gi_22156_emb_CAA44862_
                                                                   (X63177)
                   alpha-tubulin \#5 [Zea mays] >gi_450\overline{2}93 (L278\overline{15})
                   alpha-tubulin [Zea mays] >gi 452474 (U05258) alpha-tubulin
                   [Zea mays]
                   260637
Seq. No.
Contig ID
                   1606_3.R1011
5'-most EST
                   LIB3067-031-Q1-K1-D11
Method
                   BLASTN
NCBI GI
                   g450292
BLAST score
                   213
E value
                   1.0e-116
Match length
                   221
                   99
% identity
                   Zea mays alpha-tubulin mRNA, complete cds.
NCBI Description
                   >gi 452473 gb U05258 ZMU05258 Zea mays Black Mexican Sweet
                   alpha-tubulin mRNA, complete cds
                   260638
Seq. No.
                   1608 1.R1011
Contig ID
5'-most EST
                   LIB3136-049-Q1-K1-D4
Seq. No.
                   260639
Contig ID
                   1610 1.R1011
5'-most EST
                   uC-zmflmo17117c12b1
Method
                   BLASTX
NCBI GI
                   q2330840
BLAST score
                   222
E value
                   6.0e-18
Match length
                   122
% identity
                   38
NCBI Description
                  (Z98531) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                   260640
Contig ID
                   1614 1.R1011
                   LIB3075-032-Q1-K1-B1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3157927
```

BLAST score 250 E value 3.0e-21

Match length 83 % identity

NCBI Description (AC002131) Contains similarity to GDP-dissociation



inhibitor gb_L07918 from Mus musculus. [Arabidopsis
thaliana]

260641 Seq. No. 1619 1.R1011 Contig ID pmx700090735.h1 5'-most EST BLASTX Method g3184282 NCBI GI 928 BLAST score 1.0e-100 E value 288 Match length % identity 67

NCBI Description (AC004136) hypothetical protein [Arabidopsis thaliana]

 Seq. No.
 260642

 Contig ID
 1620_1.R1011

 5'-most EST
 wty700171731.h1

 Method
 BLASTX

 NCBI GI
 g4309759

 BLAST, score
 273

NCBI GI g4309759
BLAST score 273
E value 1.0e-23
Match length 73
% identity 68

NCBI Description (AC006217) unknown protein with Src homology 3 (SH3) domain

profile (PDOC50002) [Arabidopsis thaliana]

Seq. No. 260643 Contig ID 1621_1.R1011

5'-most EST LIB148-009-Q1-E1-D8

Method BLASTX
NCBI GI g3695383
BLAST score 773
E value 2.0e-82
Match length 160

% identity 86

NCBI Description (AF096370) similar to inorganic pyrophosphatase (Pfam:

PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis

thaliana]

Seq. No. 260644

Contig ID 1622 1.R1011

5'-most EST LIB189-021-Q1-E1-F2

Method BLASTX
NCBI GI g1706261
BLAST score 1711
E value 0.0e+00
Match length 360
% identity 91

NCBI Description CYSTEINE PROTEINASE 2 PRECURSOR >gi_2118129_pir__S59598

cysteine proteinase 2 precursor - maize

>gi_644490_dbj_BAA08245_ (D45403) cysteine proteinase [Zea

mays]

Seq. No. 260645

Contig ID 1624_2.R1011 5'-most EST ymt700220482.h1

Method BLASTX



```
NCBI GI
                   g2239179
BLAST score
                   267
                   8.0e-23
E value
Match length
                   81
                   59
% identity
                  (Z97208) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                   260646
Contig ID
                   1626 1.R1011
                   uC-zmrob73022a04a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3341681
BLAST score
                   902
                   3.0e-97
E value
Match length
                   190
                   95
% identity
                   (AC003672) small GTP-binding protein [Arabidopsis thaliana]
NCBI Description
                   >qi 741994 prf 2008312A GTP-binding protein [Arabidopsis
                   thaliana]
                   260647
Seq. No.
Contig ID
                   1626 2.R1011
5'-most EST
                   ymt700219022.h1
Method
                   BLASTX
NCBI GI
                   q623586
BLAST score
                   416
                   2.0e-40
E value
Match length
                   101
% identity
                   84
                  (L29273) putative [Nicotiana tabacum]
NCBI Description
                   260648
Seq. No.
                   1626 3.R1011
Contig ID
                   yyf7\overline{0}0349145.h1
5'-most EST
                   BLASTX
Method
                   g623586
NCBI GI
BLAST score
                   224
                   2.0e-18
E value
Match length
                   44
                   100
% identity
                  (L29273) putative [Nicotiana tabacum]
NCBI Description
                   260649
Seq. No.
                   1627 1.R1011
Contig ID
                   LIB3066-007-Q1-K1-D5
5'-most EST
                   BLASTX
Method
                   g2244993
NCBI GI
BLAST score
                   372
                   2.0e-43
E value
Match length
                   187
                   45
% identity
```

NCBI Description (Z97341) similarity to AMP-activated protein kinase beta

[Arabidopsis thaliana]

Seq. No. 260650 Contig ID 1629_1.R1011

5'-most EST LIB3075-031-Q1-K1-F7



```
BLASTX
Method
NCBI GI
                  q3551954
                  357
BLAST score
                  7.0e - 34
E value
Match length
                  130
                   48
% identity
                   (AF082030) senescence-associated protein 5 [Hemerocallis
NCBI Description
                  hybrid cultivar]
                  260651
Seq. No.
                  1632 1.R1011
Contig ID
                  LIB148-041-Q1-E1-E5
5'-most EST
                   260652
Seq. No.
                   1632 3.R1011
Contig ID
                   LIB148-038-Q1-E1-A10
5'-most EST
                   260653
Seq. No.
Contig ID
                   1633 1.R1011
                   wty700171744.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q984174
                   233
BLAST score
                   2.0e-19
E value
                   110
Match length
                   43
% identity
                  (Z54139) Pas7p [Saccharomyces cerevisiae]
NCBI Description
Seq. No.
                   260654
Contig ID
                   1636 1.R1011
                   wyr700235424.h1
5'-most EST
                   BLASTX
Method
                   g3980396
NCBI GI
BLAST score
                   1101
                   1.0e-120
E value
Match length
                   250
% identity
                   75
                   (AC004561) putative C-4 sterol methyl oxidase [Arabidopsis
NCBI Description
                   thaliana]
                   260655
Seq. No.
                   1637 1.R1011
Contig ID
                   LIB3075-032-Q1-K1-A11
5'-most EST
                   BLASTX
Method
                   q3386611
NCBI GI
                   186
BLAST score
                   1.0e-13
E value
                   77
Match length
                   48
% identity
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
                   260656
Seq. No.
                   1638 1.R1011
Contig ID
                   LIB148-029-Q1-E1-A10
```

BLASTN

Method g3821780 NCBI GI 36

BLAST score

5'-most EST



2.0e-10 E value 36 Match length 100 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

260657 Seq. No.

1639 1.R1011 Contig ID

5'-most EST LIB3075-032-Q1-K1-A3

260658 Seq. No.

1640 1.R1011 Contig ID zuv700356440.h1 5'-most EST

BLASTX Method g2828280 NCBI GI 920 BLAST score 1.0e-99 E value 206 Match length 84 % identity

(AL021687) putative protein [Arabidopsis thaliana] NCBI Description

>qi 2832633 emb CAA16762 (AL021711) putative protein

[Arabidopsis thaliana]

260659 Seq. No.

1646 1.R1011 Contig ID uC-zmflb73183h01b1 5'-most EST

Method BLASTX g2677830 NCBI GI BLAST score 380 2.0e-36 E value Match length 117

% identity 72

(U93168) ribosomal protein L12 [Prunus armeniaca] NCBI Description

Seq. No. 260660

Contig ID 1646 2.R1011 5'-most EST dyk700105321.h1

BLASTX Method NCBI GI q2677830 BLAST score 741 1.0e-78 E value Match length 161 % identity 92

(U93168) ribosomal protein L12 [Prunus armeniaca] NCBI Description

Seq. No. 260661

5'-most EST

% identity

Contig ID 1646 3.R1011 uC-zmrob73075f11b1

92

Method BLASTX NCBI GI g2677830 BLAST score 622 6.0e - 76E value Match length 164

NCBI Description (U93168) ribosomal protein L12 [Prunus armeniaca]

260662 Seq. No. 1646 4.R1011 Contig ID



```
pmx700088077.h1
5'-most EST
                   BLASTX
Method
                   g2677830
NCBI GI
BLAST score
                   651
                   8.0e-74
E value
                   160
Match length
                   89
% identity
                  (U93168) ribosomal protein L12 [Prunus armeniaca]
NCBI Description
                   260663
Seq. No.
                   1646 5.R1011
Contig ID
                   uC-zmroteosinte092b02b2
5'-most EST
                   BLASTX
Method
                   g2677830
NCBI GI
                   551
BLAST score
                   2.0e-56
E value
                   135
Match length
                   84
% identity
                  (U93168) ribosomal protein L12 [Prunus armeniaca]
NCBI Description
                   260664
Seq. No.
                   1646 6.R1011
Contig ID
                   uC-zmflb731234c12a1
5'-most EST
                   BLASTX
Method
                   q4371282
NCBI GI
BLAST score
                   166
                   1.0e-11
E value
                   35
Match length
                   89
% identity
                   (ACO06260) putative 60S ribosomal protein L12 [Arabidopsis
NCBI Description
                   thaliana]
                   260665
Seq. No.
                   1646 8.R1011
Contig ID
5'-most EST
                   wen7\overline{0}0333020.h1
                   BLASTX
Method
                   g2677830
NCBI GI
BLAST score
                   365
                   5.0e-35
E value
Match length
                   76
                   95
% identity
NCBI Description
                  (U93168) ribosomal protein L12 [Prunus armeniaca]
                   260666
Seq. No.
                   1646 9.R1011
Contig ID
5'-most EST
                   uC-zmf1b73232c10b1
                   BLASTX
Method
                   g3986695
NCBI GI
BLAST score
                   480
                   3.0e-48
E value
Match length
                   103
                   93
% identity
                  (AF101423) ribosomal protein L12 [Cichorium intybus]
NCBI Description
```

36073

260667

1646 10.R1011

LIB3079-042-Q1-K1-E9

Seq. No. Contig ID

5'-most EST

Contig ID

Method

NCBI GI

5'-most EST

BLAST score



```
260668
Seq. No.
                  1648 1.R1011
Contig ID
                  nbm700467394.hl
5'-most EST
                  BLASTX
Method
                  g1707998
NCBI GI
                  2234
BLAST score
                  0.0e+00
E value
                  513
Match length
                  86
% identity
                  SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi_481944_pir__S40218 glycine
                  hydroxymethyltransferase (EC 2.1.2.1) - potato
                  >gi_438247_emb_CAA81082_ (Z25863) glycine
                  hydroxymethyltransferase [Solanum tuberosum]
                   260669
Seq. No.
                   1648 2.R1011
Contig ID
                  nbm700469121.h1
5'-most EST
                   BLASTX
Method
                   g4467099
NCBI GI
                   329
BLAST score
                   7.0e-31
E value
                   95
Match length
                   75
% identity
                  (AL035538) glycine hydroxymethyltransferase like protein
NCBI Description
                   [Arabidopsis thaliana]
                   260670
Seq. No.
                   1649 1.R1011
Contig ID
                   LIB143-049-Q1-E1-B7
5'-most EST
                   BLASTX
Method
                   q2832672
NCBI GI
                   584
BLAST score
E value
                   4.0e-60
Match length
                   126
% identity
                  (AL021712) nifU-like protein [Arabidopsis thaliana]
NCBI Description
                   260671
Seq. No.
Contig ID
                   1649 2.R1011
                   LIB3075-005-Q1-K1-G3
5'-most EST
                   BLASTX
Method
                   g2832672
NCBI GI
BLAST score
                   516
E value
                   4.0e-52
Match length
                   129
% identity
                   77
NCBI Description (AL021712) nifU-like protein [Arabidopsis thaliana]
                   260672
Seq. No.
```

36074

1652 1.R1011

BLASTX

1852

g3342556

uC-zmflmo17268h07b1

5'-most EST

Seq. No.

Contig ID



```
0.0e + 00
E value
Match length
                   445
% identity
                  81
                  (AF077528) importin alpha [Arabidopsis thaliana]
NCBI Description
                  260673
Seq. No.
                  1652 2.R1011
Contig ID
5'-most EST
                  LIB3075-031-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                   g3342556
BLAST score
                   337
                   4.0e-31
E value
Match length
                   90
                   79
% identity
                  (AF077528) importin alpha [Arabidopsis thaliana]
NCBI Description
                   260674
Seq. No.
                   1653 1.R1011
Contig ID
                   xsy700211301.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2160692
BLAST score
                   686
E value
                   5.0e-72
Match length
                   184
                   69
% identity
                   (U73527) B' regulatory subunit of PP2A [Arabidopsis
NCBI Description
                   thaliana]
                   260675
Seq. No.
Contig ID
                   1653 3.R1011
                   LIB3075-031-Q1-K1-E4
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2160692
BLAST score
                   407
E value
                   6.0e-40
Match length
                   104
                   72
% identity
                  (U73527) B' regulatory subunit of PP2A [Arabidopsis
NCBI Description
                   thaliana]
                   260676
Seq. No.
                   1654 1.R1011
Contig ID
                   wyr700238945.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4138583
BLAST score
                   1933
                   0.0e+00
E value
                   486
Match length
                   77
% identity
NCBI Description (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
                   260677
Seq. No.
                   1654 2.R1011
Contig ID
```

36075

LIB3061-046-Q1-K1-D9

260678

1654 3.R1011



5'-most EST uC-zmflmo17116h12b1 Method BLASTX NCBI GI a1707364 BLAST score 209 1.0e-16 E value Match length 48 % identity 88 NCBI Description (X94626) AATP2 [Arabidopsis thaliana] 260679 Seq. No. Contig ID 1654_4.R1011 5'-most EST uC-zmflMo17084g04b1 Method BLASTX NCBI GI q4138583 BLAST score 1058 E value 1.0e-148 Match length 373 % identity 74 NCBI Description (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum] 260680 Seq. No. 1657 1.R1011 Contig ID 5'-most EST LIB3060-048-Q1-K1-B5 Method BLASTX NCBI GI q1839597 BLAST score 2043 0.0e+00E value Match length 444 95 % identity NCBI Description (S82324) calcium/calmodulin-dependent protein kinase homolog_CaM kinase homolog_MCK1 [Zea mays=maize, cv. Merit, root caps, Peptide, 625 aa [Zea mays] Seq. No. 260681 Contig ID 1660 1.R1011 $uC-z\overline{m}flb73169d04b2$ 5'-most EST Method BLASTX NCBI GI q832876 BLAST score 1712 E value 0.0e+00Match length 433 76 % identity NCBI Description (L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368 prf 2113407A ascorbate free radical reductase [Lycopersicon esculentum] 260682 Seq. No. Contig ID 1661 1.R1011 5'-most EST uC-zmflmo17103g09b1 Method BLASTX NCBI GI g3941724 BLAST score 410 E value 2.0e-39

% identity 33
NCBI Description (AB

425

Match length

(AF104913) eukaryotic protein synthesis initiation factor [Homo sapiens]



260683 Seq. No. 1661 2.R1011 Contig ID $xtd7\overline{0}0282355.h2$ 5'-most EST BLASTX Method q3738332 NCBI GI BLAST score 227 E value 4.0e-18 Match length 134 % identity 42 (AC005170) putative eukaryotic initiation factor NCBI Description [Arabidopsis thaliana] Seq. No. 260684 1662 1.R1011 Contig ID uC-zmflmo17130b02b15'-most EST Method BLASTX NCBI GI g3063693 BLAST score 485 E value 1.0e-48 Match length 168 % identity 55 NCBI Description (AL022537) putative protein [Arabidopsis thaliana] Seq. No. 260685 Contig ID 1664 1.R1011 5'-most EST uC-zmflm017016q08b1 Method BLASTX NCBI GI g3461814 BLAST score 669 E value 7.0e-70 Match length 219 58 % identity NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana] Seq. No. 260686 1666 1.R1011 Contig ID uC-zmflb73048f11b1 5'-most EST Method BLASTX NCBI GI g1076781 BLAST score 354 E value 4.0e-33 Match length 131 % identity 68 NCBI Description transcription factor HBP-la(c14) - wheat >gi 497895 dbj BAA02304 (D12920) transcription factor HBP-la(c14) [Triticum aestivum] 260687 Seq. No. Contig ID 1668 1.R1011 uwc700150460.h1 5'-most EST Method BLASTX

Match length 192 % identity 80



(AF084005) ras-like small monomeric GTP-binding protein NCBI Description [Avena fatua] 260688 Seq. No. 1668 2.R1011 Contig ID uC-zmflmo17095c06b3 5'-most EST BLASTX Method q3334323 NCBI GI 804 BLAST score 8.0e-86 E value 193 Match length 80 % identity GTP-BINDING PROTEIN SAR1A >gi_1314860 (U56929) Sar1 homolog NCBI Description [Arabidopsis thaliana] >gi_2104532_gb_AAC78700.1 (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis thaliana] >gi_2104550 (AF001535) AGAA.4 [Arabidopsis thaliana] 260689 Seq. No. 1668 3.R1011 Contig ID LIB36-005-Q1-E1-C3 5'-most EST BLASTX Method g3450893 NCBI GI 409 BLAST score 8.0e-40E value 82 Match length 96 % identity (AF084005) ras-like small monomeric GTP-binding protein NCBI Description [Avena fatua] 260690 Seq. No. Contig ID 1668 4.R1011 uC-zmflMo17086f09b1 5'-most EST BLASTX Method g3334323 NCBI GI 361 BLAST score E value 6.0e-55 Match length 137 % identity 86 GTP-BINDING PROTEIN SAR1A >gi_1314860 (U56929) Sar1 homolog NCBI Description [Arabidopsis thaliana] >gi_2104532_gb_AAC78700.1 (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis thaliana] >gi 2104550 (AF001535) AGAA.4 [Arabidopsis thaliana] 260691 Seq. No. Contig ID 1668 7.R1011 ntr700073426.h1 5'-most EST Method BLASTX NCBI GI g3450893

BLAST score 192

E value 7.0e-15 Match length 35 100 % identity

(AF084005) ras-like small monomeric GTP-binding protein NCBI Description

[Avena fatua]



Seq. No. 260692

Contig ID 1670_1.R1011

5'-most EST uC-zmflmo17287d01b1

Method BLASTX
NCBI GI g2440029
BLAST score 357
E value 1.0e-33
Match length 135
% identity 52

NCBI Description (Y14851) DAL1 protein [Arabidopsis thaliana]

>gi 2440031 emb CAA75115 (Y14850) DAL1 protein

[Arabidopsis thaliana]

Seq. No. 260693

Contig ID 1670 2.R1011

5'-most EST uC-zmflmo17046f07b1

Method BLASTX
NCBI GI g1200205
BLAST score 207
E value 9.0e-16
Match length 68
% identity 57

NCBI Description (X95753) DAG [Antirrhinum majus]

Seq. No. 260694

Contig ID 1670 3.R1011

5'-most EST uC-zmrob73033c04b1

Seq. No. 260695

Contig ID 1671_1.R1011

5'-most EST LIB3075-030-Q1-K1-F3

Method BLASTX
NCBI GI g4503523
BLAST score 898
E value 9.0e-97
Match length 312
% identity 57

NCBI Description UNKNOWN >gi 2351378 (U54558) translation initiation factor

eIF3 p66 subunit [Homo sapiens] >gi_4200328_emb_CAA18440_

(AL022313) EIF3-P66 [Homo sapiens]

Seq. No. 260696

Contig ID 1677 1.R1011

5'-most EST LIB $3\overline{0}$ 66-042-Q1-K1-H8

Method BLASTX
NCBI GI 94587526
BLAST score 529
E value 1.0e-53
Match length 257
% identity 45

NCBI Description (AC007060) Strong similarity to F19I3.2 gi_3033375 putative

berberine bridge enzyme from Arabidopsis thaliana BAC

gb_AC004238. ESTs gb_F19886, gb_Z30784 and gb_Z30785 come

from this gene

Seq. No. 260697

Contig ID 1678 1.R1011

NCBI Description



```
LIB3075-030-Q1-K1-E5
5'-most EST
                  260698
Seq. No.
Contig ID
                  1681 1.R1011
5'-most EST
                  LIB3067-048-Q1-K1-A2
                  260699
Seq. No.
                  1682 1.R1011
Contig ID
5'-most EST
                  LIB3066-006-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  q4337202
                  190
BLAST score
                   9.0e-14
E value
                  137
Match length
                   32
% identity
                  (AC006403) putative endosperm-specific protein [Arabidopsis
NCBI Description
                  thaliana]
                   260700
Seq. No.
Contig ID
                   1684 1.R1011
                  LIB3180-020-P2-M1-D5
5'-most EST
                   260701
Seq. No.
Contig ID
                   1684 2.R1011
                  LIB3075-018-Q1-K1-A9
5'-most EST
Method
                  BLASTX
NCBI GI
                   q434759
BLAST score
                   291
                   6.0e - 26
E value
Match length
                   81
% identity
                   70
                  (D21163) similar to human elongation factor 2 mRNA (HSEF2).
NCBI Description
                   [Homo sapiens]
Seq. No.
                   260702
                   1686 1.R1011
Contig ID
                   LIB3075-030-Q1-K1-A8
5'-most EST
                   BLASTX
Method
                   q2245131
NCBI GI
BLAST score
                   277
                   3.0e-24
E value
Match length
                   146
                   42
% identity
NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   260703
                   1688 1.R1011
Contig ID
                   qct701173982.h1
5'-most EST
                   BLASTX
Method
                   g4467126
NCBI GI
                   364
BLAST score
E value
                   1.0e-34
                   152
Match length
% identity
```

[Arabidopsis thaliana]

(AL035538) guanine nucleotide-exchange protein-like

Match length

% identity

313



```
260704
Seq. No.
                   1689 1.R1011
Contig ID
5'-most EST
                   LIB3088-009-Q1-K1-E4
Method
                   BLASTX
NCBI GI
                   g3377813
BLAST score
                   421
                   3.0e-41
E value
                   178
Match length
% identity
                   48
                  (AF076275) No definition line found [Arabidopsis thaliana]
NCBI Description
                   260705
Seq. No.
                   1689 2.R1011
Contig ID
                   uC-zmflmo17070g09b1
5'-most EST
Method
                   BLASTX
                   q3377813
NCBI GI
                   182
BLAST score
                   2.0e-13
E value
                   50
Match length
                   58
% identity
                  (AF076275) No definition line found [Arabidopsis thaliana]
NCBI Description
                   260706
Seq. No.
Contig ID
                   1689 3.R1011
                   wty700166256.h1
5'-most EST
                   BLASTX
Method
                   a3377813
NCBI GI
                   195
BLAST score
                   9.0e-15
E value
                   66
Match length
% identity
                   50
                  (AF076275) No definition line found [Arabidopsis thaliana]
NCBI Description
                   260707
Seq. No.
Contig ID
                   1689 4.R1011
5'-most EST
                   LIB3069-024-Q1-K1-F1
                   260708
Seq. No.
                   1690 1.R1011
Contig ID
                   qmh7\overline{0}0026277.f1
5'-most EST
                   BLASTX
Method
                   g2880048
NCBI GI
                   396
BLAST score
                   3.0e - 38
E value
Match length
                   107
                   71
% identity
                  (AC002340) unknown protein [Arabidopsis thaliana]
NCBI Description
                   260709
Seq. No.
                   1691 1.R1011
Contig ID
                   xyt700343285.h1
5'-most EST
                   BLASTX
Method
                   g4376158
NCBI GI
BLAST score
                   1346
E value
                   1.0e-149
```



NCBI Description (X98873) aspartate kinase [Arabidopsis thaliana]

Seq. No. 260710
Contig ID 1691_2.R1011
5'-most EST uC-zmflm017026e05b1
Method BLASTX
NCBI GI 92257743

Method BLASIX
NCBI GI g2257743
BLAST score 600
E value 6.0e-62
Match length 179
% identity 70

NCBI Description (U62020) lysine-sensitive aspartate kinase [Arabidopsis

thaliana]

Seq. No. 260711

Contig ID 1694_1.R1011

5'-most EST LIB189-008-Q1-E1-C12

Method BLASTX
NCBI GI g2529677
BLAST score 495
E value 2.0e-63
Match length 205
% identity 65

% identity 65 NCBI Description (AC002535) kinesin-like protein, heavy chain [Arabidopsis

thaliana]

Seq. No. 260712

Contig ID 1695_1.R1011

5'-most EST LIB3059-048-Q1-K1-G11

Seq. No. 260713 Contig ID 1695 2.R1011

5'-most EST uC-zmflb73124e03a1

Method BLASTX
NCBI GI g2950472
BLAST score 266
E value 1.0e-22
Match length 126
% identity 43

NCBI Description (AL022070) putative autophagocytosis protein

[Schizosaccharomyces pombe]

 Seq. No.
 260714

 Contig ID
 1695_3.R1011

 5'-most EST
 dyk700106387.h1

Seq. No. 260715

Contig ID 1695_4.R1011 5'-most EST wyr700244338.h1

Seq. No. 260717

Contig ID 1695_11.R1011 5'-most EST uC-zmflb73040d07b1

E value

Match length

% identity

3.0e-32 271

41



```
260718
Seq. No.
                  1695 15.R1011
Contig ID
5'-most EST
                  uC-zmflmo17376d10a1
                  260719
Seq. No.
                  1702 1.R1011
Contig ID
5'-most EST
                  fwa700098513.h1
Method
                  BLASTX
                   q4510345
NCBI GI
BLAST score
                   370
                   6.0e - 35
E value
Match length
                  168
                   43
% identity
NCBI Description
                  (AC006921) unknown protein [Arabidopsis thaliana]
                   260720
Seq. No.
                   1702 3.R1011
Contig ID
5'-most EST
                  LIB3061-013-Q1-K1-G6
                   260721
Seq. No.
Contig ID
                   1702 5.R1011
5'-most EST
                   wyr700237980.h1
                   260722
Seq. No.
Contig ID
                   1705 1.R1011
                  LIB148-027-Q1-E1-A4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2980770
BLAST score
                   1396
E value
                   1.0e-155
Match length
                   433
% identity
                   63
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   260723
                   1705 2.R1011
Contig ID
                   LIB148-004-Q1-E1-F9
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2980770
BLAST score
                   229
                   6.0e-19
E value
                   83
Match length
% identity
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]
                   260724
Seq. No.
                   1709 1.R1011
Contig ID
                   LIB3062-022-Q1-K1-A8
5'-most EST
                   BLASTX
Method
                   g4490737
NCBI GI
BLAST score
                   348
```

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]



260725 Seq. No.

1711 1.R1011 Contig ID

LIB84-013-Q1-E1-D6 5'-most EST

260726 Seq. No.

1714 1.R1011 Contig ID

uC-zmroteosinte066a08b1 5'-most EST

Method BLASTX q2493046 NCBI GI 748 BLAST score 3.0e-79E value 203 Match length 72 % identity

NCBI Description ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR

>gi_82297_pir__A41740 H+-transporting ATP synthase (EC
3.6.1.34) delta' chain precursor - sweet potato

>gi 217938 dbj BAA01511_ (D10660) mitochondrial F1-ATPase

delta subunit [Ipomoea batatas]

260727 Seq. No.

1714 2.R1011 Contig ID pmx700086953.h1 5'-most EST

BLASTX Method q2493046 NCBI GI 748 BLAST score 3.0e-79 E value 203 Match length 72 % identity

NCBI Description ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR

>gi_82297_pir__A41740 H+-transporting ATP synthase (EC

3.6.1.34) delta' chain precursor - sweet potato

>gi 217938 dbj BAA01511_ (D10660) mitochondrial F1-ATPase

delta subunit [Ipomoea batatas]

260728 Seq. No.

1714 3.R1011 Contig ID

5'-most EST LIB3059-041-Q1-K1-E6

BLASTX Method g2493046 NCBI GI BLAST score 456 2.0e-45 E value Match length 134 % identity 66

ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR NCBI Description >qi 82297 pir A41740 H+-transporting ATP synthase (EC

3.6.1.34) delta' chain precursor - sweet potato

>gi_217938_dbj_BAA01511_ (D10660) mitochondrial F1-ATPase

delta subunit [Ipomoea batatas]

260729 Seq. No.

Contig ID 1716 1.R1011

5'-most EST LIB3075-029-Q1-K1-F2

Seq. No. 260730

Contiq ID 1720 1.R1011

LIB83-016-Q1-E1-G4 5'-most EST

BLASTX Method



NCBI GI g3421123 BLAST score 824 E value 4.0e-88 Match length 230 % identity 67

NCBI Description (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis

thaliana]

Seq. No. 260731

Contig ID 1720_2.R1011 5'-most EST yyf700348517.h1

Method BLASTX
NCBI GI g4006877
BLAST score 851
E value 4.0e-91
Match length 336
% identity 57

NCBI Description (Z99707) RNA-binding like protein [Arabidopsis thaliana]

Seq. No. 260732

Contig ID 1720 3.R1011

5'-most EST LIB3136-030-Q1-K1-A5

Method BLASTX
NCBI GI g3421123
BLAST score 310
E value 3.0e-28
Match length 71
% identity 79

NCBI Description (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis

thaliana]

Seq. No. 260733

Contig ID 1720 4.R1011

5'-most EST uC-zmflmo17211b02a1

Seq. No. 260734

Contig ID 1720_6.R1011

5'-most EST LIB3061-020-Q1-K1-C3

Seq. No. 260735

Contig ID 1720_10.R1011 5'-most EST uC-zmflb73217f09b2

Method BLASTX
NCBI GI g3421123
BLAST score 360
E value 4.0e-34
Match length 89

% identity 74

NCBI Description (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis

thaliana]

Seq. No. 260736

Contig ID 1720_17.R1011 5'-most EST rv1700455038.h1

Seq. No. 260737 Contig ID 1722 1.R1011

Seq. No.

Contig ID

5'-most EST

260743

1728 2.R1011

uC-zmflb73292g01b1



```
LIB148-007-Q1-E1-D4
5'-most EST
                  BLASTX
Method
                   g4415916
NCBI GI
                   463
BLAST score
                   8.0e-46
E value
                   273
Match length
                   38
% identity
                   (AC006282) putative pectin methylesterase [Arabidopsis
NCBI Description
                   thaliana]
                   260738
Seq. No.
                   1722 3.R1011
Contig ID
                   LIB148-021-Q1-E1-D4
5'-most EST
                   260739
Seq. No.
                   1726 1.R1011
Contig ID
                   LIB3079-024-Q1-K1-H6
5'-most EST
                   BLASTX
Method
                   g4006848
NCBI GI
                   1034
BLAST score
                   1.0e-112
E value
                   310
Match length
                   63
% identity
                   (AJ131433) selenocysteine methyltransferase [Astragalus
NCBI Description
                   bisulcatus]
                   260740
Seq. No.
                   1726 3.R1011
Contig ID
                   xsy7\overline{0}0210574.h1
5'-most EST
                   260741
Seq. No.
                   1726 5.R1011
Contig ID
                   pmx700084391.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4006848
BLAST score
                   357
                   7.0e-34
E value
Match length
                   103
                   68
% identity
                   (AJ131433) selenocysteine methyltransferase [Astragalus
NCBI Description
                   bisulcatus]
                   260742
Seq. No.
                   1728 1.R1011
Contig ID
                   LIB3059-052-Q1-K1-A8
5'-most EST
Method
                   BLASTX
                   g3811007
NCBI GI
                   1845
BLAST score
                   0.0e + 00
E value
                   391
Match length
 % identity
                   (AB019327) NADP specific isocitrate dehydrogenase [Daucus
NCBI Description
                   carota]
```

% identity

NCBI Description



```
BLASTX
Method
                  g3811007
NCBI GI
                  395
BLAST score
                  3.0e-38
E value
Match length
                  86
                  86
% identity
                  (AB019327) NADP specific isocitrate dehydrogenase [Daucus
NCBI Description
                  carota]
                  260744
Seq. No.
                  1728_3.R1011
Contig ID
                  uC-zmflb73056c10b1
5'-most EST
                  BLASTX
Method
                  g3811007
NCBI GI
                   623
BLAST score
                   6.0e-65
E value
                   130
Match length
                   89
% identity
                  (AB019327) NADP specific isocitrate dehydrogenase [Daucus
NCBI Description
                   carota]
                   260745
Seq. No.
                   1728 4.R1011
Contig ID
                   uC-zmflmo17289g09b1
5'-most EST
                   BLASTX
Method
                   q3811007
NCBI GI
BLAST score
                   589
                   5.0e-61
E value
                   125
Match length
% identity
NCBI Description (AB019327) NADP specific isocitrate dehydrogenase [Daucus
                   carota]
Seq. No.
                   260746
Contig ID
                   1728 5.R1011
                   uC-zmflmo17035a07b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1708401
BLAST score
                   435
                   7.0e-43
E value
Match length
                   109
                   79
% identity
NCBI Description ISOCITRATE DEHYDROGENASE (NADP) (OXALOSUCCINATE
                   DECARBOXYLASE) (IDH) (NADP+-SPECIFIC ICDH) (IDP)
Seq. No.
                   260747
                   1737 1.R1011
Contig ID
                   uC-zmflmo17217d05b1
5'-most EST
                   BLASTX
Method
                   q3169170
NCBI GI
BLAST score
                   286
                   1.0e-25
E value
                   84
Match length
                   63
```

partial [Arabidopsis thaliana]

(AC004401) putative chloroplast envelope Ca2+-ATPase, 5'



260748 Seq. No. 1738 1.R1011 Contig ID LIB3066-037-Q1-K1-A3 5'-most EST BLASTX Method g2642213 NCBI GI 248 BLAST score 4.0e-21 E value Match length 88 % identity 57

(AF030385) nitrate-induced NOI protein [Zea mays] NCBI Description

>gi_2895781 (AF045033) nitrate-induced NOI protein [Zea

mays]

260749 Seq. No. 1739 1.R1011 . Contig ID

uC-zmflmo17164g09b1 5'-most EST

260750 Seq. No.

Contig ID 1739 2.R1011

LIB3069-029-Q1-K1-A1 5'-most EST

260751 Seq. No.

1739 3.R1011 Contig ID

uC-zmflb73176h09b2 5'-most EST

260752 Seq. No.

1739 4.R1011 Contig ID $xmt7\overline{0}0266167.h1$ 5'-most EST

260753 Seq. No.

1739 6.R1011 Contig ID

5'-most EST uC-zmflb73171e07b1

260754 Seq. No.

1739 8.R1011 Contig ID

LIB3075-029-Q1-K1-B1 5'-most EST

260755 Seq. No.

Contig ID 1744 1.R1011

uC-zmflb73073d03b3 5'-most EST

BLASTX Method NCBI GI q1449179 BLAST score 2092 E value 0.0e + 00Match length 549 79 % identity

NCBI Description (D86506) N-ethylmaleimide sensitive fusion protein

[Nicotiana tabacum]

260756 Seq. No. 1748 1.R1011 Contig ID

nbm700475981.h15'-most EST BLASTX Method NCBI GI q3108053

1091 BLAST score 1.0e-132 E value

Match length 304



```
% identity
                   (AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea
NCBI Description
                  mays]
                   260757
Seq. No.
                   1749 1.R1011
Contig ID
                  LIB3075-028-Q1-K1-G6
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2827631
BLAST score
                   367
E value
                   3.0e - 35
Match length
                   115
                   62
% identity
                  (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
                   260758
Seq. No.
                   1752 1.R1011
Contig ID
                   wyr700241888.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2980793
                   327
BLAST score
                   2.0e-33
E value
Match length
                   174
                   40
% identity
                  (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
                   260759
Seq. No.
                   1753 1.R1011
Contig ID
                   uC-zmroteosinte116b03b2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3461821
BLAST score
                   279
                   1.0e-24
E value
Match length
                   176
% identity
                   38
                   (AC004138) putative nucleoside triphosphatase [Arabidopsis
NCBI Description
                   thaliana]
                   260760
Seq. No.
                   1753 2.R1011
Contig ID
                   uC-zmroteosinte021f08b1
5'-most EST
                   BLASTX
Method
                   g3461821
NCBI GI
                   484
BLAST score
                   2.0e-48
E value
Match length
                   189
% identity
                   55
                   (AC004138) putative nucleoside triphosphatase [Arabidopsis
NCBI Description
                   thaliana]
                   260761
Seq. No.
                   1756 1.R1011
Contig ID
                   uC-z\overline{m}flmo17036g10b2
5'-most EST
                   BLASTX
Method
```

Method BLASTX
NCBI GI g2765817
BLAST score 347
E value 4.0e-43



```
280
Match length
                  36
% identity
                  (Z95352) AtMlo-h1 [Arabidopsis thaliana]
NCBI Description
                  >gi_3892049_gb_AAC78258.1_AAC78258 (AC002330) AtMlo-h1
                   [Arabidopsis thaliana]
                  260762
Seq. No.
                  1759_1.R1011
Contig ID
                  fC-zmst700336682a5
5'-most EST
                  BLASTX
Method
                  g4210330
NCBI GI
                   3583
BLAST score
                   0.0e+00
E value
                   769
Match length
                   86
% identity
                   (AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit
NCBI Description
                   [Arabidopsis thaliana]
                   260763
Seq. No.
                   1759 2.R1011
Contig ID
                   rvt700553111.hl
5'-most EST
                   BLASTX
Method
                   g4544453
NCBI GI
                   615
BLAST score
                   4.0e-73
E value
Match length
                   203
                   68
% identity
                  (AC006592) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   260764
Seq. No.
                   1760 2.R1011
Contig ID
                   LIB3066-002-Q1-K1-C11
5'-most EST
                   260765
Seq. No.
                   1761_1.R1011
Contig ID
                   LIB3075-028-Q1-K1-H8
5'-most EST
Method
                   BLASTN
                   g2314803
NCBI GI
                   45
BLAST score
                   4.0e-16
E value
                   77
Match length
 % identity
NCBI Description Oryza sativa signal recognition particle RNA sequence
                   260766
 Seq. No.
                   1767 1.R1011
 Contig ID
 5'-most EST
                   LIB3075-019-Q1-K1-E3
 Method
                   BLASTX
 NCBI GI
                   q2465923
                   677
 BLAST score
 E value
                   5.0e-71
                   226
 Match length
```

[Arabidopsis thaliana]
Seq. No. 260767

58

% identity

NCBI Description

36090

(AF024648) receptor-like serine/threonine kinase



Contig ID 1769_1.R1011

5'-most EST uC-zmflb73304h10b1

Seq. No. 260768

Contig ID 1770_1.R1011 5'-most EST ntr700074268.h1

Seq. No. 260769

Contig ID 1773_1.R1011 5'-most EST xsy700212569.h1

Method BLASTX
NCBI GI g2493147
BLAST score 596
E value 2.0e-61
Match length 165
% identity 76

NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_857574

(U27098) H+-ATPase [Oryza sativa]

Seq. No. 260770

Contig ID 1773_2.R1011 5'-most EST zla700379629.h1

Method BLASTX
NCBI GI g2493147
BLAST score 596
E value 2.0e-61
Match length 165
% identity 76

NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_857574

(U27098) H+-ATPase [Oryza sativa]

 Seq. No.
 260771

 Contig ID
 1773_3.R1011

 5'-most EST
 yyf700349139.h1

Method BLASTX
NCBI GI g137476
BLAST score 629
E value 3.0e-65
Match length 158
% identity 82

NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT

>gi_82334_pir__A40814 H+-transporting ATPase (EC 3.6.1.35)

proteolipid chain, vacuolar - oat >gi_166549 (M73232)

H+-ATPase [Avena sativa]

Seq. No. 260772

Contig ID 1773_5.R1011 5'-most EST ymt700223764.h1

Method BLASTX
NCBI GI g2493147
BLAST score 267
E value 2.0e-29
Match length 101
% identity 77

NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_857574

(U27098) H+-ATPase [Oryza sativa]



 Seq. No.
 260773

 Contig ID
 1775_1.R1011

 5'-most EST
 uC-zmflb73119g01a1

 Method
 BLASTX

Method BLASTX
NCBI GI g134598
BLAST score 805
E value 5.0e-86
Match length 152
% identity 100

NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)

Seq. No. 260774 Contig ID 1775 2.R1011

5'-most EST uC-zmflb73022c07a1

Method BLASTX
NCBI GI g134597
BLAST score 797
E value 3.0e-85
Match length 152
% identity 99

NCBI Description SUPEROXIDE DISMUTASE-4A (CU-ZN) >gi_100926_pir__S07007 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 4, cytosolic -

maize

Seq. No. 260775

Contig ID 1775 3.R1011

5'-most EST LIB189-025-Q1-E1-A9

Method BLASTX
NCBI GI g134597
BLAST score 805
E value 4.0e-86
Match length 152
% identity 100

NCBI Description SUPEROXIDE DISMUTASE-4A (CU-ZN) >qi 100926 pir S07007

superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 4, cytosolic -

maize

Seq. No. 260776

Contig ID 1775 4.R1011

5'-most EST LIB3075-028-Q1-K1-F9

Method BLASTX
NCBI GI g134598
BLAST score 788
E value 4.0e-84
Match length 152
% identity 99

NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)

Seq. No. 260777

Contig ID 1775_5.R1011

5'-most EST uC-zmflb73150g12b1

Method BLASTX
NCBI GI g134598
BLAST score 496
E value 4.0e-50
Match length 113
% identity 85

% identity



```
NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)
                  260778
Seq. No.
Contig ID
                  1775 6.R1011
                  uC-zmflb73362b01a2
5'-most EST
                  BLASTX
Method
                  q134598
NCBI GI
                  315
BLAST score
E value
                  5.0e-50
                  101
Match length
% identity
                  100
NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)
                  260779
Seq. No.
Contig ID
                  1775 12.R1011
                  uC-zmflb73119g01b1
5'-most EST
                  BLASTX
Method
                  g134598
NCBI GI
                  327
BLAST score
E value
                  2.0e-37
                  90
Match length
                  87
% identity
NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)
                  260780
Seq. No.
Contig ID
                  1775 13.R1011
                  LIB3062-009-Q1-K1-A3
5'-most EST
                  BLASTX
Method
                  g1574938
NCBI GI
BLAST score
                  343
                   2.0e-32
E value
Match length
                  86
                  77
% identity
NCBI Description (U34726) superoxide dismutase 4 [Zea mays]
Seq. No.
                   260781
                   1776 1.R1011
Contig ID
                  uC-zmflmo17321b06b1
5'-most EST
                  BLASTX
Method
                   g3337356
NCBI GI
                   2254
BLAST score
                   0.0e+00
E value
                   475
Match length
                   92
% identity
NCBI Description (AC004481) putative protein transport protein SEC61 alpha
                   subunit [Arabidopsis thaliana]
                   260782
Seq. No.
                   1776 2.R1011
Contig ID
                   ntr700077094.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3337356
                   2252
BLAST score
E value
                   0.0e + 00
Match length
                   475
```

NCBI Description (AC004481) putative protein transport protein SEC61 alpha



subunit [Arabidopsis thaliana]

 Seq. No.
 260783

 Contig ID
 1776_3.R1011

 5'-most EST
 xjt700092581.h1

 Method
 BLASTX

 NCBI GI
 g3337356

 BLAST score
 2209

E value 0.0e+00 Match length 469 % identity 91

NCBI Description (AC004481) putative protein transport protein SEC61 alpha

subunit [Arabidopsis thaliana]

Seq. No. 260784

Contig ID 1776_5.R1011

5'-most EST LIB3066-005-Q1-K1-B5

Seq. No. 260785

Contig ID 1776_6.R1011 5'-most EST ymt700221281.h1

Seq. No. 260786

Contig ID 1776 7.R1011

5'-most EST uC-zmflm017233f09b1

Method BLASTX
NCBI GI g3834321
BLAST score 361
E value 4.0e-52
Match length 129

% identity 80

NCBI Description (AC005679) Strong similarity to F13P17.9 gi_3337356 transport protein SEC61 alpha subunit homolog from

Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis

thaliana]

Seq. No. 260787

Contig ID 1776_8.R1011 5'-most EST wty700163008.h1

Seq. No. 260788

Contig ID 1780_1.R1011 5'-most EST uwc700149792.h1

Method BLASTX
NCBI GI g3193287
BLAST score 770
E value 1.0e-111
Match length 267
% identity 66

NCBI Description (AF069298) Arabidopsis predicted protein of unknown

function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]

Seq. No. 260789

Contig ID 1781 1.R1011

5'-most EST LIB3075-028-Q1-K1-D12

Seq. No. 260790



Contig ID 1784_1.R1011

5'-most EST LIB3150-032-Q1-N1-H3

Method BLASTX
NCBI GI g3868758
BLAST score 895
E value 3.0e-96
Match length 359
% identity 86

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. Contig ID

260791 1784 2.R1011

5'-most EST LIB3150-048-Q1-N1-A6

Method BLASTX
NCBI GI g2160158
BLAST score 1491
E value 1.0e-166
Match length 414
% identity 68

NCBI Description (AC000132) Similar to elongation factor 1-gamma

(gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come

from this gene. [Arabidopsis thaliana]

Seq. No. 260792 Contig ID 1784_3.R1011

5'-most EST uC-zmflb73026a02b1

Method BLASTX
NCBI GI g2997591
BLAST score 198
E value 4.0e-15
Match length 135
% identity 33

NCBI Description (AF020814) glucose-6-phosphate/phosphate-translocator

precursor [Pisum sativum]

Seq. No. 260793 Contig ID 1784 4.R1011

5'-most EST uC-zmroteosinte001b07b1

Method BLASTX
NCBI GI g2997591
BLAST score 204
E value 1.0e-15
Match length 169
% identity 33

NCBI Description (AF020814) glucose-6-phosphate/phosphate-translocator

precursor [Pisum sativum]

Seq. No. 260795 Contig ID 1784 6.R1011

5'-most EST LIB3079-026-Q1-K1-F6

Method BLASTX NCBI GI g3868758 BLAST score 767

```
E value
                   1.0e-81
Match length
                   144
% identity
                   97
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
Seq. No.
                  260796
                  1784_7.R1011
Contig ID
5'-most EST
                  uC-zmflb73073d06a1
Method
                  BLASTX
NCBI GI
                  q3868758
BLAST score
                  385
E value
                  4.0e-37
Match length
                  77
                  92
% identity
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
Seq. No.
                  260797
Contig ID
                  1784_8.R1011
5'-most EST
                  LIB3061-055-Q1-K1-H6
Method
                  BLASTX
NCBI GI
                  q3868758
BLAST score
                  275
```

E value 3.0e-24

Match length 57

% identity 91

NCRI Description (P89802) elementian factor 1D and

NCBI Description ~ (D89802) elongation factor 1B gamma [Oryza sativa]

Contig ID 1784_9.R1011
5'-most EST LIB3159-012-Q1-K1-E1
Method BLASTX
NCBI GI g3868758
BLAST score 349
E value 6.0e-33

260798

Match length 91 % identity 73

Seq. No.

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 260799

Contig ID 1784 11.R1011

5'-most EST LIB3088-002-Q1-K1-C5

Seq. No. 260800

Contig ID 1784_15.R1011 5'-most EST xmt700263371.h1

Method BLASTX
NCBI GI 93868758
BLAST score 268
E value 1.0e-23
Match length 73
% identity 73

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 260801

Contig ID 1784_17.R1011 5'-most EST fwa700099294.h1

Method BLASTX



```
NCBI GI
                  q3868758
BLAST score
                  295
E value
                  7.0e-27
Match length
                  66
% identity
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
                  260802
Seq. No.
Contig ID
                  1785 1.R1011
5'-most EST
                  ymt700222640.h1
                  260803
Seq. No.
Contig ID
                  1790 1.R1011
5'-most EST
                  LIB3180-049-P2-M1-F12
Method
                  BLASTX
                  g629692
```

NCBI GI BLAST score 2562 E value 0.0e+00Match length 933 % identity 57

NCBI Description hypothetical protein - common tobacco

>gi_506471_emb_CAA56189_ (X79794) unnamed protein product

[Nicotiana tabacum]

Seq. No. 260804 Contig ID 1790_2.R1011

5'-most EST uC-zmflmo17075f02b2

Method BLASTX NCBI GI g629692 BLAST score 501 E value 1.0e-50 Match length 146 % identity

NCBI Description hypothetical protein - common tobacco

>gi_506471 emb CAA56189 (X79794) unnamed protein product

[Nicotiana tabacum]

Seq. No. 260805 Contig ID 1792 1.R1011

5'-most EST LIB3075-028-Q1-K1-B2

Method BLASTX NCBI GI g4585987 BLAST score 295 3.0e-46 E value Match length 121 % identity 79

NCBI Description (AC005287) Similar to nucleolar protein [Arabidopsis

thaliana]

Seq. No. 260806

Contig ID 1796 1.R1011 5'-most EST xjt700093166.h1

Method BLASTX NCBI GI g1710521 BLAST score 566 E value 4.0e-58 Match length 146



% identity NCBI Description 60S RIBOSOMAL PROTEIN L24 >gi 1154859 emb CAA63960 (X94296) L24 ribosomal protein [Hordeum vulgare] 260807

Contig ID 1796 2.R1011 5'-most EST xjt700092308.h1 Method BLASTX NCBI GI g1710521 BLAST score 566 E value 5.0e-58 Match length 146

Seq. No.

79 % identity NCBI Description 60S RIBOSOMAL PROTEIN L24 >gi 1154859 emb CAA63960 (X94296) L24 ribosomal protein [Hordeum vulgare]

Seq. No. 260808 1796 3.R1011 Contig ID

5'-most EST uC-zmroteosinte117b12b1

Method BLASTX NCBI GI g1710521 BLAST score 552 E value 2.0e-56 Match length 112 % identity 95

NCBI Description 60S RIBOSOMAL PROTEIN L24 >qi 1154859 emb CAA63960

(X94296) L24 ribosomal protein [Hordeum vulgare]

Seq. No. 260809 Contig ID 1796 4.R1011

5'-most EST LIB143-057-Q1-E1-D12

Method BLASTX NCBI GI g1710521 BLAST score 508 E value 3.0e-51 Match length 112

% identity 89

NCBI Description 60S RIBOSOMAL PROTEIN L24 >gi 1154859 emb CAA63960 (X94296) L24 ribosomal protein [Hordeum vulgare]

Seq. No. 260810 Contig ID 1796 5.R1011

5'-most EST LIB3152-051-P1-K1-G8

Method BLASTX NCBI GI g1710521 BLAST score 290 E value 5.0e-26 Match length 63 % identity 87

NCBI Description 60S RIBOSOMAL PROTEIN L24 >gi 1154859 emb CAA63960

(X94296) L24 ribosomal protein [Hordeum vulgare]

Seq. No. 260811

○ Contig ID 1796 6.R1011

5'-most EST LIB83-002-Q1-E1-G9

Method BLASTN NCBI GI g1154858



BLAST score 40 E value 5.0e-13 Match length 127 % identity 83

NCBI Description H.vulgare mRNA for L24 ribosomal protein

Seq. No. Contig ID 260812 1796_7.R1011

5'-most EST

uC-zmflmo170114b01b1

Method BLASTX
NCBI GI g4415907
BLAST score 206
E value 5.0e-16
Match length 50
% identity 88

NCBI Description (AC006282) 60S ribosomal protein L24 [Arabidopsis thaliana]

>gi_4581159_gb_AAD24643.1_AC006919_21 (AC006919) putative

60S ribosomal protein L24 [Arabidopsis thaliana]

Seq. No. 260813

Contig ID 1801 1.R1011 5'-most EST uwc700151264.h1

Seq. No. 260814

Contig ID 1812 1.R1011

5'-most EST uC-zmflmo17287g05b1

Seq. No. 260815 Contig ID 1812_2.R1011

5'-most EST xyt700342730.h1

Seq. No. 260816

Contig ID 1815_1.R1011 5'-most EST nbm700469264.h1

Method BLASTX
NCBI GI g127844
BLAST score 164
E value 8.0e-11
Match length 182
% identity 29

NCBI Description N-TERMINAL ACETYLTRANSFERASE 1 (AMINO-TERMINAL,

ALPHA-AMINO, ACETYLTRANSFERASE 1) >gi_66496_pir_XYBYT1 protein N-acetyltransferase (EC 2.3.1.-) chain NAT1 - yeast (Saccharomyces cerevisiae) >gi_4028_emb_CAA33233_ (X15135) acetyltransferase (AA 1-854) [Saccharomyces cerevisiae] >gi_172028 (M23166) N-acetyltransferase [Saccharomyces cerevisiae] >gi_1279676_emb_CAA96449_ (Z71781) N-terminal

acetyltransferase [Saccharomyces cerevisiae] >gi 1431025 emb CAA98599 (Z74088) ORF YDL040c

[Saccharomyces cerevisiae]

Seq. No. 260817

Contig ID 1815 2.R1011

5'-most EST uC-zmflmo17342f02b1

Seq. No. 260818

Contig ID 1817_1.R1011

E value

Match length

1.0e-137

349



```
5'-most EST
                    LIB3075-028-Q1-K1-A6
 Seq. No.
                    260819
 Contig ID
                    1821 1.R1011
 5'-most EST
                   LIB83-002-Q1-E1-E3
 Method
                   BLASTX
 NCBI GI
                    g4490330
                   1186
 BLAST score
 E value
                    1.0e-130
 Match length
                    268
                    78
 % identity
 NCBI Description (AL035656) splicing factor-like protein [Arabidopsis
                    thaliana]
                    260820
 Seq. No.
 Contig ID
                    1821 2.R1011
 5'-most EST
                   LIB3060-005-Q1-K1-D8
                   BLASTX
 Method
 NCBI GI
                    g4490330
 BLAST score
                   3086
 E value
                    0.0e + 00
 Match length
                    644
 % identity
                    90
 NCBI Description (AL035656) splicing factor-like protein [Arabidopsis
                    thaliana]
 Seq. No.
                    260821
 Contig ID
                   1821 4.R1011
 5'-most EST
                   LIB3066-045-Q1-K1-G10
                   BLASTX
 Method
 NCBI GI
                   g4490330
 BLAST score
                   497
 E value
                    3.0e-50
 Match length
                   111
 % identity
 NCBI Description (AL035656) splicing factor-like protein [Arabidopsis
                   thaliana]
 Seq. No.
                    260822
 Contig ID
                   1824 1.R1011
                   LIB3<u>1</u>56-016-Q1-K1-D2
5'-most EST
 Method
                   BLASTN
 NCBI GI
                   g22514
 BLAST score
                   59
 E value
                   2.0e-24
 Match length
                   135
 % identity
                   87
 NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                   260823
 Seq. No.
 Contig ID
                   1826 1.R1011
 5'-most EST
                   wyr700236690.h1
 Method
                   BLASTX
 NCBI GI
                   q3258569
 BLAST score
                   1247
```



% identity NCBI Description (U89959) Similar to yeast general negative regulator of transcription subunit 1 [Arabidopsis thaliana] Seq. No. 260824 Contig ID 1826 2.R1011 5'-most EST uC-zmroteosinte106g03b2 Method BLASTX NCBI GI g3258569 BLAST score 412 E value 4.0e-40 Match length 103 % identity 80 NCBI Description (U89959) Similar to yeast general negative regulator of transcription subunit 1 [Arabidopsis thaliana] Seq. No. 260825 Contig ID 1827 1.R1011 5'-most EST LIB3075-027-Q1-K1-G3 Method BLASTX NCBI GI g3335060 BLAST score 370 E value 2.0e-42 Match length 129 % identity 60 NCBI Description (AF025842) plasma membrane-type calcium ATPase [Arabidopsis thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana] Seq. No. 260826 1832 1.R1011 Contig ID 5'-most EST LIB3075-027-Q1-K1-H1 Method BLASTX NCBI GI q3850072 BLAST score 223 E value 7.0e-18 Match length 129 % identity 36 NCBI Description (AL033385) dna-directed rna polymerase iii subunit [Schizosaccharomyces pombe] Seq. No. 260827 1833 1.R1011 gct701167652.h1 260828 Seq. No.

Contig ID 5'-most EST

Contig ID 1840 1.R1011 5'-most EST uC-zmflb73224a09b2

Method BLASTX NCBI GI q2760836 BLAST score 280 E value 2.0e-24 Match length 167 % identity

NCBI Description (AC003105) putative Ser/Thr protein kinase [Arabidopsis



Seq. No. 260829

Contig ID 1840 2.R1011

5'-most EST LIB3088-021-Q1-K1-C10

Method BLASTX
NCBI GI g1944319
BLAST score 692
E value 1.0e-72
Match length 192
% identity 65

NCBI Description (D31700) cysteine proteinase inhibitor [Glycine max]

>gi 1944342 dbj BAA19610_ (D64115) cysteine proteinase

inhibitor [Glycine max]

Seq. No. 260830 Contig ID 1840 3.R1011

5'-most EST LIB3137-016-Q1-K1-H9

Seq. No. 260831

Contig ID 1840_4.R1011 5'-most EST wty700172340.h1

Method BLASTX
NCBI GI g2760836
BLAST score 301
E value 7.0e-27
Match length 150
% identity 39

NCBI Description (AC003105) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 260832

Contig ID 1840 5.R1011

5'-most EST LIB3079-020-Q1-K1-A1

Method BLASTX
NCBI GI g1944319
BLAST score 477
E value 1.0e-47
Match length 128
% identity 66

NCBI Description (D31700) cysteine proteinase inhibitor [Glycine max]

>gi 1944342 dbj BAA19610 (D64115) cysteine proteinase

inhibitor [Glycine max]

 Seq. No.
 260833

 Contig ID
 1843_2.R1011

 5'-most EST
 wty700163757.h1

Seq. No. 260834 Contig ID 1843 3.R1011

5'-most EST LIB3061-008-Q1-K1-B7

Seq. No. 260835 Contig ID 1843_4.R1011

5'-most EST LIB3156-013-Q1-K1-B1

Seq. No. 260836
Contig ID 1844_1.R1011
5'-most EST cyk700047859.f1



```
Method
                  BLASTX
NCBI GI
                  g2832681
BLAST score
                  486
                  1.0e-48
E value
                  104
Match length
                  82
% identity
NCBI Description (AL021712) putative protein [Arabidopsis thaliana]
                  260837
Seq. No.
                  1844 2.R1011
Contig ID
                  xmt700263035.h1
5'-most EST
                  BLASTX
Method
                  g2832681
NCBI GI
BLAST score
                  486
                  1.0e-48
E value
Match length
                  106
                  79
% identity
NCBI Description
                  (AL021712) putative protein [Arabidopsis thaliana]
                  260838
Seq. No.
                  1844 3.R1011
Contig ID
                  rvt700551302.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2832681
BLAST score
                  485
                  1.0e-48
E value
                  104
Match length
% identity
                  81
NCBI Description (AL021712) putative protein [Arabidopsis thaliana]
                  260839
Seq. No.
                  1846 1.R1011
Contig ID
                  LIB143-041-Q1-E1-F2
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4468193
BLAST score
                  1535
                  1.0e-171
E value
Match length
                  497
% identity
                  (AJ010201) inosine monophosphate dehydrogenase [Glycine
NCBI Description
                  max]
                  260840
Seq. No.
Contig ID
                  1850 1.R1011
                  zuv700352782.h1
5'-most EST
                  BLASTX
Method
                  a3860247
NCBI GI
BLAST score
                  1711
E value
                  0.0e + 00
Match length
                  381
% identity
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
```

Seq. No. 260841

Contig ID 1850_2.R1011 5'-most EST yyf700352325.h1

Method BLASTX



```
NCBI GI
                   q3860247
BLAST score
                   157
E value
                   2.0e-20
Match length
                   69
                   83
% identity
NCBI Description
                  (AC005824) unknown protein [Arabidopsis thaliana]
                  260842
Seq. No.
Contig ID
                  1850 3.R1011
5'-most EST
                  LIB3066-050-Q1-K1-G1
Method
                  BLASTX
                   q3860247
NCBI GI
BLAST score
                  295
                   1.0e-26
E value
Match length
                   70
                   83
% identity
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                   260843
Seq. No.
Contig ID
                  1850 4.R1011
                   gwl700613228.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                   q4510430
BLAST score
                   543
E value
                   1.0e-55
Match length
                  128
% identity
                   80
                  (AC006929) unknown protein, 3' partial [Arabidopsis
NCBI Description
                  thalianal
Seq. No.
                   260844
Contig ID
                   1850 5.R1011
5'-most EST
                   LIB3180-035-P2-M2-G5
Method
                   BLASTX
NCBI GI
                   q3860247
BLAST score
                   201
                   1.0e-32
E value
Match length
                  115
% identity
                   65
NCBI Description
                 (AC005824) unknown protein [Arabidopsis thaliana]
                   260845
Seq. No.
                   1851 1.R1011
Contig ID
                  LIB3150-061-Q1-N1-H1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2911072
BLAST score
                  1369
                   1.0e-152
E value
```

452 Match length 61 % identity

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 260846

1851 3.R1011 Contig ID

5'-most EST $LIB3\overline{0}67-038-Q1-K1-G6$

Seq. No. 260847

BLAST score

E value Match length 166 2.0e-11

92



```
1851 7.R1011
Contig ID
5'-most EST
                  uC-zmromo17027b09a1
                  260848
Seq. No.
                  1852 1.R1011
Contig ID
                  xsy700213112.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1431629
BLAST score
                  941
E value
                  1.0e-102
                  292
Match length
% identity
                   61
NCBI Description (X99348) pectinacetylesterase precursor [Vigna radiata]
                  260849
Seq. No.
                  1856 1.R1011
Contig ID
5'-most EST
                  LIB3062-025-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                   q4309738
                   379
BLAST score
E value
                   4.0e-36
Match length
                  111
% identity
                  (AC006439) putative tubby protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  260850
Contig ID
                  1856 2.R1011
5'-most EST
                  LIB3136-022-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                   g2829918
BLAST score
                   965
E value
                   1.0e-104
Match length
                   311
% identity
                   62
NCBI Description
                  (AC002291) similar to "tub" protein gp U82468 2072162
                   [Arabidopsis thaliana]
                   260851
Seq. No.
                   1856 3.R1011
Contig ID
                   uC-zmf1b73208f02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2829918
BLAST score
                   182
E value
                   2.0e-13
Match length
                   55
% identity
NCBI Description (AC002291) similar to "tub" protein gp U82468 2072162
                   [Arabidopsis thaliana]
Seq. No.
                   260852
                   1857 1.R1011
Contig ID
                   LIB3075-027-Q1-K1-D8
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1077378
```



% identity probable membrane protein YLR222c - yeast (Saccharomyces NCBI Description cerevisiae) >qi 609371 (U19027) Ylr222cp [Saccharomyces cerevisiae] 260853 Seq. No. 1862 1.R1011 Contig ID LIB3150-049-Q1-N1-D1 5'-most EST Method BLASTX q4539460 NCBI GI BLAST score 146 1.0e-08 E value 244 Match length 21 % identity (AL049500) putative protein [Arabidopsis thaliana] NCBI Description 260854 Seq. No. 1864 1.R1011 Contig ID LIB3075-027-Q1-K1-E4 5'-most EST Method BLASTX q100226 NCBI GI 439 BLAST score E value 3.0e-43Match length 185 % identity 44 hypothetical protein - tomato >gi 19275 emb CAA78112_ NCBI Description (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf__1909366A Leu zipper protein [Lycopersicon esculentum] Seq. No. 260855 1866 1.R1011 Contig ID LIB3088-046-Q1-K1-D3 5'-most EST Seq. No. 260856 Contig ID 1868 1.R1011 5'-most EST uC-zmflmo17426e10a1 260857 Seq. No. 1868 2.R1011 Contig ID 5'-most EST LIB3075-027-Q1-K1-C1 260858 Seq. No. 1868 3.R1011 Contig ID 5'-most EST vux700162306.h1 260859 Seq. No. 1869 1.R1011 Contig ID vux700160291.h1 5'-most EST BLASTN Method

NCBI GI g1185553 BLAST score 62 E value 6.0e-26 Match length 77 % identity 47

NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2) gene, complete cds



260860 Seq. No.

Contig ID 1869 2.R1011

5'-most EST uC-zmrob73066a04b1

Method BLASTX NCBI GI g1351359 BLAST score 151 E value 1.0e-09 Match length 32 % identity 78

UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN NCBI Description

(MITOCHONDRIAL HINGE PROTEIN) (CR7) >gi_1071788_pir__S48690 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 11K protein

- potato >gi_488712_emb_CAA55860_ (X79273) ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No. 260861

1869 3.R1011 Contig ID 5'-most EST uwc700153992.h1

Method BLASTX NCBI GI g1351359 BLAST score 267 E value 3.0e-23Match length 69 % identity 70

UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PROTEIN NCBI Description

(MITOCHONDRIAL HINGE PROTEIN) (CR7) >gi_1071788_pir__S48690 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 11K protein

- potato >gi_488712_emb_CAA55860_ (X79273) ubiquinol--cytochrome c reductase [Solanum tuberosum]

260862 Seq. No.

1871 1.R1011 Contig ID ntr700073230.h1 5'-most EST

BLASTX Method q4309727 NCBI GI BLAST score 382 E value 2.0e-36 Match length 93 73 % identity

NCBI Description (AC006439) putative mitochondrial 60S ribosomal protein L6

[Arabidopsis thaliana]

Seq. No. 260863

Contig ID 1871 2.R1011

LIB143-054-Q1-E1-C8 5'-most EST

Seq. No. 260864

Contig ID 1871 3.R1011

5'-most EST LIB3088-025-Q1-K1-C10

260865 Seq. No.

Contig ID 1871 4.R1011

5'-most EST uC-zmroteosinte028a09b1

260866 Seq. No.

Contig ID 1871 5.R1011



5'-most EST xjt700092867.h1

Method BLASTX
NCBI GI g2911071
BLAST score 377
E value 1.0e-35
Match length 205
% identity 42

NCBI Description (AL021960) hypothetical protein [Arabidopsis thaliana]

Seq. No. 260867

Contig ID 1871_6.R1011

5'-most EST uC-zmflb73003b02b1

Method BLASTX
NCBI GI g2739383
BLAST score 866
E value 7.0e-93
Match length 287
% identity 63

NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 260868

Contig ID 1871_7.R1011

5'-most EST uC-zmflmo17001f10b1

Seq. No. 260869

Contig ID • 1871 8.R1011

5'-most EST uC-zmflmo17248d02b1

Seq. No. 260870

Contig ID 1871 9.R1011

5'-most EST LIB3180-001-P1-M1-B1

Seq. No. 260871

Contig ID 1871_10.R1011

5'-most EST LIB3180-061-P2-M1-H8

Seq. No. 260872

Contig ID 1871_14.R1011 5'-most EST uC-zmflb73078h07b2

Seq. No. 260873

Contig ID 1871_16.R1011 5'-most EST ymt700222094.h1

Seq. No. 260874

Contig ID 1871_18.R1011

5'-most EST uC-zmflmo17263e07b1

Method BLASTX
NCBI GI g2739383
BLAST score 439
E value 3.0e-43
Match length 144
% identity 64

NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]

Seq. No. 260875

Contig ID 1871 19.R1011



5'-most EST fwa700101423.h1 Method BLASTX NCBI GI q3377842 BLAST score 281 E value 6.0e-25 Match length 63 89 % identity NCBI Description (AF076274) No definition line found [Arabidopsis thaliana] Seq. No. 260876 1871 20.R1011 Contig ID 5'-most EST LIB3088-009-Q1-K1-F11 Seq. No. 260877 1871 22.R1011 Contig ID 5'-most EST ymt700218554.h1 Seq. No. 260878 Contig ID 1872 1.R1011 5'-most EST LIB3061-020-Q1-K1-C12 Method BLASTX NCBI GI q3603473 BLAST score 596 E value 2.0e-61 Match length 143 % identity 79 NCBI Description (AF090698) elicitor-responsive gene-3 [Oryza sativa] 260879 Seq. No. Contig ID 1873 1.R1011 5'-most EST LIB3067-029-Q1-K1-D3 Method BLASTX g3068809 NCBI GI BLAST score 454 E value 4.0e-45 Match length 137 67 % identity NCBI Description (AF059295) Skpl homolog [Arabidopsis thaliana] Seq. No. 260880 Contig ID 1874_1.R1011 LIB3059-020-Q1-K1-B12 5'-most EST Method BLASTX NCBI GI g2982299 BLAST score 440 3.0e-43E value Match length 122 % identity (AF051234) transcription factor BTF3 homolog [Picea NCBI Description

marianal

260881 Seq. No.

Contig ID 1874 2.R1011

5'-most EST LIB3158-018-Q1-K1-E6

Seq. No. 260882

Contig ID 1874_3.R1011



5'-most EST uC-zmflmo17155c05a1 Method BLASTX NCBI GI q3915866 BLAST score 1143 E value 1.0e-127 Match length 478 % identity 71 NCBI Description GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS) >gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine synthetase [Lupinus luteus] 260883 Seq. No. 1874 4.R1011 Contig ID 5'-most EST wyr700243257.hl Method BLASTX NCBI GI g3915866 BLAST score 776 E value 6.0e-83 Match length 179 % identity 77 GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS) NCBI Description >gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine synthetase [Lupinus luteus] Seq. No. 260884 1874 8.R1011 Contig ID 5'-most EST uC-zmflB73047b09b1 260885 Seq. No. Contig ID 1876 1.R1011 5'-most EST LIB3075-027-Q1-K1-D1 260886 Seq. No. Contig ID 1880 1.R1011 5'-most EST LIB3075-027-Q1-K1-A3 260887 Seq. No. 1882 1.R1011 Contig ID 5'-most EST LIB3066-043-Q1-K1-G12 Method BLASTX NCBI GI g3319357 BLAST score 1051 1.0e-114 E value Match length 375 % identity 59 (AF077407) contains similarity to phosphoenolpyruvate NCBI Description synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana] 260888 Seq. No. Contig ID 1883 1.R1011 uC-zmflmo17322b07b1 5'-most EST Method BLASTX NCBI GI

NCBI GI g4262240
BLAST score 1006
E value 1.0e-109
Match length 347
% identity 55



```
(AC006200) putative stress protein [Arabidopsis thaliana]
NCBI Description
                  260889:
Seq. No.
                  1885 1.R1011
Contig ID
5'-most EST
                  xjt700093750.h1
                  BLASTX
Method
                  g4490332
NCBI GI
                  797
BLAST score
E value
                  5.0e-85
Match length
                  245
% identity
                   63
                  (AL035656) putative protein [Arabidopsis thaliana]
NCBI Description
                  260890
Seq. No.
                  1887 1.R1011
Contig ID
                  LIB3066-037-Q1-K1-E12
5'-most EST
                   260891
Seq. No.
                  1888 1.R1011
Contig ID
5'-most EST
                  uwc700152533.h1
Method
                  BLASTX
                   q2253583
NCBI GI
                   238
BLAST score
                   4.0e-22
E value
Match length
                   81
                   74
% identity
                  (U78721) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   260892
                   1890 1.R1011
Contig ID
5'-most EST
                   LIB3075-027-Q1-K1-B6
Method
                   BLASTX
NCBI GI
                   g1572819
BLAST score
                   347
E value
                   1.0e-32
Match length
                   190
% identity
                   39
                   (U70855) similar to the RAS gene family [Caenorhabditis
NCBI Description
                   elegans]
Seq. No.
                   260893
                   1891 1.R1011
Contig ID
5'-most EST
                   LIB3075-026-Q1-K1-G6
Method
                   BLASTX
NCBI GI
                   g2827561
BLAST score
                   544
E value
                   2.0e-55
Match length
                   165
                   64
% identity
                   (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
                   >qi 3292809 emb CAA19799 (AL031018) putative protein
                   [Arabidopsis thaliana]
                   260894
Seq. No.
```

1895 1.R1011

 $xmt7\overline{0}0267114.h1$

Contig ID

5'-most EST

NCBI GI

BLAST score



```
260895
Seq. No.
                  1896 1.R1011
Contig ID
                  LIB3279-005-P1-K1-C5
5'-most EST
Method
                  BLASTX
NCBI GI
                  q71673
BLAST score
                   372
                   3.0e-35
E value
                  144
Match length
% identity
                  50
                  calmodulin - sea pansy (Renilla reniformis) (tentative
NCBI Description
                  sequence)
                  260896
Seq. No.
                  1896 2.R1011
Contig ID
5'-most EST
                  wyr700239190.hl
Method
                  BLASTX
                  q225024
NCBI GI
BLAST score
                   366
                   1.0e-34
E value
Match length
                  148
% identity
                   49
NCBI Description calmodulin [Chlamydomonas reinhardtii]
                  260897
Seq. No.
                  1900 1.R1011
Contig ID
                  ypc700798872.h1
5'-most EST
Method
                  BLASTX
                   g4210332
NCBI GI
BLAST score
                   1472
E value
                   1.0e-164
Match length
                   433
                   70
% identity
                  (AJ223803) 2-oxoglutarate dehydrogenase E2 subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   260898
Contig ID
                   1900 2.R1011
5'-most EST
                   uC-zmflb73046a04b1
Method
                   BLASTX
NCBI GI
                   q4455214
BLAST score
                   266
E value
                   5.0e-28
Match length
                   102
% identity
                   65
                   (AL035440) putative dihydrolipoamide succinyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   260899
Seq. No.
                   1900 3.R1011
Contig ID
5'-most EST
                   uC-zmflb73046g07b1
                   260900
Seq. No.
Contig ID
                   1901 1.R1011
                   xyt700343028.h1
5'-most EST
                   BLASTX
Method
```

g3236254



E value 7.0e-38 Match length 122 57 % identity (AC004684) unknown protein [Arabidopsis thaliana] NCBI Description 260901 Seq. No. Contig ID 1902 1.R1011 uC-zmroteosinte028d12b1 5'-most EST Method BLASTX NCBI GI q4567201 BLAST score 414 E value 1.0e-40 Match length 121 66 % identity (ACO07168) putative aspartate aminotransferase [Arabidopsis NCBI Description thaliana] 260902 Seq. No. 1902 2.R1011 Contig ID LIB3<u>1</u>54-004-Q1-K1-B4 5'-most EST Method BLASTX g4567201 NCBI GI BLAST score 413 2.0e-40 E value Match length 121 69 % identity (AC007168) putative aspartate aminotransferase [Arabidopsis NCBI Description thaliana] 260903 Seq. No. Contig ID 1908 1.R1011 5'-most EST uC-zmflmo17257e08b1 BLASTX Method NCBI GI q4490704 BLAST score 757 E value 2.0e-80 Match length 187 % identity 73 (AL035680) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 260904 1908 2.R1011 Contig ID LIB3069-049-Q1-K1-A1 5'-most EST Method BLASTX NCBI GI g4490704 BLAST score 1006 E value 1.0e-138 Match length 387 62

% identity

(AL035680) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 260905

1909 1.R1011 Contig ID cyk700048043.f15'-most EST

260906 Seq. No.

1909 2.R1011 Contig ID

BLAST score

E value

172

1.0e-11



```
5'-most EST
                  yyf700348849.h1
                  260907
Seq. No.
                  1911 1.R1011
Contig ID
                  LIB3069-033-Q1-K1-H3
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3420055
BLAST score
                  774
E value
                  2.0e-82
Match length
                  178
                  81
% identity
                  (AC004680) cyclophilin [Arabidopsis thaliana]
NCBI Description
                  260908
Seq. No.
                  1911 3.R1011
Contig ID
                  xsy700211127.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3420055
BLAST score
                  550
                   3.0e-56
E value
Match length
                  135
                   77
% identity
NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]
Seq. No.
                  260909
                  1911 4.R1011
Contig ID
                  LIB189-031-Q1-E1-F9
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3420055
                  595
BLAST score
E value
                   2.0e-61
Match length
                  138
% identity
                   81
NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]
                   260910
Seq. No.
Contig ID
                   1911 5.R1011
5'-most EST
                  LIB3069-054-Q1-K1-C9
Seq. No.
                   260911
Contig ID
                   1911 7.R1011
5'-most EST
                  uC-zmflmo17138d03b1
Method
                   BLASTX
NCBI GI
                   q3420055
BLAST score
                   169
                   1.0e-11
E value
                   99
Match length
% identity
NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]
Seq. No.
                   260912
Contig ID
                   1922 1.R1011
5'-most EST
                   wty700164276.h1
Method
                   BLASTX
NCBI GI
                   q4567310
```



Match length 87 % identity 46

NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]

Seq. No. 260913 Contig ID 1924 1.R1011

5'-most EST LIB3075-026-Q1-K1-G3

Seq. No. 260914 Contig ID 1924 2.R1

Contig ID 1924_2.R1011 5'-most EST kem700610957.h1

Method BLASTN
NCBI GI g3341647
BLAST score 95
E value 8.0e-46
Match length 103
% identity 98

NCBI Description Zea mays Ama gene encoding single-subunit RNA polymerase

Seq. No. 260915

Contig ID 1924 3.R1011

5'-most EST fC-zmf1700610957f1

Method BLASTX
NCBI GI g3121844
BLAST score 341
E value 2.0e-31
Match length 147
% identity 48

NCBI Description PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE

SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE)

(CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE

CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE)

>gi_1652668_dbj_BAA17588_ (D90907) phosphatidate

cytidylyltransferase [Synechocystis sp.]

Seq. No. 260916

Contig ID 1924_4.R1011 5'-most EST rv1700457250.h1

Method BLASTN NCBI GI g3341647 BLAST score 77

E value 5.0e-35 Match length 93 % identity 96

NCBI Description Zea mays Ama gene encoding single-subunit RNA polymerase

Seq. No. 260917

Contig ID 1924 5.R1011

5'-most EST LIB3062-038-Q1-K1-E8

Method BLASTX
NCBI GI g3121844
BLAST score 230
E value 9.0e-19
Match length 82
% identity 57

NCBI Description PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE

SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE)



(CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) >gi_1652668_dbj_BAA17588_ (D90907) phosphatidate cytidylyltransferase [Synechocystis sp.]

Seq. No. 260918 Contig ID 1932 1.R1011

5'-most EST LIB3137-015-Q1-K1-D3

Method BLASTX
NCBI GI g3142331
BLAST score 206
E value 1.0e-15
Match length 136
% identity 36

NCBI Description (U97327) calcyclin binding protein [Mus musculus]

Seq. No. 260919 Contig ID 1932 2.R1011

5'-most EST LIB3079-003-Q1-K1-D9

Seq. No. 260920

Contig ID 1935_1.R1011 5'-most EST ntr700076902.h1

Method BLASTX
NCBI GI g1895084
BLAST score 1838
E value 0.0e+00
Match length 336
% identity 99

NCBI Description (U89897) golgi associated protein se-wap41 [Zea mays]

Seq. No. 260921

Contig ID 1935_2.R1011

5'-most EST LIB3075-009-Q1-K1-G3

Method BLASTX
NCBI GI g1895084
BLAST score 722
E value 2.0e-76
Match length 129
% identity 100

NCBI Description (U89897) golgi associated protein se-wap41 [Zea mays]

Seq. No. 260922
Contig ID 1935 3.R1011

5'-most EST LIB3079-019-Q1-K1-A6

Method BLASTX
NCBI GI g1895084
BLAST score 577
E value 4.0e-59
Match length 249
% identity 95

NCBI Description (U89897) golgi associated protein se-wap41 [Zea mays]

 Seq. No.
 260923

 Contig ID
 1935_4.R1011

 5'-most EST
 wyr700243794.h1

Method BLASTX



```
NCBI GI
                  q1895084
BLAST score
                  453
                  6.0e-45
E value
                  112
Match length
                  98
% identity
NCBI Description
                 (U89897) golgi associated protein se-wap41 [Zea mays]
Seq. No.
                  260924
                  1954 1.R1011
Contig ID
5'-most EST
                  LIB3067-037-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  q4191616
BLAST score
                  779
                  1.0e-82
E value
                  494
Match length
                  39
% identity
NCBI Description (AF120334) GTP-binding protein NGB [Homo sapiens]
Seq. No.
                  260925
Contig ID
                  1954 2.R1011
                  LIB3070-007-Q1-N1-A6
5'-most EST
                  260926
Seq. No.
Contig ID
                  1962 1.R1011
                  wyr700237868.h1
5'-most EST
                  BLASTX
Method
                  g3482918
NCBI GI
BLAST score
                  1924
                  0.0e+00
E value
                  420
Match length
% identity
                  88
NCBI Description
                  (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
                  thaliana]
                  260927
Seq. No.
                  1962 2.R1011
Contig ID
5'-most EST
                  wyr700243094.h1
Method
                  BLASTX
NCBI GI
                  q3482918
BLAST score
                  1341
                  1.0e-148
E value
Match length
                  305
% identity
                  85
NCBI Description
                  (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
                  thaliana]
                  260928
Seq. No.
Contig ID
                  1962 3.R1011
5'-most EST
                  uC-zmflmo17267g04b1
Method
                  BLASTX
NCBI GI
                  g3482918
BLAST score
                  674
E value
                  9.0e-71
Match length
                  153
% identity
                  84
NCBI Description
                  (AC003970) Similar to ATP-citrate-lyase [Arabidopsis
```

36117

thalianal



260929 Seq. No. Contia ID 1962 4.R1011 hvj700618779.h1 5'-most EST Method BLASTX

g2497953 NCBI GI BLAST score 693 E value 1.0e-145 Match length 409 % identity 66

NCBI Description

MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi 1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] >gi_4469123 emb CAB38312 (AJ236870) molybdenum

cofactor biosynthesis enzyme [Arabidopsis thaliana]

Seq. No. 260930 1962 6.R1011 Contig ID 5'-most EST wyr700236916.hl

Method BLASTX NCBI GI g2462746 BLAST score 445 E value 4.0e-44Match length 93 % identity

(AC002292) Similar to ATP-citrate-lyase [Arabidopsis NCBI Description

thaliana]

Seq. No. 260931

Contig ID 1963 1.R1011

5'-most EST uC-zmroteosinte037e01b1

Method BLASTX NCBI GI g1709800 BLAST score 1559 E value 1.0e-174 Match length 388 79 % identity

26S PROTEASE REGULATORY SUBUNIT 8 (MSUG1 PROTEIN) NCBI Description (TAT-BINDING PROTEIN HOMOLOG 10) (TBP10) (P45/SUG)

>gi_2137798_pir__S61923 SUG1 protein - mouse
>gi_1165125_emb_CAA90961.1_ (Z54219) mSUG1 protein [Mus musculus] >gi 1262433 emb CAA61863 (X89718) 26S protease subunit [Sus scrofa] >gi 1395177 dbj BAA11938 (D83521)

proteasomal ATPase (rat SUG1) [Rattus norvegicus]

>gi_2564003_dbj_BAA22933_ (AB000491) proteasome p45/SUG [Rattus norvegicus] >gi_3193258 (AF069053) proteasome

-subunit SUG1 [Bos taurus]

260932 Seq. No. 1963 2.R1011 Contig ID

uC-zmroteosinte002d12b1 5'-most EST

Method BLASTX NCBI GI g464863 BLAST score 965 E value 1.0e-105 215

Match length % identity 87



26S PROTEASE REGULATORY SUBUNIT 8 (TAT-BINDING PROTEIN NCBI Description HOMOLOG 10) >gi_422297_pir__ JN0610 probable transcription factor DdTBP10 - slime mold (Dictyostelium discoideum) (fragment) >gi 290057 (L16579) HIV1 TAT-binding protein [Dictyostelium discoideum]

260933 Seq. No. Contig ID 1963 3.R1011

5'-most EST uC-zmflmo17277b01b1

Method BLASTX NCBI GI g3041724 BLAST score 164 E value 2.0e-23 Match length 114 57 % identity

26S PROTEASE REGULATORY SUBUNIT 8 (SUG1 HOMOLOG) (XSUG1) NCBI Description >gi 1877414 emb CAA57512 (X81986) XSUG1 [Xenopus laevis]

Seq. No. 260934

1963 6.R1011 Contig ID

5'-most EST uC-zmrob73054a11a1

260935 Seq. No.

1963 7.R1011 Contig ID 5'-most EST zla700379982.h1

Method BLASTN NCBI GI g2245466 BLAST score 46 9.0e-17 E value Match length 62

94 % identity

NCBI Description Drosophila melanogaster DUG mRNA, complete cds

260936 Seq. No.

1965 1.R1011 Contig ID $rv17\overline{0}0456451.h1$ 5'-most EST

BLASTX Method NCBI GI q4454049 BLAST score 541 2.0e-55 E value Match length 170 62 % identity

NCBI Description (AL035394) 98b like protein [Arabidopsis thaliana]

260937 Seq. No.

Contig ID 1966 1.R1011

LIB3075-025-Q1-K1-H11 5'-most EST

Method BLASTX NCBI GI q1723691 BLAST score 153 5.0e-10 E value Match length 91 % identity

NCBI Description HYPOTHETICAL 38.8 KD PROTEIN IN MIC1-SRB5 INTERGENIC REGION

> >gi 2132606 pir S64406 probable membrane protein YGR101w yeast (Saccharomyces cerevisiae) >qi 1323155 emb CAA97104

(Z72886) ORF YGR101w [Saccharomyces cerevisiae]

NCBI Description

260944

1979 2.R1011

cyk700049169.fl

Seq. No.

Contig ID

5'-most EST



```
260938
Seq. No.
Contig ID
                   1967 1.R1011
5'-most EST
                   LIB3075-018-Q1-K1-C8
Method
                   BLASTX
NCBI GI
                   q4220523
BLAST score
                   622
                   9.0e-65
E value
Match length
                   190
% identity
                   62
NCBI Description
                   (AL035356) putative alliin lyase [Arabidopsis thaliana]
                   260939
Seq. No.
Contig ID
                   1969 1.R1011
5'-most EST
                   LIB148-024-Q1-E1-E5
                   260940
Seq. No.
                   1971 1.R1011
Contig ID
5'-most EST
                   mwy7\overline{0}0442851.h1
Method
                   BLASTX
NCBI GI
                   g2245020
BLAST score
                   433
E value
                   8.0e-43
Match length
                   130
% identity
                   69
NCBI Description
                  (Z97341) growth regulator homolog [Arabidopsis thaliana]
                   260941
Seq. No.
                   1976 1.R1011
Contig ID
5'-most EST
                   LIB3075-026-Q1-K1-A10
Seq. No.
                   260942
Contig ID
                   1978 1.R1011
5'-most EST
                   LIB3075-026-Q1-K1-A2
Method
                   BLASTX
NCBI GI
                   q3355480
BLAST score
                   157
E value
                   2.0e-10
Match length
                   103
% identity
                   35
NCBI Description
                   (AC004218) Medicago nodulin N21-like protein [Arabidopsis
                   thaliana]
                   260943
Seq. No.
                   1979 1.R1011
Contig ID
5'-most EST
                   LIB3088-042-Q1-K1-D2
Method
                   BLASTX
NCBI GI
                   q4455366
BLAST score
                   501
E value
                   3.0e-50
Match length
                   186
                   56
% identity
```

36120

(AL035524) putative protein [Arabidopsis thaliana]

% identity

62



```
BLASTX
 Method
 NCBI GI
                   g1176203
 BLAST score
                   437
 E value
                   6.0e-43
Match length
                   197
                   45
 % identity
                   HYPOTHETICAL 43.1 KD PROTEIN IN RPLM-HHOA INTERGENIC REGION
 NCBI Description
                    (F375) >gi_606171 (U18997) ORF_f375 [Escherichia coli]
                   >qi 1789627 (AE000402) orf, hypothetical protein
                    [Escherichia coli]
                   260945
 Seq. No.
                   1981 1.R1011
 Contig ID
 5'-most EST
                   LIB3066-048-Q1-K1-F10
 Method
                   BLASTX
 NCBI GI
                   g3449041
 BLAST score
                   517
                    3.0e-52
 E value
 Match length
                    238
 % identity
                    41
                   (U73462) carbonic anhydrase [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    260946
 Contig ID
                    1981_2.R1011
-5'-most EST
                   LIB3075-012-Q1-K1-H1
 Method
                   BLASTX
 NCBI GI
                    q1364059
 BLAST score
                    404
 E value
                    4.0e-39
 Match length
                    189
 % identity
                    42
                   dioscorin class A precursor - Dioscorea cayenensis
 NCBI Description
                    >gi 433463 emb_CAA53781_ (X76187) storage protein
                    [Dioscorea cayenensis]
                    260947
 Seq. No.
                    1983 1.R1011
 Contig ID
                    uC-z\overline{m}flmo17287a04b1
 5'-most EST
                    BLASTN
 Method
 NCBI GI
                    g4140643
 BLAST score
                    54
                    3.0e-21
 E value
                    238
 Match length
                    90
 % identity
                    Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
 NCBI Description
                    complete sequence
                    260948
 Seq. No.
                    1985 1.R1011
 Contig ID
                    gct701179925.h1
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    q4309884
 BLAST score
                    322
 E value
                    2.0e-29
 Match length
                    93
```

36121

NCBI Description (AC006389) similar to Schizosaccharomyces pombe splicing

NCBI Description



factor; similar to PID:3395591 [Homo sapiens]

260949 Seq. No. 1986 1.R1011 Contig ID 5'-most EST LIB3150-049-Q1-N1-A8 260950 Seq. No. 1988 1.R1011 Contig ID wty700162772.h15'-most EST BLASTX Method NCBI GI g4468792 BLAST score 1076 1.0e-117 E value 211 Match length 100 % identity NCBI Description (AJ010295) Glutathione transferase III(a) [Zea mays] 260951 Seq. No. 1988 5.R1011 Contig ID xsy700217856.h1 5'-most EST BLASTX Method g66616 NCBI GI 482 BLAST score 9.0e-49 E value 98 Match length 98 % identity NCBI Description glutathione transferase (EC 2.5.1.18) III (version 1) maize >gi_22280_emb_CAA28053_ (X04455) GSTIII (aa 1-220) [Zea mays] >gi 22319 emb CAA27957_ (X04375) GSTIII (aa 1-220) [Zea mays] Seq. No. 260952 1993_1.R1011 Contig ID uC-zmflb73137g11b1 5'-most EST 260953 Seq. No. 2001_1.R1011 Contig ID hbs701183305.h1 5'-most EST BLASTX Method NCBI GI q132717 BLAST score 253 E value 2.0e-21 Match length 110 49 % identity 50S RIBOSOMAL PROTEIN L17 (BL21) >gi 71253_pir__R5BS17 NCBI Description ribosomal protein L17 - Bacillus stearothermophilus Seq. No. 260954 Contig ID 2004 1.R1011 5'-most EST LIB3136-023-Q1-K1-H4 Method BLASTX NCBI GI g3721926 BLAST score 461 E value 5.0e-46 133 Match length % identity 69

(AB017480) chloroplast FtsH protease [Nicotiana tabacum]

NCBI Description



```
260955
Seq. No.
                   2004 3.R1011
Contig ID
5'-most EST
                   LIB3066-050-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   q3128469
BLAST score
                   168
                   3.0e-25
E value
                   130
Match length
                   54
% identity
                  (AF061748) cell division protein FtsH [Streptococcus
NCBI Description
                   pneumoniae]
                   260956
Seq. No.
                   2006 1.R1011
Contig ID
                   ntr700073181.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q286124
BLAST score
                   1927
                   0.0e+00
E value
Match length
                   356
                   100
% identity
                  (D14577) glutamine synthetase [Zea mays]
NCBI Description
                   260957
Seq. No.
                   2006_2.R1011
Contig ID
                   wyr700243490.hl
5'-most EST
Method
                   BLASTX
                   q699623
NCBI GI
                   1677
BLAST score
E value
                   0.0e + 00
Match length
                   356
                   93
% identity
NCBI Description
                  (D14579) glutamine synthetase [Zea mays]
Seq. No.
                   260958
Contig ID
                   2006 3.R1011
5'-most EST
                   uC-zmflb73067e10b1
Method
                   BLASTX
NCBI GI
                   q286122
BLAST score
                   1917
E value
                   0.0e + 00
Match length
                   356
% identity
                   100
                  (D14576) glutamine synthetase [Zea mays]
NCBI Description
Seq. No.
                   260959
                   2006 4.R1011
Contig ID
                   uC-zmflmo17285b12b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q585202
BLAST score
                   1741
E value
                   0.0e+00
                   355
Match length
                   93
% identity
```

GLUTAMINE SYNTHETASE ROOT ISOZYME 2 (GLUTAMATE--AMMONIA

LIGASE) >gi_481807_pir__S39478 glutamate--ammonia ligase



(EC 6.3.1.2) 1-2, cytosolic - maize >gi_434326_emb_CAA46720_ (X65927) glutamine synthetase [Zea mays]

NCBI GI g4314387
BLAST score 971
E value 1.0e-105
Match length 218
% identity 82

NCBI Description (AC006232) putative beta-alanine synthetase [Arabidopsis

thaliana]

Seq. No. 260961

 Contig ID
 2006 6.R1011

 5'-most EST
 uwc700152411

 Method
 BLASTX

 NCBI GI
 g1934758

 BLAST score
 365

 E value
 6.0e-35

Match length 97 % identity 72

NCBI Description (Y12460) cytosolic glutamine synthetase [Brassica napus]

Seq. No. 260962

Contig ID 2006_8.R1011

5'-most EST LIB143-021-Q1-E1-D3

Method BLASTX
NCBI GI g1169926
BLAST score 585
E value 5.0e-63
Match length 145
% identity 88

NCBI Description GLUTAMINE SYNTHETASE ROOT ISOZYME 5 (GLUTAMATE--AMMONIA

LIGASE) (GS117)

Seq. No. 260963

Contig ID 2006_11.R1011 5'-most EST uC-zmflb73107g10a2

Method BLASTX
NCBI GI g2118353
BLAST score 213
E value 3.0e-17
Match length 43
% identity 93

NCBI Description glutamate--ammonia ligase (EC 6.3.1.2) 1-5, cytosolic -

maize (fragment) >gi_1360700_emb_CAA46723_ (X65930)

glutamine synthetase [Zea mays]

Seq. No. 260964

Contig ID 2006_12.R1011 5'-most EST uC-zmflmo17393h09a1

Method BLASTN NCBI GI g286123



BLAST score 262 E value 1.0e-145 Match length 297 % identity 96

NCBI Description Maize mRNA for glutamine synthetase, complete cds

Seq. No. 260965

Contig ID 2006_15.R1011 5'-most EST wuj700282046.h1

Method BLASTX
NCBI GI g4314387
BLAST score 568
E value 1.0e-58
Match length 128
% identity 81

NCBI Description (AC006232) putative beta-alanine synthetase [Arabidopsis

thaliana]

Seq. No. 260966

Contig ID 2006_18.R1011 5'-most EST uC-zmflb73296f08a1

Method BLASTN
NCBI GI 9434325
BLAST score 133
E value 9.0e-69
Match length 133
% identity 100

NCBI Description Z.mays mRNA qs1-2 for glutamine synthetase

Seq. No. 260967

Contig ID 2008_1.R1011

5'-most EST LIB3078-033-Q1-K1-D5

Method BLASTX
NCBI GI g3033396
BLAST score 290
E value 1.0e-25
Match length 102
% identity 50

NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]

Seq. No. 260968

Contig ID 2009 1.R1011

5'-most EST uC-zmflb73017h06b1

Method BLASTX
NCBI GI g3063694
BLAST score 304
E value 5.0e-27
Match length 357
% identity 35

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 260969

Contig ID 2009 2.R1011

5'-most EST uC-zmflb73274d02b1

Method BLASTX NCBI GI g3063694 BLAST score 219



E value 3.0e-34
Match length 361
% identity 40

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 260970

Contig ID 2014_1.R1011 5'-most EST uC-zmflm017092h12b1

5'-most EST uC-zmflm0170'
Method BLASTX
NCBI GI g4415912
BLAST score 280
E value 1.0e-24

E value 1.0e Match length 234 % identity 32

NCBI Description (AC006282) putative protease [Arabidopsis thaliana]

Seq. No. 260971

Contig ID 2019_1.R1011

5'-most EST LIB3075-025-Q1-K1-C9

Seq. No. 260972

Contig ID 2021_1.R1011 5'-most EST gwl700613140.h1

Method BLASTX
NCBI GI g4567250
BLAST score 379
E value 7.0e-36
Match length 164
% identity 60

NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]

Seq. No. 260973

Contig ID 2022 1.R1011

5'-most EST uC-zmflb73084e04b2

Method BLASTX
NCBI GI g4240299
BLAST score 555
E value 4.0e-56
Match length 645
% identity 31

NCBI Description (AB020712) KIAA0905 protein [Homo sapiens]

Seq. No. 260974 Contig ID 2022 3.R1011

5'-most EST uC-zmflb73339g10a1

Seq. No. 260975

Contig ID 2022 4.R1011

5'-most EST uC-zmflmo17339e10b1

Seq. No. 260976

Contig ID 2026_1.R1011

5'-most EST uC-zmflb73014e07b1

Method BLASTX
NCBI GI g1335862
BLAST score 786
E value 4.0e-84



```
Match length
                    162
                    92
 % identity
 NCBI Description (U42608) clathrin heavy chain [Glycine max]
                    260977
 Seq. No.
                    2026 2.R1011
 Contig ID
                    uC-zmflmo170112a02b1
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    q3600033
                    2204
 BLAST score
 E value
                    0.0e+00
 Match length
                    718
                    62
 % identity
                    (AF080119) contains similarity to the N terminal domain of
 NCBI Description
                    the E1 protein (Pfam: E1 N.hmm, score: 12.36) [Arabidopsis
                    thaliana]
                    260978
 Seq. No.
                    2026_5.R1011
 Contig ID
 5'-most EST
                    LIB3079-053-Q1-K1-B1
                    BLASTN
 Method
                    q3452291
 NCBI GI
 BLAST score
                    78
 E value
                    1.0e-35
                    116
 Match length
  % identity
                    93
 NCBI Description Zea mays retrotransposon Huck-2 3' LTR, partial sequence
                    260979
  Seq. No.
                    2030 1.R1011
  Contig ID
                    LIB84-004-Q1-E1-H2
  5'-most EST
                    BLASTX
 Method
  NCBI GI
                    g2062175
  BLAST score
                    540
  E value
                    1.0e-54
  Match length
                    381
                     38
% identity
  NCBI Description (AC001645) hypothetical protein [Arabidopsis thaliana]
                     260980
  Seq. No.
                     2030 2.R1011
  Contig ID
                    LIB3060-017-Q1-K1-G3
  5'-most EST
                     260981
  Seq. No.
                     2031 1.R1011
  Contig ID
                    nbm7\overline{0}0467980.h1
  5'-most EST
                    BLASTX
  Method
                     g1842111
  NCBI GI
  BLAST score
                     550
  E value
                     3.0e-56
                    156
  Match length
  % identity
                     67
```

Seq. No. 260982 Contig ID 2034_1.R1011

NCBI Description

36127

decoy [Arabidopsis thaliana]

(U87586) decoy [Arabidopsis thaliana] >gi_1931612 (U93308)



```
5'-most EST
                  LIB143-058-Q1-E1-A11
Method
                  BLASTX
                  g3334138
NCBI GI
BLAST score
                  1719
                  0.0e + 00
E value
                  442
Match length
                  71
% identity
                  CALNEXIN HOMOLOG PRECURSOR >gi 669003 (U20502) calnexin
NCBI Description
                   [Glycine max]
                  260983
Seq. No.
                  2034 2.R1011
Contig ID
                  ypc700802423.h1
5'-most EST
                  260984
Seq. No.
                  2034 3.R1011
Contig ID
                  uC-zmflb73287h06b1
5'-most EST
                  260985
Seq. No.
Contig ID
                  2034 5.R1011
                  qmh700028122.f1
5'-most EST
                  260986
Seq. No.
                  2034_6.R1011
Contig ID
                  LIB3115-034-P1-K2-H2
5'-most EST
                  BLASTN
Method
                  g1181330
NCBI GI
                  159
BLAST score
                   6.0e-84
E value
                   382
Match length
% identity
                   88
NCBI Description Z.mays CNX mRNA
                   260987
Seq. No.
Contig ID
                   2034 8.R1011
                   rvt700550964.h1
5'-most EST
                   BLASTN
Method
                   g1181330
NCBI GI
BLAST score
                   424
                   0.0e + 00
E value
Match length
                   571
                   94
% identity
NCBI Description Z.mays CNX mRNA
Seq. No.
                   260988
Contig ID
                   2034 10.R1011
                   xjt7\overline{0}0092767.h1
5'-most EST
                   BLASTX
Method
                   g3334138
NCBI GI
                   287
BLAST score
E value
                   6.0e-26
                   69
Match length
```

74 % identity

NCBI Description CALNEXIN HOMOLOG PRECURSOR >gi 669003 (U20502) calnexin

[Glycine max]

Seq. No. 260989



Contig ID 2034_11.R1011

5'-most EST LIB3151-019-Q1-K1-B7

Method BLASTN
NCBI GI g1181330
BLAST score 58
E value 7.0e-24
Match length 178
% identity 90

NCBI Description Z.mays CNX mRNA

Seq. No. 260990

Contig ID 2040_1.R1011 5'-most EST xmt700258681.h1

Method BLASTX
NCBI GI g3478700
BLAST score 1020
E value 1.0e-111
Match length 332
% identity 62

NCBI Description (AF034387) AFT protein [Arabidopsis thaliana]

Seq. No. 260991

Contig ID 2041 1.R1011

5'-most EST LIB3279-004-P1-K1-A1

Method BLASTX
NCBI GI g401238
BLAST score 805
E value 3.0e-86
Match length 200
% identity 73

NCBI Description UBIQUITIN-ACTIVATING ENZYME E1 3 >gi_170686 (M90664)

ubiquitin activating enzyme [Triticum aestivum]

Seq. No. 260992

Contig ID 2046_1.R1011 5'-most EST vux700156873.h1

Method BLASTX
NCBI GI g3025299
BLAST score 606
E value 9.0e-63
Match length 177
% identity 68

NCBI Description HYPOTHETICAL 62.3 KD PROTEIN T29M21.25 >gi_2088660

(AF002109) ABC1 isolog [Arabidopsis thaliana]

Seq. No. 260993

Contig ID 2047_1.R1011

5'-most EST LIB3070-008-Q1-N1-B8

Seq. No. 260994

Contig ID 2047 2.R1011

5'-most EST LIB3067-045-Q1-K1-G1

Seq. No. 260995

Contig ID 2052 1.R1011

5'-most EST LIB3075-020-Q1-K1-D3

Method BLASTX



NCBI GI g1172557
BLAST score 553
E value 9.0e-57
Match length 123
% identity 87
NCBI Description OUTER PL

NCBI Description OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT

ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
>gi_422030_pir__ S34146 porin por1 - maize
>gi_626044_pir__ A55017 porin, plastid - maize
>gi_313136_emb_CAA51828_ (X73429) porin [Zea mays]

Seq. No. 260996 Contig ID 2053 1.R1011

5'-most EST LIB3061-039-Q1-K1-A5

Method BLASTX
NCBI GI g3551425
BLAST score 198
E value 9.0e-15
Match length 180
% identity 33

NCBI Description (AB015291) pyrrolidone carboxyl peptidase [Pyrococcus

furiosus]

Seq. No. 260997

Contig ID 2053_2.R1011

5'-most EST uC-zmroteosinte035h06b2

 Seq. No.
 260998

 Contig ID
 2054_1.R1011

 5'-most EST
 LIB36-001-Q1-E1-C5

Method BLASTX
NCBI GI g1168782
BLAST score 316
E value 1.0e-28
Match length 165
% identity 45

NCBI Description CALCIUM-BINDING PROTEIN CAST >gi_169481 (L02830)

calcium-binding protein [Solanum tuberosum]

Seq. No. 260999

Contig ID 2054_2.R1011 5'-most EST LIB148-012-Q1-E1-E1

Method BLASTX
NCBI GI g1168782
BLAST score 333
E value 1.0e-30
Match length 173
% identity 45

NCBI Description CALCIUM-BINDING PROTEIN CAST >gi_169481 (L02830)

calcium-binding protein [Solanum tuberosum]

Seq. No. 261000

Contig ID 2054_3.R1011

5'-most EST LIB148-066-Q2-E1-D8

Method BLASTX
NCBI GI g1168782
BLAST score 204



1.0e-15 E value 68 Match length % identity 62 CALCIUM-BINDING PROTEIN CAST >gi 169481 (L02830) NCBI Description calcium-binding protein [Solanum tuberosum] 261001 Seq. No. Contig ID 2054 4.R1011 5'-most EST uC-zmflb73411c04a1 261002 Seq. No.

Contig ID 2054_5.R1011 5'-most EST dyk700102376.h1 Seq. No. 261003

Contig ID 2054_6.R1011
5'-most EST LIB148-046-Q1-E1-D6
Method BLASTX
NCBI GI g1168696
BLAST score 142
E value 9.0e-09

Match length 68 % identity 44

NCBI Description ALLERGEN BET V 3 (BET V III) >gi 629480_pir__S45011

allergen Bet v III - European white birch

>gi_1076247_pir__S46233 allergen - European white birch
>gi_488605_emb_CAA55854_ (X79267) allergen [Betula pendula]

Seq. No. 261004 Contig ID 2060 1.R1011

5'-most EST uC-zmflmo17012c04b1

Method BLASTX
NCBI GI 94512673
BLAST score 2089
E value 0.0e+00
Match length 477
% identity 83

NCBI Description (AC006931) putative phosphoprotein phosphatase [Arabidopsis

thaliana]

Seq. No. 261005

Contig ID 2060 2.R1011

5'-most EST LIB3078-024-Q1-K1-D7

Seq. No. 261006 Contig ID 2060 4.R1011

5'-most EST xmt700263392.h1

Method BLASTX
NCBI GI g4512673
BLAST score 245
E value 5.0e-21
Match length 58
% identity 79

NCBI Description (AC006931) putative phosphoprotein phosphatase [Arabidopsis

thaliana]

Seq. No. 261007

36131



```
2062 1.R1011
Contig ID
                  cat700018705.rl
5'-most EST
                  261008
Seq. No.
Contig ID
                  2065 1.R1011
                  LIB83-015-Q1-E1-A9
5'-most EST
Method
                  BLASTX
                  q3355474
NCBI GI
BLAST score
                  826
E value
                   2.0e-88
Match length
                   241
% identity
                   65
                  (AC004218) unknown protein [Arabidopsis thaliana]
NCBI Description
                   261009
Seq. No.
Contig ID
                   2066 1.R1011
                  LIB3075-024-Q1-K1-A9
5'-most EST
Seq. No.
                   261010
Contig ID
                   2071 1.R1011
                  LIB148-047-Q1-E1-C3
5'-most EST
                   BLASTN
Method
                   g3821780
NCBI GI
BLAST score
                   36
                   3.0e-10
E value
Match length
                   48
                   67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   261011
Seq. No.
Contig ID
                   2072 1.R1011
5'-most EST
                   LIB3075-022-Q1-K1-D9
Method
                   BLASTX
NCBI GI
                   q4567205
BLAST score
                   864
E value
                   7.0e-93
Match length
                   241
                   70
% identity
                  (AC007168) putative trehalose-6-phosphate phosphatase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   261012
Contig ID
                   2081 1.R1011
                   LIB3150-038-Q1-N1-E8
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2653285
BLAST score
                   1390
                   1.0e-154
E value
Match length
                   355
                   81
% identity
NCBI Description (AJ003025) enoyl-ACP reductase [Oryza sativa]
                   261013
Seq. No.
                   2081 2.R1011
Contig ID
```

Seq. No. 261014

5'-most EST

uC-zmflmo17270b03b1



```
2081 3.R1011
Contig ID
                  uC-zmflb73080e03b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3065835
BLAST score
                  611
E value
                  3.0e-63
Match length
                  195
                   64
% identity
NCBI Description
                   (AF058800) putative methyltransferase [Arabidopsis
                  thaliana]
                  261015
Seq. No.
Contig ID
                  2081 4.R1011
5'-most EST
                  uwc700153646.hl
                  BLASTX
Method
NCBI GI
                  q2653285
BLAST score
                  502
                  1.0e-50
E value
Match length
                  159
                   65
% identity
NCBI Description
                  (AJ003025) enoyl-ACP reductase [Oryza sativa]
                  261016
Seq. No.
                  2081 7.R1011
Contig ID
5'-most EST
                   fdz701161031.h1
                  BLASTX
Method
                  g3065835
NCBI GI
BLAST score
                  172
E value
                  1.0e-12
Match length
                   49
                   76
% identity
                  (AF058800) putative methyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                   261017
Seq. No.
Contig ID
                   2082 1.R1011
5'-most EST
                  hvj700620026.hl
Method
                   BLASTX
NCBI GI
                   q4567282
BLAST score
                   702
E value
                   5.0e-74
Match length
                   250
                   58
% identity
NCBI Description
                  (AC006841) putative DNAJ protein [Arabidopsis thaliana]
                   261018
Seq. No.
Contig ID
                   2085 1.R1011
5'-most EST
                   uC-zmflmo17h01b1
Method
                   BLASTX
NCBI GI
                   q320608
BLAST score
                   1196
E value
                   1.0e-132
                   247
Match length
% identity
                   51
                  ubiquitin precursor - wild oat >gi 15989 emb CAA49200
NCBI Description
```

36133

polyubiquitin [Saccharum sp.]

(X69422) tetraubiquitin [Avena fatua] >gi 777758 (L41658)



```
261019
Seq. No.
                   2085 2.R1011
Contig ID
5'-most EST
                   act701179542.hl
Method
                   BLASTX
NCBI GI
                   g2982465
BLAST score
                   308
E value
                   1.0e-27
                   190
Match length
                   39
% identity
                  (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
                   261020
Seq. No.
                   2085 3.R1011
Contig ID
                   uC-z\overline{m}flmo170113f10b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q100490
BLAST score
                   613
E value
                   9.0e-64
                   136
Match length
% identity
                   26
                   polyubiquitin - garden snapdragon (fragment)
NCBI Description
                   >gi 16071 emb_CAA48140_ (X67957) ubiquitin [Antirrhinum
                   majus]
                   261021
Seq. No.
Contig ID
                   2087 1.R1011
5'-most EST
                   LIB143-066-Q1-E1-C5
                   261022
Seq. No.
                   2091 1.R1011
Contig ID
                   LIB3076-034-Q1-K1-B3
5'-most EST
                   261023
Seq. No.
                   2091 2.R1011
Contig ID
5'-most EST
                   LIB3060-020-Q1-K1-E9
                   261024
Seq. No.
                   2093 1.R1011
Contiq ID
                   wen7\overline{0}0332212.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3881836
BLAST score
                   1101
E value
                   1.0e-120
Match length
                   283
                   73
% identity
                   (Z78019) Similarity to Yeast LPG22P protein (TR:G1151240);
NCBI Description
                   cDNA EST EMBL: T00686 comes from this gene; cDNA EST
                   EMBL:C12415 comes from this gene; cDNA EST EMBL:C12728
                   comes from this gene; cDNA EST EMBL:C10626 comes from this
                   261025
```

Seq. No. 261025 Contig ID 2093_2.R1011 5'-most EST LIB3088-007-Q1-K1-D2

Method BLASTX NCBI GI g3881836



BLAST score 2.0e-29 E value 84 Match length 74 % identity (Z78019) Similarity to Yeast LPG22P protein (TR:G1151240); NCBI Description cDNA EST EMBL: T00686 comes from this gene; cDNA EST EMBL:C12415 comes from this gene; cDNA EST EMBL:C12728 comes from this gene; cDNA EST EMBL:C10626 comes from this ge 261026 Seq. No. 2094 1.R1011 Contig ID LIB3179-023-P1-K1-A2 5'-most EST BLASTX Method NCBI GI a4510387 400 BLAST score 9.0e-39 E value 126 Match length 63 % identity (AC007017) unknown protein [Arabidopsis thaliana] NCBI Description 261027 Seq. No. 2096 1.R1011 Contig ID LIB3075-023-Q1-K1-B3 5'-most EST BLASTX Method g3850587 NCBI GI BLAST score 833 8.0e-92 E value 259 Match length 70 % identity (AC005278) Strong similarity to gi_2244780 hypothetical NCBI Description protein from Arabidopsis thaliana chromosome 4 contig gb_Z97335. [Arabidopsis thaliana] 261028 Seq. No. Contig ID 2097 1.R1011 LIB3075-023-Q1-K1-B4 5'-most EST BLASTX Method NCBI GI q1946366 BLAST score 408 1.0e-39 E value Match length 130 % identity (U93215) unknown protein [Arabidopsis thaliana] NCBI Description 261029 Seq. No. Contig ID 2100 1.R1011 LIB3060-024-Q1-K1-H5 5'-most EST Method BLASTX q1550814 NCBI GI 1358 BLAST score

E value 1.0e-150 319 Match length

87

(Y07959) 60S acidic ribosomal protein P0 [Zea mays] NCBI Description

261030 Seq. No.

% identity



```
2100 2.R1011
Contig ID
5'-most EST
                  LIB3158-005-Q1-K1-C10
                  BLASTX
Method
                   q1550814
NCBI GI
BLAST score
                   490
                   2.0e-49
E value
                   97
Match length
                   100
% identity
                  (Y07959) 60S acidic ribosomal protein P0 [Zea mays]
NCBI Description
                   261031
Seq. No.
                   2100 3.R1011
Contig ID
                   LIB3158-016-Q1-K1-H6
5'-most EST
                   BLASTX
Method
                   g1550814
NCBI GI
                   206
BLAST score
                   5.0e-16
E value
Match length
                   76
                   57
% identity
                  (Y07959) 60S acidic ribosomal protein P0 [Zea mays]
NCBI Description
                   261032
Seq. No.
                   2100 4.R1011
Contig ID
                   wty700163303.h1
5'-most EST
                   BLASTN
Method
                   g1550813
NCBI GI
BLAST score
                   266
                   1.0e-148
E value
                   333
Match length
                   95
% identity
NCBI Description Z.mays mRNA for acidic ribosomal protein PO
                   261033
Seq. No.
                   2102 1.R1011
Contig ID
                   yyf700348487.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3388157
BLAST score
                   240
                   2.0e-33
E value
                   170
Match length
                   49
% identity
                   (AF079556) poly(ADP-ribose) glycohydrolase [Drosophila
NCBI Description
                   melanogaster]
                   261034
Seq. No.
                   2104 1.R1011
Contig ID
5'-most EST
                   LIB3075-023-Q1-K1-C3
Method
                   BLASTX
NCBI GI
                   q3738338
BLAST score
                   462
                   5.0e-46
E value
Match length
                   155
% identity
                   55
                   (AC005170) putative polygalacturonase [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No. 261035

BLAST score

Match length

E value

2088

0.0e+00 599



```
2106 1.R1011
Contig ID
                  LIB3279-016-P1-K1-B9
5'-most EST
Method
                  BLASTX
                  g2190550
NCBI GI
BLAST score
                  1121
                  1.0e-123
E value
Match length
                  321
                  68
% identity
                  (AC001229) ESTs gb_T45673,gb_N37512 come from this gene.
NCBI Description
                  [Arabidopsis thaliana]
                  261036
Seq. No.
Contig ID
                  2106 2.R1011
5'-most EST
                  uC-zmflb73275g10b1
Method
                  BLASTX
                  g2190550
NCBI GI
BLAST score
                  496
                  4.0e-50
E value
                  120
Match length
                  80
% identity
                  (AC001229) ESTs gb_T45673, gb_N37512 come from this gene.
NCBI Description
                  [Arabidopsis thaliana]
                  261037
Seq. No.
Contig ID
                  2108 1.R1011
5'-most EST
                  uC-zmflmo17113d08b1
Method
                  BLASTX
                  g3169719
NCBI GI
BLAST score
                  727
E value
                  1.0e-76
Match length
                  356
% identity
                  49
NCBI Description (AF007109) similar to yeast dcpl [Arabidopsis thaliana]
                  261038
Seq. No.
Contig ID
                  2108 2.R1011
5'-most EST
                  uC-zmflmo17270g06b1
Method
                  BLASTX
NCBI GI
                  q3169719
BLAST score
                  312
E value
                   3.0e-28
Match length
                  217
% identity
                   40
NCBI Description (AF007109) similar to yeast dcpl [Arabidopsis thaliana]
Seq. No.
                   261039
Contig ID
                   2108 3.R1011
                  LIB189-028-Q1-E1-H11
5'-most EST
Seq. No.
                   261040
                   2109 1.R1011
Contig ID
5'-most EST
                  LIB3136-005-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  g4115377
```



% identity 72

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 261041

Contig ID 2109 2.R1011

5'-most EST uC-zmflb73162a12b2

Method BLASTX
NCBI GI g4115377
BLAST score 241
E value 1.0e-32
Match length 99
% identity 75

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 261042

Contig ID 2109 3.R1011

5'-most EST uC-zmrob73002b10b1

Method BLASTX
NCBI GI g1665777
BLAST score 207
E value 2.0e-16
Match length 58

% identity 64

NCBI Description (D87444) Similar to S.cerevisiae EMP70 protein precursor

(S25110) [Homo sapiens]

Seq. No. 261043

Contig ID 2109_5.R1011 5'-most EST ymt700222821.h1

Method BLASTX
NCBI GI g4115377
BLAST score 363
E value 7.0e-35
Match length 98
% identity 66

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 261044

Contig ID 2115_1.R1011

5'-most EST uC-zmflb73280a08b2

Seq. No. 261045

Contig ID 2117 1.R1011

5'-most EST LIB3150-045-Q1-N1-E6

Method BLASTX
NCBI GI g1172553
BLAST score 1136
E value 1.0e-124
Match length 276
% identity 80

NCBI Description OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN

(VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) >gi_456672_emb_CAA54788_ (X77733) voltage dependent anion

channel (VDAC) [Triticum aestivum]

Seq. No. 261046

Contig ID 2117 2.R1011



```
uC-zmflm017214c04b1
5'-most EST
                  261047
Seq. No.
Contig ID
                  2117 6.R1011
5'-most EST
                  LIB3059-030-Q1-K1-G8
                  261048
Seq. No.
                  2118 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73192d08b1
                  261049
Seq. No.
                  2118 2.R1011
Contig ID
                  LIB3150-108-P1-N1-A1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2239236
                  295
BLAST score
                  3.0e-26
E value
                  126
Match length
                  50
% identity
NCBI Description
                  (Z97211) probable involvement in ergosterol synthesis
                   [Schizosaccharomyces pombe]
Seq. No.
                   261050
Contig ID
                  2118 3.R1011
5'-most EST
                  LIB3180-022-P2-M1-C6
                   261051
Seq. No.
                   2118 4.R1011
Contig ID
5'-most EST
                  LIB3068-057-Q1-K1-G10
Seq. No.
                   261052
                   2118 5.R1011
Contig ID
5'-most EST
                   uC-zmflMo17086e12b1
Method
                   BLASTX
NCBI GI
                   q4455338
BLAST score
                   338
                   6.0e-31
E value
Match length
                   120
% identity
                   54
NCBI Description (AL035525) putative protein [Arabidopsis thaliana]
Seq. No.
                   261053
                   2118 6.R1011
Contig ID
                   LIB3088-007-Q1-K1-C5
5'-most EST
Method
                   BLASTN
NCBI GI
                   g3821794
                   36
BLAST score
                   9.0e-11
E value
                   127
Match length
                   83
% identity
NCBI Description Zea mays gene encoding protein kinase CK2 alpha subunit
                   261054
Seq. No.
                 - 2118 7.R1011
Contig ID
```

Seq. No. 261055

5'-most EST

uC-zmflmo17344c07a1

Method

BLASTN



```
2120 1.R1011
  Contig ID
                     LIB3137-028-Q1-K1-E3
5'-most EST
                     BLASTX
  Method
                     g1495251
  NCBI GI
                     741
  BLAST score
                     3.0e-78
  E value
                     366
  Match length
                     48
  % identity
                     (270314) heat-shock protein [Arabidopsis thaliana]
  NCBI Description
                     261056
  Seq. No.
                     2125 1.R1011
  Contig ID
                     fdz701161531.h1
  5'-most EST
                     261057
  Seq. No.
                     2127 1.R1011
  Contig ID
                     tzu700201871.h1
  5'-most EST
                     BLASTX
  Method
                     g3492806
  NCBI GI
                     371
  BLAST score
                     3.0e - 35
  E value
                     126
  Match length
                     67
  % identity
                     (AJ225045) adventitious rooting related oxygenase [Malus
  NCBI Description
                     domestica]
                     261058
   Seq. No.
                     2129_1.R1011
   Contig ID
                     LIB3069-003-Q1-K1-E2
   5'-most EST
                     BLASTX
  Method
                     q4220521
  NCBI GI
  BLAST score
                     825
                     7.0e-88
   E value
                     440
   Match length
                     42
   % identity
                     (AL035356) putative protein [Arabidopsis thaliana]
   NCBI Description
   Seq. No.
                     261059
                     2129 3.R1011
   Contig ID
                     uC-zmflb73297a08a1
   5'-most EST
                      261060
   Seq. No.
                      2129 4.R1011
   Contig ID
                     LIB3067-058-Q1-K1-D8
   5'-most EST
   Method
                      BLASTN
                      q4140643
   NCBI GI
   BLAST score
                      196
   E value
                      1.0e-106
   Match length
                      362
   % identity
                     Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
   NCBI Description
                      complete sequence
   Seq. No.
                      261061
                      2129 6.R1011
   Contig ID
                      gct701175284.h1
   5'-most EST
```



q4140643 NCBI GI 162 BLAST score 9.0e-86 E value 321 Match length 92 % identity Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, NCBI Description complete sequence Seq. No. 261062 2129 7.R1011 Contig ID 5'-most EST LIB3136-014-Q1-K1-D7 261063 Seq. No. 2129 9.R1011 Contig ID LIB3069-030-Q1-K1-H11 5'-most EST

BLASTN Method q4140643 NCBI GI 142 BLAST score 6.0e-74E value 316 Match length 93 % identity

NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

261064 Seq. No. 2129 11.R1011 Contig ID 5'-most EST LIB84-029-Q1-E1-E4

261065 Seq. No. 2129 15.R1011 Contig ID nbm700477164.h1 5'-most EST

BLASTX Method q4220521 NCBI GI 177 BLAST score 4.0e-13 E value Match length 75

% identity

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

261066 Seq. No. 2129 18.R1011 Contig ID

uer700581830.h1 5'-most EST

BLASTN Method g4140643 NCBI GI 105 BLAST score 7.0e-52E value Match length 242 90 % identity

Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, NCBI Description

complete sequence

261067 Seq. No.

2129 21.R1011 Contig ID hvj700621335.hl 5'-most EST

BLASTN Method g4140643 NCBI GI 59 BLAST score



1.0e-24 E value 74 Match length 96 % identity Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, NCBI Description complete sequence 261068 Seq. No. 2129 22.R1011 Contig ID 5'-most EST vux700159637.h2 BLASTN Method g4140643 NCBI GI 73 BLAST score E value 7.0e-33 199 Match length 89 % identity Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, NCBI Description complete sequence 261069 Seq. No. 2129 23.R1011 Contig ID $wen7\overline{0}0334411.h1$ 5'-most EST BLASTN Method q4140643 NCBI GI 97 BLAST score 6.0e-47E value Match length 261 % identity 95 Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, NCBI Description complete sequence 261070 Seq. No. 2130 1.R1011 Contig ID $yyf7\overline{0}0352143.h1$ 5'-most EST Method BLASTX g4510342 NCBI GI BLAST score 1504 E value 1.0e-167 451 Match length 66 % identity (AC006921) putative serine/threonine protein kinase NCBI Description [Arabidopsis thaliana] Seq. No. 261071 2130 2.R1011 Contig ID 5'-most EST uC-zmflb73270b11a1 Seq. No. 261072 Contig ID 2133 1.R1011 LIB3075-022-Q1-K1-G12 5'-most EST

 Seq. No.
 261073

 Contig ID
 2134 1.R1011

 5'-most EST
 tzu700201992.h1

 Method
 BLASTX

 NCBI GI
 g3367576

BLAST score 186 E value 4.0e-13



Match length 261 % identity 27

NCBI Description (ALO31135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No. 261074

Contig ID 2136_1.R1011

5'-most EST uC-zmflmo17186e02b1

Method BLASTX
NCBI GI g3033398
BLAST score 831
E value 5.0e-89
Match length 204
% identity 76

NCBI Description (AC004238) putative phosphoribosylaminoimidazolecarboxamide

formyltransferase [Arabidopsis thaliana]

Seq. No. 261075

Contig ID 2136 2.R1011

5'-most EST LIB83-001-Q1-E1-F6

Method BLASTX
NCBI GI g3033398
BLAST score 1297
E value 1.0e-143
Match length 302
% identity 82

NCBI Description (AC004238) putative phosphoribosylaminoimidazolecarboxamide

formyltransferase [Arabidopsis thaliana]

Seq. No. 261076

Contig ID 2138_1.R1011

5'-most EST LIB3067-019-Q1-K1-F11

Seq. No. 261077

Contig ID 2140 1.R1011

5'-most EST uC-zmflb73307e03b1

Method BLASTX
NCBI GI g2498608
BLAST score 507
E value 3.0e-51
Match length 213
% identity 51

NCBI Description L-ASPARTATE OXIDASE (QUINOLINATE SYNTHETASE B) >gi_608530

(U17232) L-aspartate oxidase [Pseudomonas aeruginosa]

Seq. No. 261078

Contig ID 2141 1.R1011

5'-most EST uC-zmflmo17045c09b1

Method BLASTX
NCBI GI g3080420
BLAST score 1564
E value 1.0e-174
Match length 556
% identity 59

NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis

thaliana]

Seq. No. 261079



```
Contig ID
                  2142 1.R1011
                  uer700579653.hl
5'-most EST
                  261080
Seq. No.
                  2142 2.R1011
Contig ID
                  LIB3059-021-Q1-K1-F6
5'-most EST
                  261081
Seq. No.
                  2151 1.R1011
Contig ID
                  LIB3067-001-Q1-K1-A11
5'-most EST
                  BLASTX
Method
                  g3108209
NCBI GI
                  518
BLAST score
                  1.0e-52
E value
Match length
                  118
                   80
% identity
                   (AF028809) eukaryotic cap-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   261082
Seq. No.
                   2151 2.R1011
Contig ID
                   hvj700624001.h1
5'-most EST
                   BLASTX
Method
                   g3108209
NCBI GI
                   795
BLAST score
                   6.0e-85
E value
                   179
Match length
                   78
% identity
                  (AF028809) eukaryotic cap-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   261083
Seq. No.
                   2153 1.R1011
Contig ID
                   uC-zmflm017026b02b1
5'-most EST
                   BLASTX
Method
                   q1854386
NCBI GI
                   864
BLAST score
                   7.0e-93
E value
                   257
Match length
                   63
% identity
                   (AB001375) similar to soluble NSF attachment protein [Vitis
NCBI Description
                   vinifera]
                   261084
Seq. No.
                   2153 2.R1011
Contig ID
                   LIB3059-021-Q1-K1-D10
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1854386
BLAST score
                   355
                   3.0e - 33
E value
                   83
Match length
 % identity
                   (AB001375) similar to soluble NSF attachment protein [Vitis
NCBI Description
                   vinifera]
                    261085
 Seq. No.
```

36144

2154 1.R1011

Contig ID



```
ntr700071659.h1
5'-most EST
                  BLASTX
Method
                  a629772
NCBI GI
BLAST score
                  1887
                  0.0e + 00
E value
                  421
Match length
                  86
% identity
                  beta-ketoacyl-ACP synthase - barley
NCBI Description
                  >gi 498740 emb CAA84022 (Z34268) beta-ketoacyl-ACP
                  synthase [Hordeum vulgare]
                  261086
Seq. No.
                  2154 2.R1011
Contig ID
                  uC-zmflmo17159c10a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q629775
                  223
BLAST score
                  7.0e-18
E value
                  59
Match length
                  76
% identity
NCBI Description beta-ketoacyl-ACP synthase - barley (fragment)
                   261087
Seq. No.
                   2157 1.R1011
Contig ID
5'-most EST
                   pmx700090750.h1
                   BLASTX
Method
                   q2507229
NCBI GI
                   548
BLAST score
                   6.0e-56
E value
                   265
Match length
                   45
% identity
                   40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE)
NCBI Description
                   (ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED
                   PROTEIN) (ESTROGEN RECEPTOR BINDING CYCLOPHILIN)
                   >gi 423247_pir__A46579 estrogen receptor-binding
                   cyclophilin - bovine >gi_393300_dbj_BAA03159_ (D14074)
                   cyclophilin [Bos taurus]
                   261088
Seq. No.
                   2159 1.R1011
Contig ID
                   uC-zmflB73042e09b1
5'-most EST
Method
                   BLASTX
                   q4455129
NCBI GI
                   344
BLAST score
                   6.0e - 32
E value
Match length
                   128
% identity
                   52
NCBI Description (AF127761) ribonucleoprotein ZRNP1 [Homo sapiens]
Seq. No.
                   261089
                   2159 2.R1011
Contig ID
                   LIB143-013-Q1-E1-G10
5'-most EST
```

261090

2159 4.R1011

uC-zmflmo17397c03a1

Seq. No.

Contig ID 5'-most EST



```
261091
Seq. No.
                  2163 1.R1011
Contig ID
                  uC-zmflmo17113b07b1
5'-most EST
                  BLASTX
Method
                  g3763933
NCBI GI
BLAST score
                  487
                  9.0e-49
E value
                  214
Match length
                  53
% identity
                 (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
                  261092
Seq. No.
Contig ID
                  2166 1.R1011
5'-most EST
                  ceu700433128.h1
Seq. No.
                  261093
Contig ID
                  2169 1.R1011
5'-most EST
                  wty700163308.hl
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
                  2.0e-10
E value
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  261094
                  2170 1.R1011
Contig ID
5'-most EST
                  LIB148-027-Q1-E1-D6
Seq. No.
                  261095
                  2171 1.R1011
Contig ID
5'-most EST
                  LIB3075-015-Q1-K1-A11
Seq. No.
                  261096
                  2173 1.R1011
Contiq ID
                  uC-zmflmo17310f09b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3860253
BLAST score
                  215
                  2.0e-17
E value
                  89
Match length
% identity
NCBI Description (AC005824) hypothetical protein [Arabidopsis thaliana]
                  261097
Seq. No.
Contig ID
                  2174 1.R1011
5'-most EST
                  uC-zmroteosinte084h07b1
Method
                  BLASTX
NCBI GI
                  g4530591
BLAST score
                  426
```

Method BLASTX
NCBI GI g4530591
BLAST score 426
E value 9.0e-42
Match length 111
% identity 70

NCBI Description (AF132475) heme oxygenase 1 [Arabidopsis thaliana]

>gi_4530593_gb_AAD22108.1_ (AF132476) heme oxygenase 1

[Arabidopsis thaliana]



261098 Seq. No. 2174 2.R1011 Contig ID uC-zmflmo17168e09b15'-most EST BLASTX Method g2760833 NCBI GI 695 BLAST score 5.0e-73E value 188 Match length 70 % identity

NCBI Description (AC003105) unknown protein [Arabidopsis thaliana]

 Seq. No.
 261099

 Contig ID
 2174_3.R1011

 5'-most EST
 LIB3075-022-Q1-K1-A1

 Method
 BLASTX

NCBI GI g2760833
BLAST score 349
E value 4.0e-33
Match length 98
% identity 62

NCBI Description (AC003105) unknown protein [Arabidopsis thaliana]

 Seq. No.
 261100

 Contig ID
 2175_1.R1011

 5'-most EST
 nwy700446740.h1

 Method
 RLASTX

Method BLASTX
NCBI GI 94455208
BLAST score 1292
E value 1.0e-143
Match length 393
% identity 68

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

 Seq. No.
 261101

 Contig ID
 2176_1.R1011

 5'-most EST
 qmh700029275.f1

Seq. No. 261102 Contig ID 2183_1.R1011

5'-most EST uC-zmflmo17130a01b1

Method BLASTX
NCBI GI g2135053
BLAST score 198
E value 1.0e-14
Match length 148
% identity 30

NCBI Description E1B 19K/Bcl-2-interacting protein Nip2 - human >gi_558844 (U15173) BCL2/adenovirus E1B 19kD-interacting protein 2

[Homo sapiens]

Seq. No. 261103 Contig ID 2186_1.R1011

5'-most EST LIB189-027-Q1-E1-E2

Seq. No. 261104 Contig ID 2188_1.R1011

36147



```
uC-zmflb73239a10b2
5'-most EST
                  BLASTX
Method
                  g551288
NCBI GI
                   2845
BLAST score
                   0.0e + 00
E value
                   553
Match length
                   98
% identity
                  (Z33611) phosphoglycerate mutase [Zea mays]
NCBI Description
                   261105
Seq. No.
                   2188 2.R1011
Contig ID
                   LIB3115-020-P1-K1-H5
5'-most EST
                   BLASTX
Method
                   q1076820
NCBI GI
BLAST score
                   428
                   7.0e-42
E value
                   146
Match length
% identity
                   63
                  phosphoglycerate mutase (EC 5.4.2.1) - maize
NCBI Description
                   261106
Seq. No.
                   2188 3.R1011
Contig ID
                   LIB3180-043-P2-M2-B11
5'-most EST
                   BLASTX
Method
                   g551288
NCBI GI
                   580
BLAST score
                   7.0e-60
E value
Match length
                   112
                   97
% identity
                  (Z33611) phosphoglycerate mutase [Zea mays]
NCBI Description
                   261107
Seq. No.
                   2188_7.R1011
Contig ID
                   uC-zmroteosinte005a10b1
5'-most EST
                   BLASTX
Method
                   q1076820
NCBI GI
BLAST score
                   150
                   1.0e-09
E value
                   52
Match length
                   62
% identity
NCBI Description phosphoglycerate mutase (EC 5.4.2.1) - maize
                   261108
Seq. No.
                   2189 1.R1011
Contig ID
                   LIB3075-021-Q1-K1-G3
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4263818
BLAST score
                   280
E value
                   9.0e-25
                   146
Match length
% identity
NCBI Description (AC006067) unknown protein [Arabidopsis thaliana]
                   261109
Seq. No.
```

2192 1.R1011 Contig ID ntr700077041.h1 5'-most EST

Method BLASTX



q1652733 NCBI GI BLAST score 458 1.0e-61 E value 215 Match length 58 % identity

(D90908) glycogen operon protein GlgX [Synechocystis sp.] NCBI Description

261110 Seq. No.

2199 1.R1011 Contig ID pmx700090694.h1 5'-most EST

261111 Seq. No.

2199 2.R1011 Contig ID xmt700258333.h1 5'-most EST

261112 Seq. No.

Contig ID 2202 1.R1011

LIB3078-014-Q1-K1-E10 5'-most EST

BLASTX Method g3758827 NCBI GI BLAST score 384 9.0e-37 E value 146 Match length 51 % identity

(AJ011921) amino acid selective channel protein [Hordeum NCBI Description

vulgare]

Seq. No. 261113

2204 1.R1011 Contig ID

 $uC-z\overline{m}flmo17277g08b1$ 5'-most EST

BLASTX Method NCBI GI g113456 1953 BLAST score 0.0e + 00E value 387 Match length 97 % identity

NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)

>gi_22162_emb_CAA40781_ (X57556) adenine nucleotide

translocator [Zea mays]

261114 Seq. No.

2204 2.R1011 Contig ID

uC-zmflb73233a11b15'-most EST

Method BLASTX NCBI GI q113460 BLAST score 646 E value 1.0e-67 Match length 134 % identity 95

ADP, ATP CARRIER PROTEIN 2 PRECURSOR (ADP/ATP TRANSLOCASE 2) NCBI Description

(ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2)

>gi_100851_pir__S16568 ADP,ATP carrier protein precursor - maize >gi_22164_emb_CAA41812_ (X59086) adenine nucleotide

translocator [Zea mays]

Seq. No. 261115

Seq. No.

Contig ID

261119

2206 2.R1011



```
2204_3.R1011
Contig ID
                   uC-zmflm017211c05b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q113456
BLAST score
                   349
E value
                   1.0e-32
Match length
                   70
                   100
% identity
                   ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                   >gi_22162_emb_CAA40781_ (X57556) adenine nucleotide
                   translocator [Zea mays]
                   261116
Seq. No.
                   2204 4.R1011
Contig ID
5'-most EST
                   LIB3079-015-Q1-K1-F8
                   BLASTX
Method
                   g4587567
NCBI GI
BLAST score
                   197
E value
                   5.0e-15
Match length
                   91
                   47
% identity
                  (AC006550) F1003.7 [Arabidopsis thaliana]
NCBI Description
                   261117
Seq. No.
                   2204_8.R1011
Contig ID
5'-most EST
                   ymt700223189.h1
                   BLASTX
Method
                   g113460
NCBI GI
                   790
BLAST score
E value
                   3.0e - 84
                   165
Match length
                   93
% identity
NCBI Description ADP, ATP CARRIER PROTEIN 2 PRECURSOR (ADP/ATP TRANSLOCASE 2)
                    (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2)
                   >gi_100851_pir__S16568 ADP,ATP carrier protein precursor -
maize >gi_22164_emb_CAA41812_ (X59086) adenine nucleotide
                   translocator [Zea mays]
                   261118
Seq. No.
Contig ID
                   2206 1.R1011
                   LIB3062-035-Q1-K1-C6
5'-most EST
Method
                   BLASTX
NCBI GI
                   g112994
BLAST score
                   207
E value
                   4.0e-16
Match length
                   44
% identity
                   91
                   GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                   >qi 82685 pir S04536 embryonic abundant protein,
                   glycine-rich - maize >gi 22313 emb CAA31077 (X12564)
                   ABA-inducible gene protein [Zea mays]
                   >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                   mays]
```

36150

Seq. No.

261124



```
uC-zmflmo17271d07b1
5'-most EST
                  BLASTX
Method
                  g2425066
NCBI GI
                  2156
BLAST score
                  0.0e+00
E value
                  454
Match length
% identity
                  91
                  (AF019147) cysteine proteinase Mir3 [Zea mays]
NCBI Description
                  261120
Seq. No.
                  2206 3.R1011
Contig ID
                  LIB3088-021-Q1-K1-B2
5'-most EST
                  BLASTN
Method
                  g22312
NCBI GI
                  259
BLAST score
                  1.0e-144
E value
                   343
Match length
                   95
% identity
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                  abscisic acid)
                   261121
Seq. No.
                   2206 5.R1011
Contig ID
                  LIB3078-001-Q1-K1-E2
5'-most EST
                   BLASTN
Method
                   g22312
NCBI GI
                   206
BLAST score
E value
                   1.0e-112
Match length
                   218
                   99
% identity
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                   abscisic acid)
                   261122
Seq. No.
                   2206_6.R1011
Contig ID
                   xjt700094529.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1917019
                   988
BLAST score
                   1.0e-107
E value
                   232
Match length
% identity
                  (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
NCBI Description
                   261123
Seq. No.
                   2206_7.R1011
Contig ID
5'-most EST
                   LIB3078-032-Q1-K1-G8
Method
                   BLASTN
NCBI GI
                   q22312
BLAST score
                   174
                   4.0e-93
E value
Match length
                   293
% identity
                   97
                   Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                   abscisic acid)
```

36151



```
2206 8.R1011
Contig ID
                  fwa700101251.hl
5'-most EST
                  BLASTX
Method
                  g2425066
NCBI GI
                  1628
BLAST score
                   0.0e+00
E value
                   361
Match length
                   85
% identity
                  (AF019147) cysteine proteinase Mir3 [Zea mays]
NCBI Description
                   261125
Seq. No.
                   2206 9.R1011
Contig ID
                   uC-zmflmo17099d09b1
5'-most EST
                   BLASTX
Method
                   g2425066
NCBI GI
BLAST score
                   901
                   3.0e-97
E value
Match length
                   204
                   81
% identity
                  (AF019147) cysteine proteinase Mir3 [Zea mays]
NCBI Description
                   261126
Seq. No.
                   2206 10.R1011
Contig ID
                   wyr700242329.h1
5'-most EST
                   BLASTX
Method
                   g1917019
NCBI GI
BLAST score
                   972
                   1.0e-105
E value
Match length
                   230
% identity
                   85
                  (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
NCBI Description
                   261127
Seq. No.
                   2206 11.R1011
Contig ID
                   uC-zmflmo17042c03b1
5'-most EST
                   BLASTX
Method
                   q4218535
NCBI GI
BLAST score
                   440
                   2.0e-43
E value
Match length
                   91
                   85
% identity
NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]
                   261128
Seq. No.
                   2206_12.R1011
Contig ID
                   uC-z\overline{m}flmo17059b11a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1917019
                   155
BLAST score
                   4.0e-10
E value
                   41
Match length
% identity
NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
                   261129
Seq. No.
```

36152

2206 13.R1011

LIB3115-028-P1-K1-G12

Contig ID

5'-most EST

Contig ID

5'-most EST



```
BLASTX
Method
NCBI GI
                   g4218535
                   477
BLAST score
E value
                   8.0e-48
                   104
Match length
                   82
% identity
                  (AJ010829) GRAB1 protein [Triticum sp.]
NCBI Description
                   261130
Seq. No.
                   2206 14.R1011
Contig ID
5'-most EST
                   LIB36-013-Q1-E1-G7
Method
                   BLASTX
                   q1917019
NCBI GI
                   235
BLAST score
E value
                   2.0e-19
                   68
Match length
% identity
                   75
                  (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
NCBI Description
                   261131
Seq. No.
                   2206_15.R1011
Contig ID
                   uC-zmrob73019e07b1
5.'-most EST
Method
                   BLASTN
NCBI GI
                   g22312
                   200
BLAST score
E value
                   1.0e-108
                   260
Match length
                   94
% identity
                   Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                   abscisic acid)
                   261132
Seq. No.
Contig ID
                   2206 20.R1011
                   LIB143-046-Q1-E1-E7
5'-most EST
Method
                   BLASTN
NCBI GI
                   g22312
BLAST score
                   176
                   2.0e-94
E value
                   200
Match length
                   97
% identity
NCBI Description Maize ABA-inducible gene for glycine-rich protein ( ABA =
                   abscisic acid)
                   261133
Seq. No.
                   2206 28.R1011
Contig ID
                   uer700579266.h1
5'-most EST
                   BLASTX
Method
                   g2425066
NCBI GI
                   387
BLAST score
                   8.0e-38
E value
                   77
Match length
                   95
% identity
                  (AF019147) cysteine proteinase Mir3 [Zea mays]
NCBI Description
Seq. No.
                   261134
```

36153

2206_34.R1011 pwr700451803.h1



```
BLASTX
Method
NCBI GI
                   g2425066
BLAST score
                   426
E value
                   3.0e-42
Match length
                   97
                   96
% identity
                  (AF019147) cysteine proteinase Mir3 [Zea mays]
NCBI Description
Seq. No.
                   261135
                   2206_35.R1011
Contig ID
5'-most EST
                   nwy700448429.h1
                   BLASTX
Method
NCBI GI
                   q2425066
BLAST score
                   180
E value
                   3.0e-17
Match length
                   67
% identity
                  (AF019147) cysteine proteinase Mir3 [Zea mays]
NCBI Description
Seq. No.
                   261136
                   2206 37.R1011
Contig ID
5'-most EST
                   uC-zmflb73286c08b1
Method
                   BLASTX
NCBI GI
                   g1917019
BLAST score
                   356
E value
                   5.0e-36
Match length
                   93
% identity
                   90
NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
                   261137
Seq. No.
                   2219 1.R1011
Contig ID
                   uC-zmflb73184c08b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4490303
                   278
BLAST score
                   2.0e-28
E value
Match length
                   122
                   52
% identity
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
Seq. No.
                   261138
                   2222 1.R1011
Contig ID
5'-most EST
                   LIB3067-038-Q1-K1-D1
                   {\tt BLASTX}
Method
NCBI GI
                   g4432854
BLAST score
                   280
                   6.0e-24
E value
                   241
Match length
                   32
% identity
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]
                   261139
Seq. No.
```

 Seq. No.
 261139

 Contig ID
 2222_2.R1011

 5'-most EST
 uC-zmflb73193e11a1

Seq. No. 261140



```
2222 3.R1011
Contig ID
                  LIB3137-001-Q1-K1-G4
5'-most EST
                  BLASTX
Method
                  g2191150
NCBI GI
BLAST score
                  1380
                  1.0e-153
E value
                   355
Match length
                   77
% identity
                   (AF007269) similar to mitochondrial carrier family
NCBI Description
                   [Arabidopsis thaliana]
                   261141
Seq. No.
                   2222 5.R1011
Contig ID
                  uC-zmflb73192f05b1
5'-most EST
                   BLASTX
Method
                   g4388820
NCBI GI
                   268
BLAST score
                   2.0e-23
E value
                   69
Match length
                   72
% identity
                   (AC006528) putative myb DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   261142
Seq. No.
                   2222 6.R1011
Contig ID
                   uC-zmf1b73249g10b3
5'-most EST
                   BLASTX
Method
                   g2651302
NCBI GI
BLAST score
                   401
                   9.0e - 39
E value
Match length
                   228
% identity
                   41
                  (AC002336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   261143
Seq. No.
Contig ID
                   2222 7.R1011
5'-most EST
                   uC-zmflb73127b07b2
                   261144
Seq. No.
                   2222 10.R1011
Contig ID
5'-most EST
                   uC-zmflb73100d07b1
                   261145
Seq. No.
                   2222 14.R1011
Contig ID
                   uC-zmflmo17074g06b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2191150
BLAST score
                   296
E value
                   1.0e-26
                   75
Match length
                   80
% identity
                   (AF007269) similar to mitochondrial carrier family
NCBI Description
```

Seq. No. 261146 Contig ID 2226_1.R1011

5'-most EST wyr700243928.h1

[Arabidopsis thaliana]



```
Method
                  BLASTX
                  g4101473
NCBI GI
BLAST score
                  901
                  3.0e-97
E value
Match length
                  254
% identity
                  70
                  (AF003382) KEA1 [Arabidopsis thaliana]
NCBI Description
                  261147
Sea. No.
                  2226 2.R1011
Contig ID
                  fC-zmle700443881d5
5'-most EST
                  BLASTN
Method
                  g168436
NCBI GI
                  34
BLAST score
                  2.0e-09
E value
Match length
                   66
                   88
% identity
NCBI Description Zea mays catalase (Cat3) gene, complete cds
Seq. No.
                   261148
                   2227 2.R1011
Contig ID
                   uC-zmflb73020g06b1
5'-most EST
Seq. No.
                   261149
                   2227 3.R1011
Contig ID
                   uC-zmflmo17039b07b1
5'-most EST
Seq. No.
                   261150
                   2227_4.R1011
Contig ID
                   uC-z\overline{m}f1b73134b05b1
5'-most EST
                   BLASTX
Method
                   g1781299
NCBI GI
                   337
BLAST score
                   4.0e-31
E value
                   93
Match length
                   69
% identity
                  (Y09506) transformer-SR ribonucleoprotein [Nicotiana
NCBI Description
                   tabacum]
                   261151
Seq. No.
                   2227 5.R1011
Contig ID
5'-most EST
                   uC-zmroteosinte083d07b1
Seq. No.
                   261152
                   2227 6.R1011
Contig ID
                   nbm700469814.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1781299
BLAST score
                   164
                   4.0e-11
E value
Match length
                   47
% identity
NCBI Description
```

(Y09506) transformer-SR ribonucleoprotein [Nicotiana tabacum]

261153 Seq. No. Contig ID 2228 1.R1011



```
uC-zmflmo17061e02b1
5'-most EST
                     261154
Seq. No.
                     2231 1.R1011
Contig ID
                     LIB3066-031-Q1-K1-D4
5'-most EST
                     BLASTX
Method
                     g4587526
NCBI GI
                     357
BLAST score
                     2.0e-37
E value
                     155
Match length
                     45
% identity
                     (ACO07060) Strong similarity to F19I3.2 gi_3033375 putative
NCBI Description
                     berberine bridge enzyme from Arabidopsis thaliana BAC
                     gb AC004238. ESTs gb F19886, gb Z30784 and gb Z30785 come
                     from this gene
                     261155
Seq. No.
                     2234 1.R1011
Contig ID
                     LIB3069-003-Q1-K1-F12
5'-most EST
                     261156
Seq. No.
                     2237 1.R1011
Contig ID
                     LIB3<u>1</u>36-008-Q1-K1-E8
5'-most EST
                     BLASTX
Method
                     g3915023
NCBI GI
                      1414
BLAST score
                      1.0e-157
E value
Match length
                      474
                      60
% identity
                     SUCROSE-PHOSPHATE SYNTHASE 1
NCBI Description
                      (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1)
                      >gi 2588888_dbj_BAA23213_ (AB005023) sucrose-phosphate
                      synthase [Citrus unshiu]
                      261157
Seq. No.
                      2237_2.R1011
Contig ID
5'-most EST
                      uC-zmflb73233d01b1
Method
                      BLASTX
NCBI GI
                      a115511
                      762
BLAST score
                      6.0e-81
E value
Match length
                      149
% identity
                      100
                     CALMODULIN >gi 231682_sp P29612_CALM_ORYSA CALMODULIN >gi 71682_pir MCBH calmodulin = barley >gi 100666_pir S24952 calmodulin 1 (clone lambda DASH) - rice >gi 20188_emb_CAA78287 (Z12827) calmodulin [Oryza sativa] >gi 167008 (M27303) calmodulin [Hordeum vulgare]
NCBI Description
                      >qi 170072 (L01431) calmodulin [Glycine max] >gi_310315
                      (L18913) calmodulin [Oryza sativa] >gi_506850 (L\overline{2}0691)
                      calmodulin [Vigna radiata] >gi 1478370 bbs_176852 (S81594)
                      auxin-regulated calmodulin, arCaM [Vigna radiata=mung bean,
                      Wilczek, seedling, Peptide, 149 aa] [Vigna radiata]
                      >gi 1742989_emb_CAA70982_ (Y09853) CaM protein [Cicer
                      arietinum] \overline{>}gi \overline{1754991} (\overline{U}48242) calmodulin TaCaM1-1
```

[Triticum aestivum] >gi_1754993 (U48688) calmodulin TaCaM1-2 [Triticum aestivum] >gi 1754995 (U48689)



calmodulin TaCaM1-3 [Triticum aestivum] >gi 1755003 (U48693) calmodulin TaCaM3-1 [Triticum aestivum] >gi 1755005 (U49103) calmodulin TaCaM3-2 [Triticum aestivum] >gi 1755007 (U49104) calmodulin TaCaM3-3 [Triticum aestivum] >gi 1755009 (U49105) calmodulin TaCaM4-1 [Triticum aestīvum] >gi_3617842 (AF042840) calmodulin [Oryza sativa] >gi 226769_prf_ 1604476A calmodulin [Hordeum vulgare var. distichum] >gi 1583768_prf__2121384B calmodulin [Glycine max]

261158 Seq. No. 2237 3.R1011 Contig ID $wen7\overline{0}0335565.h1$ 5'-most EST BLASTX Method g115511 NCBI GI BLAST score 762 6.0e-81 E value Match length 149

100

% identity NCBI Description

CALMODULIN >gi 231682 sp P29612 CALM_ORYSA CALMODULIN >gi 71682 pir MCBH calmodulin - barley >gi 100666 pir S24952 calmodulin 1 (clone lambda DASH) rice >gi_20188_emb_CAA78287_ (Z12827) calmodulin [Oryza sativa] >gi_167008 (M27303) calmodulin [Hordeum vulgare] >gi_170072 (L01431) calmodulin [Glycine max] >gi_310315 (L1 $\overline{8}$ 913) calmodulin [Oryza sativa] >gi_506850 (L $\overline{2}$ 0691) calmodulin [Vigna radiata] >gi_1478370_bbs_176852 (S81594) auxin-regulated calmodulin, arCaM [Vigna radiata=mung bean, Wilczek, seedling, Peptide, 149 aa] [Vigna radiata] >gi_1742989_emb_CAA70982_ (Y09853) CaM protein [Cicer arietinum] >gi 1754991 (U48242) calmodulin TaCaM1-1 [Triticum aestivum] >gi_1754993 (U48688) calmodulin TaCaM1-2 [Triticum aestīvum] >gi_1754995 (U48689) calmodulin TaCaM1-3 [Triticum aestivum] >gi 1755003 (U48693) calmodulin TaCaM3-1 [Triticum aestivum] >gi_1755005 (U49103) calmodulin TaCaM3-2 [Triticum aestivum] >gi_1755007 (U49104) calmodulin TaCaM3-3 [Triticum aestivum] >gi_1755009 (U49105) calmodulin TaCaM4-1 [Triticum aestīvum] >gi 3617842 (AF042840) calmodulin [Oryza sativa] >gi_226769_prf__1604476A calmodulin [Hordeum vulgare var. distichum] >qi 1583768 prf 2121384B calmodulin [Glycine max]

261159 Seq. No. 2237 4.R1011 Contig ID $xsy7\overline{0}0208976.h1$ 5'-most EST BLASTX Method g115511 NCBI GI 762 BLAST score 6.0e-81 E value

Match length 149 100 % identity

NCBI Description

sativa] >gi_167008 (M27303) calmodulin [Hordeum vulgare]



>qi 170072 (L01431) calmodulin [Glycine max] >gi_310315 (L18913) calmodulin [Oryza sativa] >gi_506850 (L20691) calmodulin [Vigna radiata] >gi_1478370_bbs_176852 (S81594) auxin-regulated calmodulin, arCaM [Vigna radiata=mung bean, Wilczek, seedling, Peptide, 149 aa] [Vigna radiata] >gi 1742989_emb_CAA70982_ (Y09853) CaM protein [Cicer arietinum] >gi 1754991 (U48242) calmodulin TaCaM1-1 [Triticum aestivum] >gi_1754993 (U48688) calmodulin TaCaM1-2 [Triticum aestivum] >gi_1754995 (U48689) calmodulin TaCaM1-3 [Triticum aestivum] >gi_1755003 (U48693) calmodulin TaCaM3-1 [Triticum aestivum] >gi_1755005 (U49103) calmodulin TaCaM3-2 [Triticum aestivum] >gi 1755007 (U49104) calmodulin TaCaM3-3 [Triticum aestivum] >gi_1755009 (U49105) calmodulin TaCaM4-1 [Triticum aestivum] >gi 3617842 (AF042840) calmodulin [Oryza sativa] >gi 226769 prf 1604476A calmodulin [Hordeum vulgare var. distichum] >gi 1583768 prf 2121384B calmodulin [Glycine max]

261160 Seq. No. 2237 5.R1011 Contig ID ntr700076405.h1 5'-most EST BLASTX Method g20186 NCBI GI 761 BLAST score 8.0e-81 E value 149 Match length % identity 100

NCBI Description (X65016) calmodulin [Oryza sativa]

>gi_3336950_emb_CAA74307_ (Y13974) calmodulin [Zea mays]
>gi_4103961 (AF030034) calmodulin [Phaseolus vulgaris]

Seq. No. 261161 Contig ID 2237_6.R1011

5'-most EST LIB3062-023-Q1-K1-E2

Method BLASTX
NCBI GI g20186
BLAST score 761
E value 8.0e-81
Match length 149
% identity 100

NCBI Description (X65016) calmodulin [Oryza sativa]

>gi_3336950_emb_CAA74307_ (Y13974) calmodulin [Zea mays]
>gi_4103961 (AF030034) calmodulin [Phaseolus vulgaris]

Seq. No. 261162

Contig ID 2237 7.R1011

5'-most EST uC-zmflmo17116e05b1

Method BLASTX
NCBI GI g3915019
BLAST score 962
E value 1.0e-109
Match length 262
% identity 77

NCBI Description SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE

GLUCOSYLTRANSFERASE) >gi_421958_pir__S34172

sucrose-phosphate synthase (EC $\overline{2}$.4. $\overline{1}$.14) - potato



>gi 313265 emb CAA51872 (X73477) sucrose-phosphate synthase [Solanum tuberosum]

261163 Seq. No. 2237 9.R1011 Contig ID LIB3116-026-P1-K2-D3 5'-most EST BLASTX Method g115511 NCBI GI 437 BLAST score 6.0e-63 E value Match length 130 62 % identity NCBI Description

CALMODULIN >gi_231682_sp_P29612_CALM_ORYSA CALMODULIN

>gi_71682_pir__MCBH calmodulin - barley >gi_100666_pir__S24952 calmodulin 1 (clone lambda DASH) -

rice >gi_20188_emb_CAA78287_ (Z12827) calmodulin [Oryza sativa] >gi_167008 (M27303) calmodulin [Hordeum vulgare] >gi_170072 (L01431) calmodulin [Glycine max] >gi_310315 (L18913) calmodulin [Oryza sativa] $>gi_506850$ (L20691) calmodulin [Vigna radiata] $>gi_1478370$ bbs_176852 (S81594) auxin-regulated calmodulin, arCaM [Vigna radiata=mung bean, Wilczek, seedling, Peptide, 149 aa] [Vigna radiata] >gi_1742989_emb_CAA70982_ (Y09853) CaM protein [Cicer [Triticum $aest\overline{i}vum$] >gi_1754993 (U48688) calmodulin TaCaM1-2 [Triticum aestivum] >gi_1754995 (U48689) calmodulin TaCaM1-3 [Triticum aestivum] >gi_1755003 (U48693) calmodulin TaCaM3-1 [Triticum aestivum] >gi_1755005 (U49103) calmodulin TaCaM3-2 [Triticum aestivum] >gi_1755007 (U49104) calmodulin TaCaM3-3

[Triticum aestivum] >gi_1755009 (U49105) calmodulin TaCaM4-1 [Triticum aestīvum] >gi 3617842 (AF042840) calmodulin [Oryza sativa] >gi_226769_prf__1604476A

calmodulin [Hordeum vulgare var. distichum]

>gi 1583768 prf 2121384B calmodulin [Glycine max]

Seq. No. 261164 2237 24.R1011 Contig ID cat700016752.rl 5'-most EST

261165 Seq. No. Contig ID 2239 1.R1011 5'-most EST uC-zmflb73055f05b1

261166 Seq. No. 2241 1.R1011 Contig ID

5'-most EST uC-zmromo17102g03a1

Method BLASTX NCBI GI q4567273 BLAST score 1214 1.0e-134 E value Match length 361 % identity

(AC006841) putative vacuolar proton ATPase subunit NCBI Description

[Arabidopsis thaliana]

Seq. No. 261167

36160



```
2241 2.R1011
Contig ID
                  uC-zmflmo17067f11a1
5'-most EST
Method
                  BLASTX
                  g4567273
NCBI GI
BLAST score
                  342
E value
                   6.0e-32
Match length
                  92
                  72
% identity
NCBI Description
                   (AC006841) putative vacuolar proton ATPase subunit
                   [Arabidopsis thaliana]
                  261168
Seq. No.
Contig ID
                  2243 1.R1011
5'-most EST
                  xsy700212795.h1
Method
                  BLASTN
NCBI GI
                   q3821780
BLAST score
                   36
E value
                   2.0e-10
Match length
                   36
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   261169
Contig ID
                   2243 4.R1011
5'-most EST
                   cat700021179.rl
                   261170
Seq. No.
Contig ID
                   2244 1.R1011
                   LIB3075-021-Q1-K1-A10
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1706319
BLAST score
                   659
                   6.0e-69
E value
Match length
                   227
% identity
                   55
                  HISTIDINE DECARBOXYLASE (HDC) (TOM92)
NCBI Description
                   >gi 481829 pir S39554 histidine decarboxylase (EC
                   4.1.1.22) - tomato >gi_416534_emb_CAA50719_ (X71900)
                   histidine decarboxylase [Lycopersicon esculentum]
                   261171
Seq. No.
                   2246 1.R1011
Contig ID
5'-most EST
                   LIB3075-020-Q1-K1-G9
Seq. No.
                   261172
                   2248 1.R1011
Contig ID
                   LIB3075-020-Q1-K1-H10
5'-most EST
                   BLASTX
Method
                   q2735841
NCBI GI
```

Method BLASTX
NCBI GI g2735841
BLAST score 369
E value 3.0e-35
Match length 168

% identity 51

NCBI Description (AF010283) No definition line found [Sorghum bicolor]

Seq. No. 261173

Contig ID 2249 1.R1011

Contig ID

5'-most EST



```
uC-zmflmo17128h03b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q4538895
BLAST score
                  43
                  8.0e-15
E value
Match length
                  107
                  85
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8
NCBI Description
                   (ESSA project)
Seq. No.
                  261174
                  2249 2.R1011
Contig ID
5'-most EST
                  xjt700096756.h1
Method
                  BLASTX
NCBI GI
                  q4538911
BLAST score
                   1166
E value
                   1.0e-128
Match length
                   323
                   69
% identity
NCBI Description
                  (AL049482) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   261175
Contig ID
                   2249 3.R1011
5'-most EST
                  uC-zmflb73037c01b2
Method
                  BLASTX
NCBI GI
                   q4538911
BLAST score
                   221
E value
                  8.0e-37
Match length
                  141
% identity
                   58
NCBI Description (ALO49482) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   261176
                   2254 1.R1011
Contig ID
5'-most EST
                  ntr700076731.h1
Method
                  BLASTX
NCBI GI
                   g2224901
BLAST score
                   211
E value
                   1.0e-16
Match length
                   59
                   59
% identity
NCBI Description (U67134) PcMYB1 protein [Petroselinum crispum]
Seq. No.
                   261177
Contig ID
                   2259 1.R1011
5'-most EST
                  LIB148-007-Q1-E1-C3
                  BLASTX
Method
NCBI GI
                   g1871186
BLAST score
                   385
                   1.0e-51
E value
                  177
Match length
% identity
                   61
NCBI Description (U90439) protein kinase isolog [Arabidopsis thaliana]
Seq. No.
                   261178
```

36162

2260 1.R1011

LIB3088-001-Q1-K1-H12



```
Method
                  BLASTX
                  g3341687
NCBI GI
BLAST score
                  169
                  2.0e-11
E value
Match length
                  59
                  54
% identity
                  (AC003672) putative ras protein [Arabidopsis thaliana]
NCBI Description
                  261179
Seq. No.
                  2260 3.R1011
Contig ID
                  LIB3066-043-Q1-K1-H1
5'-most EST
Method
                  BLASTX
                   g2245125
NCBI GI
BLAST score
                   152
E value
                   9.0e-10
Match length
                   68
                   43
% identity
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   261180
Seq. No.
                   2264 1.R1011
Contig ID
                   LIB3075-020-Q1-K1-F6
5'-most EST
Method
                   BLASTX
                   q2493459
NCBI GI
                   259
BLAST score
                   5.0e-22
E value
                   147
Match length
% identity
                   35
                  PROTEIN KINASE C SUBSTRATE, 60.1 KD PROTEIN, HEAVY CHAIN
NCBI Description
                   (PKCSH) (80K-H PROTEIN) >gi 1215746 (U49178) 60 kDa protein
                   kinase C substrate [Bos taurus]
Seq. No.
                   261181
                   2266 1.R1011
Contig ID
                   LIB148-053-Q1-E1-C10
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4467146
BLAST score
                   1167
                   1.0e-128
E value
                   499
Match length
                   44
% identity
                  (AL035540) galactosidase like protein [Arabidopsis
NCBI Description
                   thaliana]
                   261182
Seq. No.
Contig ID
                   2274_1.R1011
5'-most EST
                   wty700165026.hl
Method
                   BLASTX
NCBI GI
                   q3885334
                   1190
BLAST score
                   1.0e-131
E value
Match length
                   302
% identity
                   73
                   (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
```

Seq. No. 261183

thaliana]

% identity

75



```
Contig ID
                   2274 2.R1011
                  uC-zmflb73276e01b1
5'-most EST
Method
                   BLASTX
                   q3885334
NCBI GI
BLAST score
                   2021
                   0.0e + 00
E value
Match length
                   561
% identity
                   68
                  (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   261184
                   2274 4.R1011
Contig ID
                   uC-zmflb73154b03a1
5'-most EST
Seq. No.
                   261185
                   2274 5.R1011
Contig ID
                   LIB3076-046-Q1-K1-F5
5'-most EST
                   BLASTX
Method
                   q3885334
NCBI GI
                   461
BLAST score
                   4.0e-46
E value
Match length
                   122
                   75
% identity
                  (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   261186
                   2274 7.R1011
Contig ID
5'-most EST
                   uC-zmflb73085g01a1
                   261187
Seq. No.
Contig ID
                   2274 8.R1011
5'-most EST
                   uC-zmflmo17329h11a1
                   BLASTX
Method
NCBI GI
                   g3885334
BLAST score
                   156
E value
                   3.0e-10
Match length
                   60
                   50
% identity
                  (AC005623) putative argonaute protein [Arabidopsis
NCBI Description
                   thalianal
                   261188
Seq. No.
                   2274_10.R1011
Contig ID
                   uC-zmflb73129h07a1
5'-most EST
Seq. No.
                   261189
Contig ID
                   2275 1.R1011
5'-most EST
                   LIB3075-020-Q1-K1-D8
Method
                   BLASTX
NCBI GI
                   q2982285
BLAST score
                   342
E value
                   4.0e-32
Match length
                   68
```

NCBI Description (AF051227) GASA5-like protein [Picea mariana]



261190 Seq. No. 2276 1.R1011 Contig ID $nbm7\overline{0}0476117.h1$ 5'-most EST BLASTX Method g549061 NCBI GI 427 BLAST score 6.0e-42 E value 158 Match length 56 % identity T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA) NCBI Description (CCT-ZETA-1) >gi_631655_pir__S43063 CCT (chaperonin containing TCP-1) zeta chain - mouse >gi 468554_emb_CAA83432_ (Z31557) CCT (chaperonin containing TCP-1) zeta subunit [Mus musculus] 261191 Seq. No. 2278 1.R1011 Contig ID LIB3066-044-Q1-K1-A8 5'-most EST BLASTX Method g2459428 NCBI GI 155 BLAST score 8.0e-10 E value 49 Match length 71 % identity (AC002332) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 261192 2278 2.R1011 Contig ID LIB3066-002-Q1-K1-D11 5'-most EST 261193 Seq. No. 2278 3.R1011 Contig ID LIB148-034-Q1-E1-E3 5'-most EST 261194 Seq. No. Contig ID 2280 1.R1011 LIB3066-036-Q1-K1-F6 5'-most EST Method BLASTX NCBI GI a3080436 BLAST score 326 E value 4.0e-57 Match length 204 59 % identity NCBI Description (AL022605) putative protein [Arabidopsis thaliana] Seq. No. 261195 Contig ID 2280 2.R1011 5'-most EST LIB3075-020-Q1-K1-E2 261196 Seq. No.

2283 1.R1011 Contig ID

LIB3150-057-Q1-N1-D7 5'-most EST

Method BLASTX NCBI GI g2632252 BLAST score 1528 E value 1.0e-170



Match length 427 % identity 68

NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No. 261197

Contig ID 2283_2.R1011

5'-most EST uC-zmflmo17055e05b1

Method BLASTX
NCBI GI g3885328
BLAST score 432
E value 2.0e-42
Match length 116
% identity 72

NCBI Description (AC005623) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 261198

Contig ID 2283_5.R1011

5'-most EST LIB3075-020-Q1-K1-E7

Method BLASTX
NCBI GI g2632254
BLAST score 513
E value 4.0e-52
Match length 121
% identity 78

NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No. 261199
Contig ID 2283_6.R1011
5'-most EST qmh700028251.f1

Method BLASTX
NCBI GI g3885328
BLAST score 426
E value 3.0e-46
Match length 134
% identity 66

NCBI Description (AC005623) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 261200

Contig ID 2285_1.R1011 5'-most EST rvt700548955.h1

Method BLASTX
NCBI GI g1737492
BLAST score 1321
E value 1.0e-146
Match length 475
% identity 76

NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No. 261201 Contig ID 2285_2.R1011

5'-most EST LIB3150-069-P2-K1-D5

Method BLASTX NCBI GI g1737492 BLAST score 268 E value 2.0e-23



Match length 81 % identity 72

NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No. 261202

Contig ID 2288_1.R1011

5'-most EST LIB148-062-Q1-E1-D7

Method BLASTX
NCBI GI g2529707
BLAST score 944
E value 1.0e-102
Match length 318

% identity 53

NCBI Description (AF001434) Hpast [Homo sapiens]

Seq. No. 261203

Contig ID 2289_1.R1011

5'-most EST LIB3150-068-P1-N1-F2

Method BLASTX
NCBI GI g3043618
BLAST score 283
E value 9.0e-25
Match length 123
% identity 40

NCBI Description (AB011119) KIAA0547 protein [Homo sapiens]

Seq. No. 261204 Contig ID 2289 2.R1011

5'-most EST uC-zmflmo17210f11a1

Seq. No. 261205

Contig ID 2292_1.R1011

5'-most EST LIB3075-020-Q1-K1-C4

Method BLASTN
NCBI GI g3821794
BLAST score 94
E value 3.0e-45
Match length 170
% identity 89

NCBI Description Zea mays gene encoding protein kinase CK2 alpha subunit

Seq. No. 261206

Contig ID 2293_1.R1011

5'-most EST uC-zmflb73056c12b1

Method BLASTX
NCBI GI g2129740
BLAST score 821
E value 2.0e-87
Match length 220
% identity 71

NCBI Description small nuclear ribonucleoprotein - Arabidopsis thaliana

>gi_2129756_pir__S71411 U1 snRNP 70K protein - Arabidopsis

thaliana >gi_1255711 (M93439) small nuclear

ribonucleoprotein [Arabidopsis thaliana] >gi_1354469 (U52909) U1 snRNP 70K protein [Arabidopsis thaliana]

Seq. No. 261207



2293 2.R1011 Contig ID 5'-most EST uC-zmflb73135h11b2 Method BLASTX g2129740 NCBI GI BLAST score 172 6.0e-12 E value Match length 43 % identity 72 small nuclear ribonucleoprotein - Arabidopsis thaliana NCBI Description >qi 2129756 pir S71411 U1 snRNP 70K protein - Arabidopsis thaliana >gi 1255711 (M93439) small nuclear ribonucleoprotein [Arabidopsis thaliana] >gi_1354469 (U52909) U1 snRNP 70K protein [Arabidopsis thaliana] 261208 Seq. No. 2294 1.R1011 Contig ID LIB3075-020-Q1-K1-C8 5'-most EST Method BLASTX NCBI GI g729135 BLAST score 1715 E value 0.0e + 00Match length 364 % identity 90 CAFFEIC ACID 3-O-METHYLTRANSFERASE NCBI Description (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi 283034 pir S28612 catechol O-methyltransferase ($\overline{\text{EC}}$ $\overline{2}$.1.1.6) - $\overline{\text{maize}}$ >gi 168532 (M73235) O-methyltransferase [Zea mays] Seq. No. 261209 2294 2.R1011 Contig ID uC-zmroteosinte119g02b2 5'-most EST Method BLASTX NCBI GI g729135 435 BLAST score E value 8.0e-4390 Match length 93 % identity NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir___S28612 catechol O-methyltransferase (EC 2.1.1.6) - maize >gi 168532 (M73235) O-methyltransferase [Zea mays] Seq. No. 261210 Contig ID 2294 3.R1011 wyr700242782.hl 5'-most EST Method BLASTX NCBI GI q729135 BLAST score 252 E value 1.0e-21 Match length 65 % identity 83 NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID

36168

3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir__S28612 catechol O-methyltransferase (EC 2.1.1.6) - maize



>gi 168532 (M73235) O-methyltransferase [Zea mays]

Seq. No. 261211 2294 5.R1011 Contig ID 5'-most EST LIB189-016-Q1-E1-B8 Method BLASTX NCBI GI g729135 BLAST score 206 E value 4.0e-16 Match length 41 % identity 95 NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir___S28612 catechol O-methyltransferase (EC 2.1.1.6) - maize >gi 168532 (M73235) O-methyltransferase [Zea mays] 261212 Seq. No. Contig ID 2294_7.R1011 5'-most EST pmx700091158.h1 Method BLASTX NCBI GI q729135 BLAST score 295 E value 8.0e-27 Match length 91 % identity 69 NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir__S28612 catechol O-methyltransferase (EC 2.1.1.6) - maize >gi 168532 (M73235) O-methyltransferase [Zea mays] Seq. No. 261213 2296 1.R1011 Contig ID 5'-most EST uC-zmflb73070a05b1 Method BLASTX NCBI GI g1296955 BLAST score 608 E value 1.0e-62 Match length 153 35 % identity NCBI Description (X95402) duplicated domain structure protein [Oryza sativa] 261214 Seq. No. Contig ID 2297 1.R1011

5'-most EST uC-zmflMo17065f12b1

Method . BLASTX NCBI GI g1076800 BLAST score 1120 E value 1.0e-123 247 Match length % identity 87

NCBI Description L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate peroxidase [Zea mays] >gi_1096503_prf__2111423A ascorbate

peroxidase [Zea mays]



```
261215
 Seq. No.
                    2297 3.R1011
 Contig ID
5'-most EST
                    mwy700438636.h1
                    BLASTN
 Method
                    g600115
 NCBI GI
                    389
 BLAST score
                    0.0e+00
 E value
                    515
 Match length
                    97
 % identity
 NCBI Description
                   Z.mays apx gene encoding cytosolic ascorbate peroxidase
                    261216
 Seq. No.
                    2297 4.R1011
 Contig ID
                    uC-zmflb73069d09a1
 5'-most EST
                    BLASTN
 Method
 NCBI GI
                    q600115
 BLAST score
                    317
                    1.0e-178
 E value
                    346
 Match length
                    98
  % identity
                    Z.mays apx gene encoding cytosolic ascorbate peroxidase
 NCBI Description
                    261217
 Seq. No.
                    2298 1.R1011
 Contig ID
                    wyr700237367.h1
  5'-most EST
 Method
                    BLASTX
 NCBI GI
                    g4239889
 BLAST score
                    1884
                     0.0e + 00
 E value
                    398
 Match length
                     91
  % identity
  NCBI Description
                   (AB016802) MAP kinase 5 [Zea mays]
                    261218
  Seq. No.
  Contig ID
                     2298_4.R1011
  5'-most EST
                    uC-zmflb73119a09a1
  Method
                    BLASTN
  NCBI GI
                     g4239888
                     75
  BLAST score
                     5.0e-34
  E value
  Match length
                     324
                     87
  % identity
  NCBI Description Zea mays mRNA for MAP kinase 5, complete cds
                     261219
  Seq. No.
                     2299 1.R1011
  Contig ID
  5'-most EST
                    uC-zmflmo17257a07b1
  Method
                     BLASTX
  NCBI GI
                     q3881976
  BLAST score
                     932
  E value
                     1.0e-101
  Match length
                     260
  % identity
                    (AJ012409) hypothetical protein [Homo sapiens]
  NCBI Description
```

36170

261220

2299_3.R1011

Seq. No. Contig ID

BLAST score

E value Match length 1020 1.0e-111

217



```
uC-zmrob73016e03a1
5'-most EST
                  BLASTX
Method
                  g3881976
NCBI GI
BLAST score
                  267
                  3.0e-23
E value
                  60
Match length
                  80
% identity
                  (AJ012409) hypothetical protein [Homo sapiens]
NCBI Description
                  261221
Seq. No.
                   2299 5.R1011
Contig ID
                  LIB3180-011-P2-M1-C9
5'-most EST
                   261222
Seq. No.
                   2302 1.R1011
Contig ID
5'-most EST
                   tzu700204437.h1
                  BLASTX
Method
                   g3746431
NCBI GI
                   878
BLAST score
                   1.0e-145
E value
                   278
Match length
                   94
% identity
                  (AF038585) pyruvate dehydrogenase kinase isoform 1; PDK1
NCBI Description
                   [Zea mays]
                   261223
Seq. No.
Contig ID
                   2302 2.R1011
5'-most EST
                   uC-zmflmo17333h09b1
                   BLASTX
Method
                   g3746431
NCBI GI
BLAST score
                   923
                   1.0e-100
E value
                   193
Match length
                   93
% identity
                  (AF038585) pyruvate dehydrogenase kinase isoform 1; PDK1
NCBI Description
                   [Zea mays]
                   261224
Seq. No.
                   2302 3.R1011
Contig ID
5'-most EST
                   uer700582463.hl
Method
                   BLASTX
NCBI GI
                   q3746431
BLAST score
                   434
E value
                   1.0e-42
Match length
                   90
                   92
% identity
                   (AF038585) pyruvate dehydrogenase kinase isoform 1; PDK1
NCBI Description
                   [Zea mays]
                   261225
Seq. No.
                   2302 4.R1011
Contig ID
5'-most EST
                   wty700165260.h1
Method
                   BLASTX
                   g3746431
NCBI GI
```

36171



% identity (AF038585) pyruvate dehydrogenase kinase isoform 1; PDK1 NCBI Description [Zea mays] 261226 Seq. No. 2302 7.R1011 Contig ID yyf700349147.hl 5'-most EST BLASTX Method g3746431 NCBI GI 308 BLAST score 1.0e-35 E value Match length 101 81 % identity (AF038585) pyruvate dehydrogenase kinase isoform 1; PDK1 NCBI Description [Zea mays] 261227 Seq. No. 2303 1.R1011 Contig ID LIB148-009-Q1-E1-F6 5'-most EST BLASTX Method g3785989 NCBI GI 838 BLAST score 6.0e-90 E value 261 Match length 61 % identity (AC005560) unknown protein [Arabidopsis thaliana] NCBI Description 261228 Seq. No. 2304 1.R1011 Contig ID cyk700050457.f1 5'-most EST BLASTX Method g2852640 NCBI GI 347 BLAST score 6.0e - 32E value 192 Match length 40 % identity NCBI Description (AF007157) unknown [Homo sapiens] 261229 Seq. No. 2305 1.R1011 Contig ID xyt700344454.h1 5'-most EST Method BLASTX q4056507 NCBI GI 253 BLAST score E value 2.0e-21 80 Match length % identity (AC005896) putative RNA binding protein [Arabidopsis NCBI Description thaliana]

Seq. No. 261230 Contig ID 2308_1.R1011 5'-most EST LIB3075-007-Q1-K1-E8

Method BLASTX
NCBI GI g960289
BLAST score 966
E value 1.0e-105



Match length 251 % identity 75 NCBI Description (L34343) anthranilate synthase alpha subunit [Ruta

graveolens]

261231 Seq. No. 2308_2.R1011 Contig ID

LIB3059-046-Q1-K1-E7 5'-most EST

Method BLASTX NCBI GI g960289 BLAST score 537 E value 5.0e-55 Match length 146 % identity 72

NCBI Description (L34343) anthranilate synthase alpha subunit [Ruta

graveolens]

Seq. No. 261232 Contig ID 2310 1.R1011 5'-most EST xjt700092223.h1 Method BLASTX

NCBI GI q2826884 BLAST score 624 E value 2.0e-64 Match length 382 42 % identity

NCBI Description (AJ223635) transcription factor IIA large subunit

[Arabidopsis thaliana]

Seq. No. 261233 Contig ID 2317 1.R1011

5'-most EST LIB3066-005-Q1-K1-G2

Method BLASTN NCBI GI q22455 BLAST score 473 E value 0.0e + 00Match length 533 % identity 98

NCBI Description Z.mays pollen specific mRNA C-terminal (clone 3A6)

Seq. No. 261234 Contig ID 2318 1.R1011

5'-most EST LIB3066-006-Q1-K1-E3

Method BLASTX NCBI GI g2623248 BLAST score 584 E value 7.0e-60 259 Match length 49 % identity

NCBI Description (AF030882) SU1 isoamylase [Zea mays]

Seq. No. 261235

Contig ID 2321 1.R1011

5'-most EST LIB148-028-Q1-E1-G10

Method BLASTX NCBI GI g2809243 312 BLAST score



E value 2.0e-28 Match length 95 % identity 58

(AC002560) F21B7.12 [Arabidopsis thaliana] NCBI Description

261236 Seq. No. 2326 1.R1011 Contig ID uC-zmrob73004f12b1 5'-most EST

Seq. No. 261237 Contig ID 2328_1.R1011

5'-most EST LIB3066-043-Q1-K1-F10

Method BLASTX NCBI GI q1491710 BLAST score 270 E value 1.0e-23 Match length 91 54 % identity

(X96506) alpha subunit; forms heterodimer with NC2 NCBI Description

alpha/Dr1 [Homo sapiens]

261238 Seq. No. Contig ID 2328 2.R1011 5'-most EST cjh700195359.h1BLASTX Method

NCBI GI g1491710 BLAST score 272 E value 1.0e-23 Match length 114 48 % identity

NCBI Description (X96506) alpha subunit; forms heterodimer with NC2

alpha/Dr1 [Homo sapiens]

261239 Seq. No. 2329 1.R1011 Contig ID

5'-most EST uC-zmroteosinte069e08b1

Method BLASTX NCBI GI q4127988 BLAST score 1317 E value 1.0e-145 Match length 367 % identity

(AJ005940) GTP-binding protein [Homo sapiens] >gi 4218945 NCBI Description

(AF078103) developmentally regulated GTP-binding protein

[Homo sapiens]

Seq. No. 261240

2334 1.R1011 Contig ID

uC-zmflmo17257e06b1 5'-most EST

BLASTX Method NCBI GI q2497486 BLAST score 790 E value 4.0e-84 Match length 191 % identity 80

NCBI Description URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP

KINASE) >gi 2121275 (AF000147) UMP/CMP kinase [Arabidopsis



thaliana]

```
Seq. No.
                  261241
                  2334 3.R1011
Contig ID
                  LIB148-060-Q1-E1-F1
5'-most EST
                  BLASTX
Method
                  q2497486
NCBI GI
                  165
BLAST score
                  2.0e-11
E value
                  35
Match length
                  86
% identity
                  URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP
NCBI Description
                  KINASE) >gi 2121275 (AF000147) UMP/CMP kinase [Arabidopsis
                  thaliana]
```

Seq. No. 261242 2334 4.R1011 Contig ID

LIB148-039-Q1-E1-A12 5'-most EST

Method BLASTX q2497486 NCBI GI BLAST score 328 2.0e-30 E value Match length 85

84 % identity

URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP NCBI Description

KINASE) >gi 2121275 (AF000147) UMP/CMP kinase [Arabidopsis

thaliana]

261243 Seq. No. 2334 6.R1011 Contig ID vux700157618.h1 5'-most EST

Seq. No. 261244

2335 1.R1011 Contig ID

LIB3076-041-Q1-K1-E6 5'-most EST

BLASTX Method NCBI GI q4154281 BLAST score 2421 0.0e + 00E value Match length 465 % identity

(AF082347) C13 endopeptidase NP1 precursor [Zea mays] NCBI Description

Seq. No. 261245

2335 2.R1011 Contig ID

5'-most EST LIB3060-051-Q1-K1-G12

Method BLASTX NCBI GI q4154281 BLAST score 456 4.0e-46 E value Match length 139 % identity

(AF082347) C13 endopeptidase NP1 precursor [Zea mays] NCBI Description

261246 Seq. No. 2335 3.R1011 Contig ID 5'-most EST uC-zmflb73019d05b1

Seq. No.

Contig ID 5'-most EST



```
BLASTX
Method
NCBI GI
                  g4154281
                   642
BLAST score
                   3.0e-67
E value
Match length
                  144
                   87
% identity
                  (AF082347) C13 endopeptidase NP1 precursor [Zea mays]
NCBI Description
                   261247
Seq. No.
                   2335 4.R1011
Contig ID
                  uC-z\overline{m}rob73045e08a1
5'-most EST
                  BLASTX
Method
NCBI GI
                   q4154281
BLAST score
                   212
                   9.0e-17
E value
Match length
                   42
                   95
% identity
                  (AF082347) C13 endopeptidase NP1 precursor [Zea mays]
NCBI Description
                   261248
Seq. No.
                   2335 6.R1011
Contig ID
                  uer700578409.h1
5'-most EST
                   BLASTN
Method
                   g4154280
NCBI GI
BLAST score
                   93
                   5.0e-45
E value
Match length
                   113
% identity
                   96
NCBI Description Zea mays C13 endopeptidase NP1 precursor, mRNA, complete
                   cds
Seq. No.
                   261249
Contig ID
                   2337 1.R1011
5'-most EST
                   LIB148-040-Q1-E1-D5
Seq. No.
                   261250
Contig ID
                   2338 1.R1011
5'-most EST
                   LIB3061-036-Q1-K1-F5
                   261251
Seq. No.
                   2339 1.R1011
Contig ID
5'-most EST
                   kem700612180.h1
                   261252
Seq. No.
                   2343 1.R1011
Contig ID
5'-most EST
                   LIB3075-019-Q1-K1-E4
Method
                   BLASTX
NCBI GI
                   g2943792
BLAST score
                   930
E value
                   1.0e-101
Match length
                   235
% identity
NCBI Description (AB006809) PV72 [Cucurbita sp.]
```

36176

261253

2348 1.R1011

uC-zmflmo17181e01b1



Method BLASTX NCBI GI q2388580 BLAST score 987 E value 1.0e-107 Match length 320 56 % identity

(AC000098) Similar to Sequence 10 from patent 5477002 NCBI Description

(gb 1253956). [Arabidopsis thaliana]

261254 Seq. No. Contig ID 2353 1.R1011 5'-most EST uwc700149613.hl

BLASTX Method NCBI GI q729882 BLAST score 426 1.0e-41 E value 169 Match length 56 % identity

CASEIN KINASE II BETA' CHAIN (CK II) NCBI Description

>gi_1076300_pir__S47968 casein kinase II (EC 2.7.1.-) beta chain CKB2 - Arabidopsis thaliana >gi_467975 (U03984) casein kinase II beta subunit CKB2 [Arabidopsis thaliana] >gi 2245122_emb_CAB10544_ (Z97343) unnamed protein product

[Arabidopsis thaliana]

Seq. No. 261255 Contig ID 2355 1.R1011

5'-most EST LIB3137-003-Q1-K1-B6

Method BLASTX NCBI GI g3757515 BLAST score 873 E value 9.0e - 94293 Match length % identity 62

NCBI Description (AC005167) hypothetical protein [Arabidopsis thaliana]

>gi 4581130 gb AAD24620.1 AC005825 27 (AC005825)

hypothetical protein [Arabidopsis thaliana]

261256 Seq. No. 2355 2.R1011 Contig ID

LIB3150-094-P2-K1-C6 5'-most EST

Seq. No. 261257

2355 3.R1011 Contig ID 5'-most EST $gw17\overline{0}0615369.h1$

Method BLASTX g3757515 NCBI GI BLAST score 221 E value 1.0e-17 Match length 101 % identity 52

(AC005167) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi_4581130_gb_AAD24620.1_AC005825 27 (AC005825)

hypothetical protein [Arabidopsis thaliana]

261258

Seq. No. Contig ID 2358_1.R1011



```
LIB3069-044-Q1-K1-F2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g115577
                  1795
BLAST score
                  0.0e + 00
E value
Match length
                  365
                  95
% identity
                 PHOSPHOENOLPYRUVATE CARBOXYLASE, HOUSEKEEPING ISOZYME
NCBI Description
                  (PEPCASE) >gi_348536_pir__S28614 phosphoenolpyruvate
                  carboxylase (EC 4.1.1.31) - sugarcane hybrid H32-8560
                  >gi 169844 (M86661) phosphoenolpyruvate carboxylase
                   [Saccharum sp.]
                  261259
Seq. No.
                  2359 1.R1011
Contig ID
5'-most EST
                  ceu700433756.h1
                  261260
Seq. No.
                  2359 2.R1011
Contig ID
                  LIB3076-001-Q1-K1-B2
5'-most EST
                  261261
Seq. No.
                  2359 3.R1011
Contig ID
                  uC-zmflb73224h04b1
5'-most EST
                  261262
Seq. No.
                  2360 1.R1011
Contig ID
                  LIB3075-018-Q1-K1-B12
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1495273
                  192
BLAST score
E value
                  1.0e-14
                  58
Match length
                   67
% identity
NCBI Description (Z50752) sugar transporter [Arabidopsis thaliana]
Seq. No.
                  261263
Contig ID
                  2361 1.R1011
                  LIB3075-018-Q1-K1-C9
5'-most EST
                   261264
Seq. No.
Contig ID
                   2363 1.R1011
                  LIB3075-010-Q1-K1-G7
5'-most EST
Method
                  BLASTN
NCBI GI
                  g902585
BLAST score
                   40
E value
                   4.0e-13
Match length
                  72
% identity
                   89
NCBI Description Zea mays clone MubG9 ubiquitin gene, complete cds
```

Seq. No. 261265

Contig ID 2365_1.R1011 5'-most EST uwc700154308.h1

Method BLASTX NCBI GI g2641619 BLAST score 734



```
1.0e-77
E value
Match length
                   148
% identity
                   89
NCBI Description
                   (AF032468) ubiquitin-conjugating enzyme protein E2 [Zea
                   mays]
                   261266
Seq. No.
                   2365_2.R1011
Contig ID
5'-most EST
                   uC-zmflB73106h10b1
Method
                   BLASTX
NCBI GI
                   g2641619
BLAST score
                   162
                   6.0e-11
E value
Match length
                   30
                   100
% identity
NCBI Description
                  (AF032468) ubiquitin-conjugating enzyme protein E2 [Zea
                   mays]
                   261267
Seq. No.
Contig ID
                   2365 3.R1011
                   uC-z\overline{m}f1b73073b05b3
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2641619
BLAST score
                   750
E value
                   1.0e-79
                   148
Match length
% identity
                   92
NCBI Description
                  (AF032468) ubiquitin-conjugating enzyme protein E2 [Zea
                   mays]
Seq. No.
                   261268
                   2365 4.R1011
Contig ID
5'-most EST
                   uC-zmflmo17035g12b1
Method
                   BLASTX
NCBI GI
                   g2624417
BLAST score
                   725
E value
                   2.0e-76
Match length
                   168
                   80
% identity
NCBI Description
                  (AJ002959) Ubiquitin carrier protein [Zea mays]
Seq. No.
                   261269
Contig ID
                   2365 6.R1011
5'-most EST
                   uC-zmflb73178f12b1
Method
                   BLASTX
NCBI GI
                   g2624417
BLAST score
                   822
E value
                   5.0e-88
Match length
                   158
% identity
```

Seq. No. 261270 Contig ID 2365 8.R1011

NCBI Description

5'-most EST uC-zmflm017092c06b1

Method BLASTX NCBI GI g2624417

(AJ002959) Ubiquitin carrier protein [Zea mays]



BLAST score 249 E value 2.0e-21 Match length 46 % identity 93

NCBI Description (AJ002959) Ubiquitin carrier protein [Zea mays]

Seq. No. 261271

Contig ID 2366_1.R1011 5'-most EST pmx700085903.h1

Method BLASTX
NCBI GI g1351905
BLAST score 2035
E value 0.0e+00
Match length 417
% identity 95

NCBI Description ASPARTOKINASE 2 / HOMOSERINE DEHYDROGENASE 2 CHLOROPLAST

PRECURSOR (AK-HSDH 2) (AKHSDH2) >gi_500853 (L33913) aspartate kinase-homoserine dehydrogenase [Zea mays]

Seq. No. 261272

Contig ID 2367_1.R1011

5'-most EST LIB3075-019-Q1-K1-B7

Seq. No. 261273

Contig ID 2369 1.R1011

5'-most EST LIB3079-054-Q1-K1-H8

Seq. No. 261274

Contig ID 2373 1.R1011

5'-most EST uC-zmflmo17340h04b1

Seq. No. 261275

Contig ID 2373_2.R1011

5'-most EST uC-zmflB73005g12b1

Seq. No. 261276

Contig ID 2373 3.R1011

5'-most EST uC-zmflb73130c12b2

Seq. No. 261277

Contig ID 2373 4.R1011

5'-most EST LIB3078-027-Q1-K1-H11

Method BLASTN NCBI GI g3821780

BLAST score 36
E value 3.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 261278

Contig ID 2373 5.R1011

5'-most EST uC-zmflmo17197g04b1

Seq. No. 261279

Contig ID 2373 6.R1011

5'-most EST LIB3066-015-Q1-K1-H9



261280 Seq. No.

2373 7.R1011 Contig ID

uC-zmflmo17305c05a1 5'-most EST

261281 Seq. No.

2373 15.R1011 Contig ID

LIB3078-033-Q1-K1-B6 5'-most EST

261282 Seq. No.

2375 2.R1011 Contig ID

LIB3180-058-P2-M1-C3 5'-most EST

261283 Seq. No.

Contig ID 2376 1.R1011 5'-most EST nbm700476804.h1

BLASTX Method NCBI GI q626464 BLAST score 177 2.0e-12 E value 75 Match length 44 % identity

NCBI Description VPS27 protein - yeast (Saccharomyces cerevisiae)

>gi_496723_emb_CAA54574_ (X77395) N2038 [Saccharomyces
cerevisiae] >gi_1302478_emb_CAA96282_ (Z71620) ORF YNR006w

[Saccharomyces cerevisiae]

Seq. No. 261284

Contig ID 2378 1.R1011

LIB3075-018-Q1-K1-H7 5'-most EST

Method BLASTX NCBI GI g3386621 BLAST score 818 2.0e-87 E value 223 Match length 70 % identity

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 261285

2378 2.R1011 Contig ID 5'-most EST tzu700204669.h1

Method BLASTX NCBI GI g3386621 BLAST score 341 5.0e-32 E value 85 Match length % identity 78

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No. 261286

2378 4.R1011 Contig ID

5'-most EST LIB3079-012-Q1-K1-A1

261287 Seq. No.

Contig ID 2379 1.R1011

LIB3075-018-Q1-K1-H8 5'-most EST



```
Seq. No.
                   261288
                   2380 1.R1011
Contig ID
5'-most EST
                  LIB3068-036-Q1-K1-E2
Method
                   BLASTX
NCBI GI
                   g2078350
BLAST score
                   1596
                   1.0e-178
E value
Match length
                   372
                   83
% identity
                  (U95923) transaldolase [Solanum tuberosum]
NCBI Description
Seq. No.
                   261289
Contig ID
                   2380 2.R1011
                   uC-zmflmo17129f06b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2078350
BLAST score
                   288
                   6.0e-27
E value
Match length
                   94
% identity
                  (U95923) transaldolase [Solanum tuberosum]
NCBI Description
                   261290
Seq. No.
Contig ID
                   2380 3.R1011
                   pmx700083979.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2078350
BLAST score
                   299
E value
                   6.0e-27
Match length
                   83
                   70
% identity
                  (U95923) transaldolase [Solanum tuberosum]
NCBI Description
Seq. No.
                   261291
                   2382 1.R1011
Contig ID
                   LIB3075-019-Q1-K1-A3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1657382
BLAST score
                   658
                   3.0e-69
E value
                   145
Match length
                   84
% identity
                   (Y09101) cholinephosphate cytidylyltransferase [Pisum
NCBI Description
                   sativum]
Seq. No.
                   261292
                   2384 1.R1011
Contig ID
5'-most EST
                   LIB3075-019-Q1-K1-A5
Method
                   BLASTX
                   g2293566
NCBI GI
                   937
BLAST score
                   1.0e-101
E value
Match length
                   181
                   100
% identity
```

Seq. No. 261293

NCBI Description

(AF012896) ADP-ribosylation factor 1 [Oryza sativa]



2384 2.R1011 Contig ID 5'-most EST yyf700349992.h1 Method BLASTX

g2293566 NCBI GI BLAST score 937 E value 1.0e-101 181 Match length 100 % identity

(AF012896) ADP-ribosylation factor 1 [Oryza sativa] NCBI Description

261294 Seq. No.

Contig ID 2384 3.R1011

5'-most EST uC-zmflmo17292b11b1

Method BLASTX NCBI GI g1351974 931 BLAST score 1.0e-100 E value Match length 181 99 % identity

ADP-RIBOSYLATION FACTOR >gi 1076788 pir S49325 NCBI Description

ADP-ribosylation factor - maize >gi_1076789_pir_ S53486 ADP-ribosylation factor - maize >gi 556686 emb CAA56351_

(X80042) ADP-ribosylation factor [Zea mays]

261295 Seq. No. 2384 4.R1011 Contig ID

5'-most EST LIB3061-012-Q1-K1-C4

BLASTX Method g543841 NCBI GI 897 BLAST score 9.0e-97 E value Match length 173 99 % identity

ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 NCBI Description

ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi 2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236)

ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No. 261296

Contig ID 2384 5.R1011 5'-most EST xmt700258055.h1

BLASTX Method NCBI GI q543841 BLAST score 928 E value 1.0e-100 Match length 181 % identity 98

NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 322518 pir S28875

> ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >qi 2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No. 261297



```
2384 7.R1011
Contig ID
5'-most EST
                  LIB189-019-Q1-E1-G4
Method
                  BLASTX
NCBI GI
                  q543841
BLAST score
                   442
                  8.0e-44
E value
Match length
                  85
% identity
                  100
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi 322518 pir S28875
                  ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586
                   (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
                  >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis
                   thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236)
                  ADP-ribosylation factor [Arabidopsis thaliana]
Seq. No.
                  261298
Contig ID
                  2384 11.R1011
5'-most EST
                  LIB3079-045-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                  g2293566
BLAST score
                  344
E value
                   5.0e-32
Match length
                  67
                  97
% identity
NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
                  261299
Seq. No.
                  2384 15.R1011
Contig ID
                  ntr700072510.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2293566
BLAST score
                  437
E value
                   4.0e-43
Match length
                  125
% identity
                   78
NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
Seq. No.
                   261300
Contig ID
                  2388 1.R1011
                  pmx700087403.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2506139
BLAST score
                  2080
E value
                  0.0e + 00
Match length
                  523
% identity
                  78
NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
                   (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962)
                  archain/delta-COP [Oryza sativa]
```

 Seq. No.
 261301

 Contig ID
 2388_2.R1011

 5'-most EST
 uC-zmflb73254f09a1

 Method
 BLASTX

 NCBI GI
 g2506139

 BLAST score
 343

4.0e-32

E value

```
Match length
                  80
% identity
                  82
                  COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
NCBI Description
                   (ARCHAIN) >gi 1314049 emb CAA91901 (Z67962)
                  archain/delta-COP [Oryza sativa]
                  261302
Seq. No.
Contig ID
                  2388_3.R1011
5'-most EST
                  uC-zmflmo17280b04b1
Method
                  BLASTX
NCBI GI
                  q2506139
BLAST score
                  400
                  7.0e - 39
E value
Match length
                  109
% identity
                  77
                  COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
NCBI Description
                   (ARCHAIN) >gi 1314049 emb CAA91901 (Z67962)
                  archain/delta-COP [Oryza sativa]
Seq. No.
                  261303
Contig ID
                  2388 4.R1011
5'-most EST
                  uC-zmflb73276e06b1
Method
                  BLASTX
NCBI GI
                  q2506139
BLAST score
                  549
E value
                  2.0e-56
Match length
                  126
                  79
% identity
NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
                   (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962)
                  archain/delta-COP [Oryza sativa]
Seq. No.
                  261304
Contig ID
                  2388 6.R1011
5'-most EST
                  LIB3062-006-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  g2506139
BLAST score
                  216
E value
                  2.0e-17
Match length
                  113
% identity
                  47
NCBI Description
                  COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
                   (ARCHAIN) >gi 1314049 emb CAA91901 (Z67962)
                  archain/delta-COP [Oryza sativa]
Seq. No.
                  261305
Contig ID
                  2388 8.R1011
5'-most EST
                  LIB3150-116-P2-K1-A9
Method
                  BLASTX
NCBI GI
                  q2506139
BLAST score
                  230
E value
                  5.0e-19
                  55
Match length
                  82
% identity
NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)
                  (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962)
```

36185

archain/delta-COP [Oryza sativa]



```
Seq. No.
                  261306
                  2391 1.R1011
Contig ID
5'-most EST
                  LIB3075-018-Q1-K1-F9
Seq. No.
                  261307
Contig ID
                  2393 1.R1011
5'-most EST
                  dyk700105389.h1
Method
                  BLASTX
NCBI GI
                  g3510253
BLAST score
                  445
E value
                  3.0e-43
Match length
                  412
% identity
                  30
NCBI Description (AC005310) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  261308
Contig ID
                  2393 2.R1011
5'-most EST
                  LIB3069-052-Q1-K1-B12
Seq. No.
                  261309
Contig ID
                  2393 4.R1011
5'-most EST
                  LIB3079-001-Q1-K1-H12
Seq. No.
                  261310
                  2395 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17193h09b1
Method
                  BLASTX
NCBI GI
                  g2244990
BLAST score
                  2652
E value
                  0.0e+00
                  730
Match length
                  73
% identity
NCBI Description (297340) similarity to LIM homeobox protein -
                  Caenorhabditis [Arabidopsis thaliana]
Seq. No.
                  261311
Contig ID
                  2395 2.R1011
5'-most EST
                  uC-zmflmo17053a01a1
Method
                  BLASTX
NCBI GI
                  g2244990
BLAST score
                  212
E value
                  6.0e-17
Match length
                  44
% identity
                  95
NCBI Description (297340) similarity to LIM homeobox protein -
```

NCBI Description (Z97340) similarity to LIM homeobox p Caenorhabditis [Arabidopsis thaliana]

Seq. No. 261312 Contig ID 2397_1.R1011 5'-most EST LIB3062-011-Q1-K1-F10

 Seq. No.
 261313

 Contig ID
 2401 1.R1011

 5'-most EST
 gwl700618618.h1

 Method
 BLASTY

Method BLASTX NCBI GI g3549666



```
339
BLAST score
                  1.0e-31
E value
                  80
Match length
                  81
% identity
                  (AL031394) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  261314
                  2409_1.R1011
Contig ID
                  dyk7\overline{0}0106501.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4585875
BLAST score
                  885
                   2.0e-95
E value
Match length
                  245
                   67
% identity
                  (AC005850) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   261315
Seq. No.
                   2409 2.R1011
Contig ID
                  uC-zmroB73028b12b1
5'-most EST
                  BLASTX
Method
                   g4585875
NCBI GI
BLAST score
                   390
                   9.0e-38
E value
                   114
Match length
                   62
% identity
NCBI Description
                  (AC005850) Unknown protein [Arabidopsis thaliana]
                   261316
Seq. No.
                   2410 1.R1011
Contig ID
                   uC-zmflB73025h11b2
5'-most EST
Method
                  BLASTX
NCBI GI
                   q1717957
BLAST score
                   1268
E value
                   1.0e-140
Match length
                   273
% identity
                   89
                  UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT
NCBI Description
                   PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP)
                   >gi_100923_pir__A41607 ubiquinol--cytochrome-c reductase
                   (EC 1.10.2.2) iron-sulfur protein precursor - maize
                   >gi 168607 (M77224) Rieske Fe-S protein [Zea mays]
                   261317
Seq. No.
                   2410 2.R1011
Contig ID
5'-most EST
                   uC-zmflmo17068d09a1
Method
                   BLASTX
NCBI GI
                   g1717957
BLAST score
                   233
E value
                   2.0e-19
Match length
                   44
% identity
                   91
                  UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT
NCBI Description
```

36187

PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP)

>gi 168607 (M77224) Rieske Fe-S protein [Zea mays]

>gi_100923_pir__A41607 ubiquinol--cytochrome-c reductase
(EC 1.10.2.2) iron-sulfur protein precursor - maize

BLAST score

E value

1578

1.0e-176



```
261318
       Seq. No.
       Contig ID
                          2416 1.R1011
       5'-most EST
                          LIB3066-052-Q1-K1-B10
       Seq. No.
                          261319
                          2417 1.R1011
       Contig ID
                          rv1700454147.h1
       5'-most EST
       Method
                          BLASTX
       NCBI GI
                          g4539006
       BLAST score
                          219
                          2.0e-17
       E value
       Match length
                          143
       % identity
                          41
                          (AL049481) putative protein [Arabidopsis thaliana]
       NCBI Description
       Seq. No.
                          261320
       Contig ID
                          2424_1.R1011
       5'-most EST
                          uC-zmflmo17238c09b1
                          261321
       Seq. No.
                          2429 1.R1011
       Contig ID
                          wen7\overline{0}0332641.h1
       5'-most EST
                          261322
       Seq. No.
       Contig ID
                          2431 1.R1011
       5'-most EST
                          qmh700027956.f1
                          BLASTX
       Method
       NCBI GI
                          q3236240
       BLAST score
                          562
       E value
                          2.0e-57
       Match length
                          176
                          60
       % identity
       NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]
                          261323
       Seq. No.
Contig ID
5'-most EST
                          2431 2.R1011
                          LIB3150-026-Q1-N1-C8
       Method
                          BLASTX
       NCBI GI
                          g3236240
       BLAST score
                          337
       E value
                          2.0e-31
       Match length
                          87
       % identity
       NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]
       Seq. No.
                          261324
       Contig ID
                          2432 1.R1011
       5'-most EST
                          wen700333391.hl
                          261325
       Seq. No.
       Contig ID
                          2436 1.R1011
       5'-most EST
                          LIB143-030-Q1-E1-C6
       Method
                          BLASTX
                          g3318613
       NCBI GI
```

36188



Match length 353 % identity 88

NCBI Description (AB016064) mitochondrial phosphate transporter [Zea mays]

Seq. No. 261326

Contig ID 2436 3.R1011

5'-most EST uC-zmrob73019a05b1

Method BLASTX
NCBI GI g3318613
BLAST score 790
E value 3.0e-84
Match length 175
% identity 90

NCBI Description (AB016064) mitochondrial phosphate transporter [Zea mays]

Seq. No. 261327

Contig ID 2439 1.R1011 5'-most EST yyf700350287.h1

Method BLASTX
NCBI GI g4106694
BLAST score 2317
E value 0.0e+00
Match length 495
% identity 89

NCBI Description (D85751) glutathione reductase [Oryza sativa]

>gi_4153883_dbj_BAA37092.1_ (AB009592) cytosolic

glutathione reductase [Oryza sativa]

 Seq. No.
 261328

 Contig ID
 2443_1.R1011

 5'-most EST
 fdz701160388.h1

Method BLASTX
NCBI GI g4415926
BLAST score 145
E value 6.0e-09
Match length 76
% identity 42

NCBI Description (AC006282) unknown protein [Arabidopsis thaliana]

Seq. No. 261329

Contig ID 2444 1.R1011

5'-most EST LIB3075-018-Q1-K1-B9

Method BLASTX
NCBI GI g1708462
BLAST score 432
E value 1.0e-42
Match length 140
% identity 58

NCBI Description IAA-AMINO ACID HYDROLASE HOMOLOG 2 PRECURSOR >gi 902791

(U23796) ILL2 [Arabidopsis thaliana]

Seq. No. 261330 Contig ID 2445 1.R1011

5'-most EST LIB3067-002-Q1-K1-G5

Method BLASTX NCBI GI g2979552 BLAST score 778



E value 7.0e-83 Match length 212 % identity 67

NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]

Seq. No. 261331

Contig ID 2447 1.R1011

5'-most EST uC-zmflmo17321c01b1

Method BLASTX
NCBI GI g2499708
BLAST score 4170
E value 0.0e+00
Match length 812
% identity 96

NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)

(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)

>gi_1020409_dbj_BAA11135_ (D73410) phospholipase D [Zea

mays]

Seq. No. 261332

Contig ID 2447_2.R1011

5'-most EST uC-zmflmo17153e02a1

Method BLASTX
NCBI GI g2499708
BLAST score 325
E value 4.0e-30
Match length 61
% identity 98

NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)

(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)

>gi_1020409_dbj_BAA11135_ (D73410) phospholipase D [Zea

mays]

Seq. No. 261333

Contig ID 2447_5.R1011 5'-most EST pmx700091663.h1

Method BLASTN
NCBI GI g1020408
BLAST score 91

E value 1.0e-43 Match length 216 % identity 95

NCBI Description Zea mays mRNA for phospholipase D, complete cds

Seq. No. 261334 Contig ID 2448 1.R1011

5'-most EST LIB3075-018-Q1-K1-C2

Seq. No. 261335

Contig ID 2449_1.R1011

5'-most EST LIB3068-043-Q1-K1-C2

Method BLASTX
NCBI GI g4589852
BLAST score 1645
E value 0.0e+00
Match length 383
% identity 77



```
NCBI Description
                  (AB025968) cycloartenol synthase [Glycyrrhiza glabra]
                   261336
Seq. No.
Contig ID
                   2449 2.R1011
                  wty700168739.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                   q2627181
BLAST score
                   1181
E value
                   1.0e-130
Match length
                   244
                   82
% identity
                  (D89619) cycloartenol synthase [Pisum sativum]
NCBI Description
                   261337
Seq. No.
Contig ID
                   2449 3.R1011
                  nbm700471185.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q3688598
BLAST score
                   217
E value
                  2.0e-17
Match length
                   62
% identity
                   65
                  (AB009029) Cycloartenol Synthase [Panax ginseng]
NCBI Description
Seq. No.
                   261338
                   2450 1.R1011
Contig ID
5'-most EST
                   rv1700457886.h1
Method
                   BLASTX
NCBI GI
                   q4507071
BLAST score
                   446
E value
                   4.0e-44
Match length
                   220
                   39
% identity
NCBI Description
                  SWI/SNF related, matrix associated, actin dependent
                   regulator of chromatin, subfamily a, member 3
                   >gi_1082441_pir__A56095 HIP116 protein - human >gi_531196
                   (L34673) ATPase [Homo sapiens]
Seq. No.
                   261339
Contig ID
                   2451 1.R1011
5'-most EST
                   hbs701184330.h1
Method
                  BLASTX
NCBI GI
                   g3337367
BLAST score
                   231
E value
                   6.0e-19
Match length
                   100
% identity
NCBI Description
                  (AC004481) hypothetical protein [Arabidopsis thaliana]
```

Seq. No. 261340 Contig ID 2451 2

Contig ID 2451_2.R1011 5'-most EST ceu700424991.h1

Seq. No. 261341 Contig ID 2451 3.R1011

5'-most EST LIB3075-017-Q1-K1-H2

Method BLASTN



```
g3821780
NCBI GI
BLAST score
                  36
E value
                  2.0e-10
                  36
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  261342
Seq. No.
                  2451 4.R1011
Contig ID
5'-most EST
                  uC-zmflmo17046c02b1
                  261343
Seq. No.
                  2451 6.R1011
Contig ID
5'-most EST
                  qmh700026978.f1
Method
                  BLASTX
NCBI GI
                  g2982245
BLAST score
                  380
                  3.0e-36
E value
                  135
Match length
                  56
% identity
                 (AF051205) hypothetical protein [Picea mariana]
NCBI Description
                  261344
Seq. No.
                  2451 7.R1011
Contig ID
5'-most EST
                  LIB3068-006-Q1-K1-E4
Seq. No.
                  261345
Contig ID
                  2451 8.R1011
                  uC-zmflmo17305d11a1
5'-most EST
                  261346
Seq. No.
Contig ID
                  2451 9.R1011
5'-most EST
                  LIB3061-004-Q1-K1-E11
                  BLASTX
Method
NCBI GI
                  g2760330
BLAST score
                   253
E value
                   2.0e-21
                  98
Match length
% identity
                   56
NCBI Description (AC002130) F1N21.15 [Arabidopsis thaliana]
Seq. No.
                   261347
                  2454_1.R1011
Contig ID
5'-most EST
                  LIB3075-017-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  g2462911
BLAST score
                   436
```

E value 4.0e-43Match length 153 % identity

(Z83832) UDP-glucose:sterol glucosyltransferase [Avena NCBI Description

sativa]

Seq. No. 261348 Contig ID 2466 1.R1011

5'-most EST LIB3075-017-Q1-K1-F6

Method BLASTX



```
g2827621
NCBI GI
BLAST score
                  526
                  3.0e-53
E value
                  307
Match length
                  38
% identity
                  (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
                  261349
Seq. No.
                  2469 1.R1011
Contig ID
                  uer700580254.h1
5'-most EST
                  BLASTN
Method
NCBI GI
                  q22192
BLAST score
                  61
                  2.0e-25
E value
                  133
Match length
                  87
% identity
                  Z.mays B-I gene for B transcriptional activator
NCBI Description
                   261350
Seq. No.
                  2469 2.R1011
Contig ID
                  uC-zmrob73075d09b1
5'-most EST
Method
                  BLASTX
                   g2764802
NCBI GI
                   995
BLAST score
                   1.0e-108
E value
                   193
Match length
% identity
                   99
                  (X77795) ras-like gene [Zea mays]
NCBI Description
                   261351
Seq. No.
                   2469 3.R1011
Contig ID
                   uC-zmroteosinte095f03b2
5'-most EST
                   BLASTN
Method
                   q722327
NCBI GI
                   133
BLAST score
E value
                   2.0e-68
Match length
                   308
                   92
% identity
                  Zea mays clone Zm-Rab2-B GTP binding protein (rab2) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   261352
                   2469 4.R1011
Contig ID
                   LIB3159-018-Q1-K1-C8
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1346957
BLAST score
                   858
E value
                   1.0e-102
```

Match length 192 % identity

NCBI Description RAS-RELATED PROTEIN RAB-2-B >gi_722328 (U22433) GTP binding

protein [Zea mays]

Seq. No. 261353 2469 6.R1011 Contig ID

5'-most EST uC-zmromo17009e12a1

Method BLASTX



```
g4099090
NCBI GI
BLAST score
                  546
E value
                   2.0e-55
Match length
                  200
% identity
                   50
                  (U83178) unknown [Arabidopsis thaliana]
NCBI Description
                  261354
Seq. No.
Contig ID
                  2469 7.R1011
5'-most EST
                  clt700045010.f1
                  BLASTX
Method
NCBI GI
                  g2130042
BLAST score
                  2479
E value
                  0.0e + 00
                  525
Match length
                  91
% identity
                  Mg-chelatase chain Xantha-f - barley >gi_861199 (U26916)
NCBI Description
                  protoporphyrin IX Mg-chelatase subunit precursor [Hordeum
                  vulgare]
Seq. No.
                   261355
                  2469 8.R1011
Contig ID
                  LIB3136-020-Q1-K1-H8
5'-most EST
                  BLASTN
Method
                  g22192
NCBI GI
BLAST score
                   64
E value
                   2.0e-27
Match length
                  88
                   93
% identity
NCBI Description Z.mays B-I gene for B transcriptional activator
Seq. No.
                   261356
Contig ID
                   2469 9.R1011
                  LIB3150-092-P2-K1-D3
5'-most EST
Method
                   BLASTN
NCBI GI
                   g22192
BLAST score
                   85
                   9.0e-40
E value
Match length
                   126
% identity
NCBI Description Z.mays B-I gene for B transcriptional activator
Seq. No.
                   261357
Contig ID
                   2469 10.R1011
5'-most EST
                   LIB3136-022-Q1-K1-H7
Method
                   BLASTN
NCBI GI
                   g2623247
BLAST score
                   77
E value
                   6.0e-35
Match length
                   105
```

93 % identity

NCBI Description Zea mays SU1 isoamylase (sugary1) gene, complete cds

Seq. No. 261358

2469 11.R1011 Contig ID 5'-most EST fdz701164519.h1

BLASTN Method



```
g3821780
NCBI GI
BLAST score
                  37
                  3.0e-11
E value
                  61
Match length
% identity
                  56
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  261359
Seq. No.
                  2469 14.R1011
Contig ID
5'-most EST
                  uC-zmrob73062a04a1
                  BLASTN
Method
NCBI GI
                  g2623247
BLAST score
                  74
                  2.0e-33
E value
                  118
Match length
                  91
% identity
NCBI Description Zea mays SU1 isoamylase (sugary1) gene, complete cds
                  261360
Seq. No.
                  2469 15.R1011
Contig ID
5'-most EST
                  LIB3059-049-Q1-K1-B9
Method
                  BLASTX
NCBI GI
                  g1346956
BLAST score
                  388
E value
                   3.0e-37
                  93
Match length
% identity
                  84
NCBI Description RAS-RELATED PROTEIN RAB-2-A >gi 722326 (U22432) GTP binding
                  protein [Zea mays]
Seq. No.
                  261361
Contig ID
                  2469 16.R1011
5'-most EST
                  gct701173144.h1
Method
                  BLASTX
                  g642121
NCBI GI
BLAST score
                   364
E value
                  1.0e-34
Match length
                  136
                   60
% identity
NCBI Description (L35845) small GTP-binding protein [Oryza sativa]
Seq. No.
                   261362
Contig ID
                   2469 17.R1011
5'-most EST
                  LIB148-064-Q1-E1-F1
Method
                  BLASTX
NCBI GI
                  g1765896
BLAST score
                   292
E value
                   2.0e-26
Match length
                   56
% identity
NCBI Description (Y09314) Rab2-like protein [Arabidopsis thaliana]
```

Seq. No. 261363

Contig ID 2469 21.R1011 5'-most EST wty700166615.h1

Method BLASTX NCBI GI g2130042



```
BLAST score 158
E value 2.0e-10
Match length 32
% identity 91
```

NCBI Description Mg-chelatase chain Xantha-f - barley >gi_861199 (U26916) protoporphyrin IX Mg-chelatase subunit precursor [Hordeum

vulgare]

Seq. No. 261364

Contig ID 2469_22.R1011 5'-most EST nwy700445402.h1

Method BLASTN
NCBI GI g2764801
BLAST score 172
E value 8.0e-92
Match length 224
% identity 95

NCBI Description Z.mays yptm3 mRNA

Seq. No. 261365

Contig ID 2469_24.R1011 5'-most EST uC-zmflb73210b11b1

Method BLASTX
NCBI GI g2829894
BLAST score 194
E value 1.0e-14
Match length 61
% identity 62

NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No. 261366

Contig ID 2470 1.R1011

5'-most EST LIB3075-016-Q1-K1-H10

Seq. No. 261367

Contig ID 2472_1.R1011

5'-most EST uC-zmflmo17101c01b1

Seq. No. 261368

Contig ID 2472_2.R1011 5'-most EST uC-zmflb73096e11b1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36

% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 261369

Contig ID 2472_3.R1011

5'-most EST LIB3136-002-P1-K1-A3

Seq. No. 261370

Contig ID 2480_1.R1011

5'-most EST uC-zmflb73241g05b2



```
261371
Seq. No.
                  2480 2.R1011
Contig ID
                  uC-zmflb73222b01b1
5'-most EST
                  261372
Seq. No.
Contig ID
                  2480 3.R1011
                  LIB3069-006-Q1-K1-C4
5'-most EST
                  261373
Seq. No.
                  2480 5.R1011
Contig ID
5'-most EST
                  uC-zmflb73088e09b2
                  261374
Seq. No.
Contig ID
                  2481 1.R1011
5'-most EST
                  uC-zmflb73077c05b2
Seq. No.
                  261375
                  2482 1.R1011
Contig ID
                  LIB3075-017-Q1-K1-E2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2072356
BLAST score
                  580
                  5.0e-60
E value
                  146
Match length
                  75
% identity
NCBI Description (U96713) aminoalcoholphosphotransferase [Brassica rapa]
Seq. No.
                  261376
                  2483 1.R1011
Contig ID
5'-most EST
                  uC-zmflB73005a03b1
Method
                  BLASTX
NCBI GI
                  g4467137
BLAST score
                   666
E value
                   8.0e-70
Match length
                  180
                   70
% identity
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
                   261377
Seq. No.
                   2488 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17071d08b1
Method
                  BLASTX
NCBI GI
                   q4539401
BLAST score
                   342
E value
                   1.0e-31
Match length
                   240
% identity
                   54
NCBI Description (AL035526) putative protein [Arabidopsis thaliana]
Seq. No.
                   261378
                   2490 1.R1011
Contig ID
```

 Seq. No.
 261378

 Contig ID
 2490_1.R1011

 5'-most EST
 LIB3079-025-Q1-K1-E1

 Method
 BLASTX

 NCBI GI
 g4589965

NCBI GI g4589965 BLAST score 1051 E value 1.0e-114 Match length 337



% identity (AC007169) putative glyoxalase II [Arabidopsis thaliana] NCBI Description 261379 Seq. No. 2491 1.R1011 Contig ID 5'-most EST LIB3150-052-Q1-N1-H9 Method BLASTX NCBI GI g4165861 BLAST score 735 1.0e-77 E value Match length 356 22 % identity (AF006603) histone deacetylase mHDA2 [Mus musculus] NCBI Description 261380 Seq. No.

Contig ID 2498 1.R1011 5'-most EST LIB3152-015-P1-K1-D1 Method BLASTX NCBI GI g1708463

BLAST score 800 3.0e-85E value Match length 339 47 % identity

NCBI Description IAA-AMINO ACID HYDROLASE >gi 887785 (U23794) ILR1

[Arabidopsis thaliana]

Seq. No. 261381 2498 2.R1011 Contig ID

LIB3066-014-Q1-K1-F9 5'-most EST

Method BLASTX NCBI GI g1708463 BLAST score 537 E value 8.0e-55 Match length 201 50 % identity

NCBI Description IAA-AMINO ACID HYDROLASE >gi 887785 (U23794) ILR1

[Arabidopsis thaliana]

Seq. No. 261382 Contig ID 2500 1.R1011

5'-most EST LIB3059-006-01-K1-G5

Method BLASTX NCBI GI q729704 BLAST score 201 E value 3.0e-15 Match length 97 % identity 7

NCBI Description DNA-BINDING PROTEIN HEXBP (HEXAMER-BINDING PROTEIN)

>gi_1078700_pir__A47156 hexamer-binding protein HEXBP -Leishmania major >gi_159342 (M94390) HEXBP DNA binding

protein [Leishmania major]

Seq. No. 261383 2500 2.R1011 Contig ID

5'-most EST LIB3150-063-P2-K1-D1

Seq. No. 261384



```
Contig ID
                  2502 1.R1011
                  yyf700352560.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1519251
BLAST score
                  925
                  1.0e-100
E value
                  202
Match length
                  91
% identity
                  (U65957) GF14-c protein [Oryza sativa]
NCBI Description
                  261385
Seq. No.
                  2502 2.R1011
Contig ID
5'-most EST
                  rv1700454127.h1
                  BLASTX
Method
                  q1519251
NCBI GI
BLAST score
                   441
E value
                  1.0e-43
                  99
Match length
% identity
                   91
                  (U65957) GF14-c protein [Oryza sativa]
NCBI Description
                   261386
Seq. No.
                   2502 3.R1011
Contig ID
5'-most EST
                  tzu700206126.hl
                  BLASTX
Method
                   g1519251
NCBI GI
BLAST score
                   443
                   4.0e-44
E value
Match length
                   103
% identity
                   87
NCBI Description (U65957) GF14-c protein [Oryza sativa]
                   261387
Seq. No.
Contig ID
                   2503 1.R1011
                   LIB3075-017-Q1-K1-D12
5'-most EST
Method
                   BLASTX
                   q2911067
NCBI GI
                   411
BLAST score
E value
                   2.0e-40
Match length
                   122
% identity
                   70
                  (AL021960) UV-damaged DNA-binding protein-like [Arabidopsis
NCBI Description
                   thaliana]
                   261388
Seq. No.
                   2505 1.R1011
Contig ID
                   uC-zmflmo17175b11b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1335862
                   3640
BLAST score
                   0.0e + 00
E value
Match length
                   898
% identity
                   89
NCBI Description (U42608) clathrin heavy chain [Glycine max]
```

36199

Seq. No.

261389

Contig ID

2505 2.R1011



5'-most EST LIB3088-019-Q1-K1-F4 Method BLASTX g1335862 NCBI GI BLAST score 199 4.0e-15 E value Match length 59 64 % identity (U42608) clathrin heavy chain [Glycine max] NCBI Description Seq. No. 261390 Contig ID 2505 3.R1011 5'-most EST xsy700214964.h1 261391 Seq. No. Contig ID 2505 4.R1011

5'-most EST uC-zmflb73156c06b1 BLASTX Method NCBI GI q1335862

BLAST score 212 E value 1.0e-16 Match length 75 61 % identity

NCBI Description (U42608) clathrin heavy chain [Glycine max]

Seq. No. 261392 2507 1.R1011 Contig ID 5'-most EST uC-zmflb73299f12b1 Method BLASTX

NCBI GI q129916 1799 BLAST score E value 0.0e + 00402 Match length 90 % identity

NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat

>gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase

(AA 1 - 401) [Triticum aestivum]

Seq. No. 261393 2507 2.R1011 Contig ID 5'-most EST uC-zmflb73221a10b1

Seq. No. 261394 Contig ID 2507 3.R1011

5'-most EST LIB3059-036-Q1-K1-E2

Seq. No. 261395 Contig ID 2507 4.R1011

5'-most EST LIB3279-052-P1-K1-D3

Seq. No. 261396 2507 5.R1011 Contig ID

5'-most EST LIB3079-003-Q1-K1-F7

Seq. No. 261397 Contig ID 2507 7.R1011 5'-most EST pmx700085449.h1



Seq. No.

261398

Contig ID

2507 9.R1011

5'-most EST

LIB3150-084-P2-N2-C11

Seq. No.

261399

Contig ID 5'-most EST

2507 11.R1011 wty700169321.h1

Seq. No.

261400

Contig ID

2507 14.R1011

5'-most EST

LIB3060-011-Q1-K1-A10

Method NCBI GI BLASTX q129916

BLAST score E value

380

Match length

6.0e-44 117

% identity

83

NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi 66911 pir TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase (AA 1 - 401) [Triticum aestivum]

Seq. No.

261401

Contig ID 5'-most EST 2507 15.R1011 tfd700574401.hl

Seq. No.

261402

Contig ID

2507 17.R1011

5'-most EST

uC-zmflb73181g04b2

Seq. No.

261403

Contig ID

2507 18.R1011

5'-most EST

LIB3079-043-Q1-K2-C3

Seq. No.

261404

Contig ID

2507 22.R1011

5'-most EST

LIB3079-021-Q1-K1-H6

Seq. No.

261405

Contig ID

2507 23.R1011

5'-most EST

LIB3078-033-Q1-K1-G2

Seq. No.

261406

Contig ID

2507 27.R1011 ymt700218586.h1

5'-most EST

Seq. No.

261407

Contig ID

2507 29.R1011 wty700163015.h1

5'-most EST

Seq. No.

261408

Contig ID

2507 31.R1011

5'-most EST

 $uC-z\overline{m}flmo17320b03a1$

Seq. No.

261409

Contig ID

2507 32.R1011



ypc700805505.h1 5'-most EST BLASTX Method NCBI GI g2257598 BLAST score 217 E value 2.0e-17 Match length 89 % identity 56 NCBI Description (AB005551) phosphoglycerate kinase [Robinia pseudoacacia] Seq. No. 261410 2507 33.R1011 Contig ID 5'-most EST LIB3059-026-Q1-K1-E2 Seq. No. 261411 Contig ID 2507 34.R1011 5'-most EST cjh700194794.h1 261412 Seq. No. 2509 1.R1011 Contig ID 5'-most EST LIB3180-049-P2-M1-C8 261413 Seq. No. Contig ID 2509 2.R1011 5'-most EST LIB3066-018-Q1-K1-G6 Seq. No. 261414 Contig ID 2511 1.R1011 5'-most EST LIB3075-017-Q1-K1-E1 Method BLASTX NCBI GI g2250699 BLAST score 793 E value 1.0e-84 Match length 299 53 % identity NCBI Description (AB001517) PWP2 protein [Homo sapiens] Seq. No. 261415 Contig ID 2513 1.R1011 5'-most EST LIB3075-017-Q1-K1-A7 Seq. No. 261416 Contig ID 2515 1.R1011 5'-most EST LIB84-024-Q1-E1-C6 Method BLASTX NCBI GI g4581156 BLAST score 321 E value 2.0e-29 Match length 153 % identity 41 NCBI Description (AC006919) putative pyruvate kinase [Arabidopsis thaliana]

Seq. No. 261417

Contig ID 2523 1.R1011 5'-most EST uC-zmflb73013g12b1

Method BLASTX NCBI GI g2370461 BLAST score 244



E value 4.0e-40 Match length 102 % identity 80

NCBI Description (Y14675) putative glycoprotein [Sorghum bicolor]

Seq. No. 261418

Contig ID 2523 2.R1011

5'-most EST LIB3150-086-P2-N2-D5

Seq. No. 261419

Contig ID 2523 3.R1011

5'-most EST LIB3069-020-Q1-K1-H4

Method BLASTN
NCBI GI g2370460
BLAST score 152
E value 8.0e-80
Match length 202
% identity 95

NCBI Description Sorghum bicolor mRNA for putative glycoprotein

Seq. No. 261420

Contig ID 2527 1.R1011

5'-most EST LIB3\(\bar{1}\)37-020-Q1-K1-H11

Method BLASTX
NCBI GI g4325345
BLAST score 346
E value 2.0e-32
Match length 100
% identity 66

NCBI Description (AF128393) similar to thioredoxin-like proteins (Pfam:

PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42,

N=1) [Arabidopsis thaliana]

Seq. No. 261421

Contig ID 2527_2.R1011

5'-most EST LIB3075-016-Q1-K1-F12

Method BLASTX
NCBI GI g4325345
BLAST score 158
E value 1.0e-10
Match length 49
% identity 57

NCBI Description (AF128393) similar to thioredoxin-like proteins (Pfam:

PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42,

N=1) [Arabidopsis thaliana]

Seq. No. 261422

Contig ID 2532 1.R1011 5'-most EST wyr700240989.h1

Seq. No. 261423

Contig ID 2532 2.R1011 5'-most EST zla700380656.h1

Seq. No. 261424



2533 1.R1011 Contig ID LIB3075-016-Q1-K1-H11 5'-most EST BLASTX Method NCBI GI q4406769 BLAST score 649 8.0e-68 E value 206 Match length 63 % identity (AC006836) putative translin [Arabidopsis thaliana] NCBI Description Seq. No. 261425 Contig ID 2534 1.R1011 5'-most EST uC-zmflmo17176b07b1 261426 Seq. No. 2534 2.R1011 Contig ID 5'-most EST LIB3075-016-Q1-K1-H9 261427 Seq. No. 2536 1.R1011 Contig ID uC-zmflmo17330f04b1 5'-most EST Method BLASTX NCBI GI g2632254 BLAST score 1063 1.0e-116 E value Match length 306 67 % identity (Y12465) serine/threonine kinase [Sorghum bicolor] NCBI Description 261428 Seq. No. 2536 2.R1011 Contig ID 5'-most EST uC-zmrob73054b09a1 Method BLASTX NCBI GI q2632254 708 BLAST score E value 1.0e-74Match length 216 % identity 66 (Y12465) serine/threonine kinase [Sorghum bicolor] NCBI Description Seq. No. 261429 Contig ID 2536 3.R1011 uC-zmflb73014d11b1 5'-most EST Method BLASTX NCBI GI q2632252 BLAST score 421 E value 5.0e-41Match length 134 % identity 60

NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No. 261430 2537 1.R1011 Contig ID xyt700343007.h1 5'-most EST

Seq. No. 261431 Contig ID 2538 1.R1011



```
5'-most EST
                  LIB3075-017-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  q120507
BLAST score
                  1151
                  1.0e-126
E value
                  277
Match length
                  83
% identity
                  FERRITIN 1 PRECURSOR >gi_82687_pir__S22498 ferritin
NCBI Description
                  precursor (clone FM1) - maize (fragment)
                  >gi 22276_emb_CAA43663_ (X61391) ferritin [Zea mays]
                  261432
Seq. No.
Contig ID
                  2538 2.R1011
                  uC-zmflMo17016b07b1
5'-most EST
                  BLASTX
Method
                  g2342477
NCBI GI
BLAST score
                  278
                   4.0e-24
E value
Match length
                  117
                   49
% identity
                  (AB006679) ATP binding protein [Homo sapiens]
NCBI Description
                   261433
Seq. No.
Contig ID
                   2538 3.R1011
                  uC-zmflb73244f04a1
5'-most EST
                   261434
Seq. No.
                   2538 4.R1011
Contig ID
5'-most EST
                   LIB3078-053-Q1-K1-E4
Method
                   BLASTX
                   q120510
NCBI GI
                   567
BLAST score
                   1.0e-79
E value
Match length
                   161
                   98
% identity
NCBI Description FERRITIN 2 PRÉCURSOR >gi_82688_pir__S24057 ferritin
                   precursor (clone FM2) - maize >gi 22278_emb_CAA43664_
                   (X61392) ferritin [Zea mays]
                   261435
Seq. No.
                   2538 5.R1011
Contig ID
                   uC-zmflb73193a01a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2130128
                   262
BLAST score
                   1.0e-22
E value
                   88
Match length
                   66
% identity
NCBI Description ferritin 2 precursor - maize >gi_1103630_emb_CAA58147_
                   (X83077) ferritin [Zea mays]
                   261436
Seq. No.
```

2538 6.R1011 Contig ID uC-zmflmo17248c07a1 5'-most EST

BLASTX Method

q2130128 NCBI GI 347 BLAST score

BLAST score

E value Match length 1.0e-145



```
E value
                  9.0e-33
Match length
                  77
                  90
% identity
                  ferritin 2 precursor - maize >gi_1103630_emb_CAA58147_
NCBI Description
                   (X83077) ferritin [Zea mays]
Seq. No.
                  261437
                  2538 7.R1011
Contig ID
                  uC-zmflmo17368h05a1
5'-most EST
                  BLASTX
Method
                  q2130128
NCBI GI
BLAST score
                  407
                  9.0e-40
E value
Match length
                  84
% identity
                  96
                  ferritin 2 precursor - maize >gi_1103630_emb_CAA58147_
NCBI Description
                   (X83077) ferritin [Zea mays]
                  261438
Seq. No.
                  2538 9.R1011
Contig ID
                  LIB143-056-Q1-E1-D10
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2130127
BLAST score
                   525
                  1.0e-53
E value
Match length
                  110
                   93
% identity
                  ferritin 1 precursor - maize >gi_1103628 emb_CAA58146
NCBI Description
                   (X83076) ferritin [Zea mays]
                   261439
Seq. No.
                   2538 12.R1011
Contig ID
                   wyr700244294.h1
5'-most EST
                   261440
Seq. No.
                   2541 1.R1011
Contig ID
                   LIB148-063-Q1-E1-E8
5'-most EST
Method
                   BLASTX
                   g2135800
NCBI GI
                   186
BLAST score
                   2.0e-13
E value
                   193
Match length
                   27
% identity
NCBI Description nerve terminal protein - human >gi_307426 (L19760) nerve
                   terminal protein [Homo sapiens] >gi_521174 (L09253) this
                   product utilizes exon 5a [Gallus gallus]
                   >gi_2116628_dbj_BAA20151_ (AB003991) SNAP-25A [Rattus
                   rattus]
Seq. No.
                   261441
                   2544 1.R1011
Contiq ID
                   cyk700051677.f1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3046731
                   1199
```



```
% identity
                  (AJ005373) protein kinase [Craterostigma plantagineum]
NCBI Description
                  261442
Seq. No.
                  2551 1.R1011
Contig ID
                  LIB148-064-Q1-E1-G12
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3420055
BLAST score
                  592
                  5.0e-61
E value
                  180
Match length
                  67
% identity
                 (AC004680) cyclophilin [Arabidopsis thaliana]
NCBI Description
                  261443
Seq. No.
                  2551 4.R1011
Contig ID
                  LIB148-039-Q1-E1-B8
5'-most EST
                  BLASTX
Method
                  g3420055
NCBI GI
BLAST score
                  293
E value
                  2.0e-26
                  72
Match length
                  75
% identity
NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]
Seq. No.
                  261444
Contig ID
                  2555 1.R1011
                  LIB3075-016-Q1-K1-A12
5'-most EST
                  261445
Seq. No.
                  2560 1.R1011
Contig ID
                  LIB3079-033-Q1-K1-A2
5'-most EST
Method
                  BLASTX
                  q2342735
NCBI GI
                  404
BLAST score
E value
                   6.0e-39
Match length
                  127
% identity
NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]
                   261446
Seq. No.
Contig ID
                   2563 1.R1011
5'-most EST
                   pmx700084731.h1
                   BLASTX
Method
NCBI GI
                   g136140
BLAST score
                   778
E value
                   5.0e-83
                   236
Match length
% identity
                   61
                  PUTATIVE AC9 TRANSPOSASE >gi_72973 pir TQZMCA probable
NCBI Description
                   transposase - maize transposon Ac9
Seq. No.
                   261447
```

Contig ID 2565_1.R1011 5'-most EST wyr700241489.h1

Method BLASTX NCBI GI g1652572



BLAST score 173 E value 7.0e-12 Match length 175 % identity 33 NCBI Description (D90906

NCBI Description (D90906) hypothetical protein [Synechocystis sp.]

Seq. No. 261448 Contig ID 2567_1.R1011

5'-most EST uC-zmflb73127h06b2

Method BLASTX
NCBI GI g2224663
BLAST score 1459
E value 1.0e-162
Match length 578
% identity 52

NCBI Description (AB002359) KIAA0361 [Homo sapiens]

Seq. No. 261449 Contig ID 2567 2.R1011

5'-most EST fC-zmle700432067r2

Seq. No. 261450

Contig ID 2568_1.R1011

5'-most EST LIB3075-016-Q1-K1-A10

Method BLASTX
NCBI GI g2827631
BLAST score 399
E value 8.0e-39
Match length 104
% identity 70

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 261451 Contig ID 2571_1.R1011

5'-most EST LIB3150-002-Q1-N1-G4

Method BLASTX
NCBI GI 94510356
BLAST score 872
E value 9.0e-94
Match length 386
% identity 44

NCBI Description (AC006921) putative kinesin-related protein TKRP125

[Arabidopsis thaliana]

Seq. No. 261452 Contig ID 2574_1.R1011

5'-most EST LIB148-023-Q1-E1-G4

Seq. No. 261454 Contig ID 2580_1.R1011

5'-most EST LIB $3\overline{0}$ 75-015-Q1-K1-F9

Seq. No. 261455



```
2582 1.R1011
Contig ID
                  LIB3075-015-Q1-K1-G4
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4510348
BLAST score
                  181
E value
                  3.0e-13
Match length
                  73
% identity
                  48
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
                  261456
Seq. No.
                  2583 1.R1011
Contiq ID
5'-most EST
                  LIB3075-015-Q1-K1-E7
Seq. No.
                  261457
Contig ID
                  2586 1.R1011
                  LIB3059-028-Q1-K1-A11
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3912919
BLAST score
                  406
E value
                  2.0e-39
Match length
                  149
% identity
                  58
NCBI Description (AF001308) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  261458
                  2587 1.R1011
Contig ID
                  LIB3076-019-Q1-K1-F1
5'-most EST
Method
                  BLASTX
                  g126066
NCBI GI
BLAST score
                  991
E value
                  1.0e-108
Match length
                  201
% identity
                  100
NCBI Description L-LACTATE DEHYDROGENASE (LDH) >gi_82704_pir__S22492
                  L-lactate dehydrogenase (EC 1.1.1.27) chain Ldh1 - maize
                  >gi 22353 emb CAA77808 (Z11754) lactate dehydrogenase [Zea
                  mays]
                  261459
Seq. No.
                  2588 1.R1011
Contig ID
5'-most EST
                  LIB3066-009-Q1-K1-A6
                  261460
Seq. No.
```

Contig ID 2590_1.R1011

5'-most EST LIB3075-015-Q1-K1-E10

Method BLASTX
NCBI GI g2498731
BLAST score 456
E value 2.0e-45
Match length 156
% identity 53

NCBI Description PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1

>gi_1362013_pir__S57611 zeta-crystallin homolog Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)

zeta-crystallin homologue [Arabidopsis thaliana]



```
Seq. No.
                    261461
 Contig ID
                    2593 1.R1011
 5'-most EST
                    LIB3076-006-01-K1-F4
 Method
                    BLASTX
 NCBI GI
                    q1877397
 BLAST score
                    195
 E value
                    8.0e-15
 Match length
                    51
 % identity
                    67
 NCBI Description
                    (Y11591) shaggy-like kinase [Ricinus communis]
 Seq. No.
                    261462
 Contig ID
                    2597 1.R1011
 5'-most EST
                    zuv700356023.h1
 Method
                    BLASTX
 NCBI GI
                    q3297809
 BLAST score
                    170
 E value
                    6.0e-12
 Match length
                    118
 % identity
                    37
 NCBI Description (AL031032) putative protein [Arabidopsis thaliana]
 Seq. No.
                    261463
... Contig ID
                    2600 1.R1011
 5'-most EST
                    LIB3075-015-Q1-K1-B7
 Seq. No.
                    261464
                    2601 1.R1011
 Contig ID
 5'-most EST
                    uC-zmflmo17125a11b1
 Method
                    BLASTX
 NCBI GI
                    g4539423
 BLAST score
                    1426
 E value
                    0.0e+00
 Match length
                    422
 % identity
                    80
 NCBI Description
                     (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
                     [Arabidopsis thaliana]
 Seq. No.
                    261465
 Contig ID
                    2602 1.R1011
 5'-most EST
                    LIB3075-015-Q1-K1-B9
 Seq. No.
                    261466
 Contig ID
                    2604 1.R1011
 5'-most EST
                    cyk700049985.f1
 Method
                    BLASTX
 NCBI GI
                    g2829870
 BLAST score
                    219
 E value
                    6.0e-28
```

Match length 96 % identity

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 261467 2607 1.R1011 Contig ID

5'-most EST LIB148-057-Q1-E1-E3



261468 Seq. No.

Contig ID 2609 1.R1011 5'-most EST pmx700091447.h1

BLASTX Method g3702336 NCBI GI BLAST score 562 6.0e-58E value Match length 151 72 % identity

NCBI Description (AC005397) putative 3-methyl-2-oxobutanoate

hydroxy-methyl-transferase [Arabidopsis thaliana]

261469 Seq. No.

2610 1.R1011 Contig ID

LIB3069-008-Q1-K1-C6 5'-most EST

BLASTX Method NCBI GI q1176658 BLAST score 271 9.0e-33 E value 179 Match length 48 % identity

HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II NCBI Description

>gi 726363 (U23168) No definition line found

[Caenorhabditis elegans]

Seq. No. 261470

Contig ID 2613 1.R1011

5'-most EST uC-zmflb73284b07a1

Method BLASTX NCBI GI g927428 BLAST score 2268 E value 0.0e+00Match length 552

76 % identity

NCBI Description (X86733) fis1 [Linum usitatissimum]

Seq. No. 261471

2616_1.R1011 Contig ID

5'-most EST LIB3075-015-Q1-K1-A2

Method BLASTX NCBI GI q4218011 BLAST score 517 E value 2.0e-52 Match length 186 52 % identity

(AC006135) putative protein kinase [Arabidopsis thaliana] NCBI Description

>gi_4309721_gb_AAD15491_ (AC006439) putative
serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 261472

2617 1.R1011 Contig ID

5'-most EST uC-zmrob73066b05b1

Method BLASTX NCBI GI g4417280 BLAST score 681 2.0e-71 E value Match length 243

E value

Match length

4.0e-10

61



% identity NCBI Description (AC007019) putative ATP synthase [Arabidopsis thaliana] 261473 Seq. No. Contig ID 2617 2.R1011 5'-most EST uC-zmflb73208d05b1 BLASTX Method NCBI GI g1084358 351 BLAST score 1.0e-46 E value Match length 172 % identity 62 NCBI Description ATP synthase - soybean 261474 Seq. No. 2619 1.R1011 Contig ID uC-zmflmo17269d10b15'-most EST Method BLASTX g1657382 NCBI GI BLAST score 1012 1.0e-110 E value Match length 248 % identity 75 (Y09101) cholinephosphate cytidylyltransferase [Pisum NCBI Description sativum] Seq. No. 261475 2621 1.R1011 Contig ID 5'-most EST LIB3180-002-P1-M1-B1 Method BLASTX NCBI GI g1699370 BLAST score 1321 E value 1.0e-146 Match length 471 55 % identity NCBI Description (S82620) prolidase=peptidase D/imidopeptidase {EC 3.4.13.9} [mice, liver, Peptide, 493 aa] [Mus sp.] Seq. No. 261476 2624 1.R1011 Contig ID 5'-most EST xjt700096937.h1 Method BLASTX NCBI GI g4204260 BLAST score 167 E value 5.0e-11 Match length 61 % identity 54 NCBI Description (AC005223) 25568 [Arabidopsis thaliana] 261477 Seq. No. Contig ID 2624 2.R1011 5'-most EST LIB3061-056-Q1-K1-H9 Method BLASTX NCBI GI g4204260 BLAST score 160

% identity NCBI Description (AC005223) 25568 [Arabidopsis thaliana] Seq. No. 261478 Contig ID 2624 4.R1011 5'-most EST uC-zmflb73160d02a1 Seq. No. 261479 Contig ID 2628 1.R1011 5'-most EST LIB3137-057-Q1-K1-A6 Method BLASTX NCBI GI q549063 BLAST score 661 E value 4.0e-69 Match length 167 74 % identity TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) NCBI Description >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi 303835 dbj BAA02151 (D12626) 21kd polypeptide [Oryza sativa] 261480 Seq. No. 2628_2.R1011 Contig ID 5'-most EST LIB3067-060-Q1-K1-H4 Method BLASTX NCBI GI q451193 BLAST score 1012 E value 1.0e-110 Match length 222 % identity NCBI Description (L28008) wali7 [Triticum aestivum] >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum] Seq. No. 261481 Contig ID 2628 3.R1011 5'-most EST LIB3150-038-Q1-N1-E3 Method BLASTX NCBI GI g549063 BLAST score 486

Method BLASTX
NCBI GI g549063
BLAST score 486
E value 8.0e-49
Match length 130
% identity 71

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 261482

Contig ID 2628 4.R1011

5'-most EST LIB3059-042-Q1-K1-G1

Method BLASTX
NCBI GI g451193
BLAST score 1012
E value 1.0e-110
Match length 222
% identity 89

NCBI Description (L28008) wali7 [Triticum aestivum]



>gi 1090845 prf 2019486B wali7 gene [Triticum aestivum]

Seq. No. 261483

Contig ID 2628 5.R1011

5'-most EST LIB3059-032-Q1-K1-A10

Method BLASTX NCBI GI q4193388 BLAST score 188 7.0e-18 E value 64 Match length 75 % identity

(AF091455) translationally controlled tumor protein [Hevea NCBI Description

brasiliensis]

Seq. No. 261484

2628 6.R1011 Contig ID

5'-most EST LIB3067-004-Q1-K1-B3

BLASTX Method g549063 NCBI GI BLAST score 650 6.0e-68 E value Match length 167 % identity 72

TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) NCBI Description

>gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi 303835 dbj BAA02151 (D12626)

21kd polypeptide [Oryza sativa]

261485 Seq. No. 2628 7.R1011 Contig ID

LIB3150-014-Q1-N1-B8 5'-most EST

Method BLASTX NCBI GI g2827656 BLAST score 492 5.0e-49E value Match length 331

% identity 44

NCBI Description (AL021637) DAG-like protein [Arabidopsis thaliana]

261486 Seq. No.

2628 8.R1011 Contig ID

5'-most EST LIB3078-020-Q1-K1-B4

Method BLASTX NCBI GI g549063 BLAST score 335 7.0e-40E value Match length 129 % identity 73

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

> >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 261487

Contig ID 2628 11.R1011

5'-most EST LIB3156-001-Q1-K1-A1



```
Seq. No.
                  261488
                  2628 12.R1011
Contig ID
5'-most EST
                  LIB3059-040-Q1-K1-A5
Method
                  BLASTX
                  g2970051
NCBI GI
                  211
BLAST score
E value
                  1.0e-16
                  51
Match length
                  76
% identity
                  (AB012110) ARG10 [Vigna radiata]
NCBI Description
Seq. No.
                  261489
                  2628 13.R1011
Contig ID
                  uC-zmflb73247a05b3
5'-most EST
Method
                  BLASTX
NCBI GI
                   q451193
BLAST score
                   391
E value
                  7.0e-38
Match length
                   111
% identity
                  75
                  (L28008) wali7 [Triticum aestivum]
NCBI Description
                  >gi 1090845 prf 2019486B wali7 gene [Triticum aestivum]
                   261490
Seq. No.
                   2628 14.R1011
Contig ID
                  uC-zmflb73233h01b1
5'-most EST
Seq. No.
                  261491
                   2628 15.R1011
Contig ID
                   uC-zmflm017233e07b1
5'-most EST
Method
                   BLASTX
                   g451193
NCBI GI
BLAST score
                   220
                   8.0e-18
E value
                   56
Match length
                   80
% identity
                   (L28008) wali7 [Triticum aestivum]
NCBI Description
                   >gi 1090845 prf 2019486B wali7 gene [Triticum aestivum]
                   261492
Seq. No.
                   2628 16.R1011
Contig ID
5'-most EST
                   fdz701164336.h1
                   261493
Seq. No.
                   2628 18.R1011
Contig ID
5'-most EST
                   uC-zmflmo17151f09b1
Method
                   BLASTX
NCBI GI
                   q549063
```

Method BLASTX
NCBI GI g549063
BLAST score 286
E value 3.0e-25
Match length 93
% identity 61

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)

21kd polypeptide [Oryza sativa]



```
Seq. No.
                  261494
                  2628 29.R1011
Contig ID
5'-most EST
                  uC-zmflb73276e06a1
                  261495
Seq. No.
                  2628 30.R1011
Contig ID
5'-most EST
                  uC-zmflmo17221a11b1
                  261496
Seq. No.
                  2628 33.R1011
Contig ID
                  vux700157633.hl
5'-most EST
                  BLASTX
Method
                  g2970051
NCBI GI
BLAST score
                  281
                  7.0e-25
E value
Match length
                  70
                  79
% identity
                 (AB012110) ARG10 [Vigna radiata]
NCBI Description
Seq. No.
                  261497
                  2628 37.R1011
Contig ID
                  xyt700342682.hl
5'-most EST
                  261498
Seq. No.
                  2632 1.R1011
Contig ID
                  LIB3066-018-Q1-K1-G10
5'-most EST
Seq. No.
                   261499
                  2635 1.R1011
Contig ID
                  xsy700217693.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4006924
                   1107
BLAST score
E value
                   1.0e-121
                   487
Match length
                   45
% identity
                  (Z99708) beta-galactosidase like protein [Arabidopsis
NCBI Description
                   thaliana]
                   261500
Seq. No.
                   2635 2.R1011
Contig ID
5'-most EST
                   uC-zmflb73214b10a1
Method
                   BLASTX
NCBI GI
                   g4006924
                   209
BLAST score
E value
                   2.0e-16
Match length
                   74
% identity
                   47
                  (Z99708) beta-galactosidase like protein [Arabidopsis
NCBI Description
                   thaliana]
```

 Seq. No.
 261501

 Contig ID
 2637_1.R1011

 5'-most EST
 LIB3066-031-Q1-K1-A9

 Method
 BLASTX

Method BLASTX NCBI GI g4262250 BLAST score 1617



E value 0.0e+00 Match length 364 % identity 85

NCBI Description (AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No. 261502

Contig ID 2642_1.R1011 5'-most EST pmx700086842.h1

Method BLASTX
NCBI GI g585417
BLAST score 385
E value 7.0e-63
Match length 239
% identity 50

NCBI Description LIPOXYGENASE 1 >gi_629724_pir__S44940 lipoxygenase (EC

1.13.11.12) - potato >gi 486619_emb_CAA55724_ (X79107)

lipoxygenase [Solanum tuberosum]

Seq. No. 261503 Contig ID 2643_1.R1011

5'-most EST LIB3150-092-P1-N1-C7

Method BLASTX
NCBI GI g300265
BLAST score 702
E value 3.0e-74
Match length 172
% identity 81

NCBI Description HSP68=68 kda heat-stress DnaK homolog [Lycopersicon

peruvianum=tomatoes, Peptide Mitochondrial Partial, 580 aa]

Seq. No. 261504

Contig ID 2648_1.R1011

5'-most EST uC-zmflmo17183e10a1

Seq. No. 261505

Contig ID 2650_1.R1011 5'-most EST xtj700377851.h1

Method BLASTX
NCBI GI g3924823
BLAST score 282
E value 1.0e-24
Match length 142
% identity 40

NCBI Description (Z83113) cDNA EST yk491a11.5 comes from this gene; cDNA EST

yk491a11.3 comes from this gene [Caenorhabditis elegans]

Seq. No. 261506 Contig ID 2650_2.R1011

5'-most EST LIB3116-001-Q1-K1-C8

Seq. No. 261507 Contig ID 2650 3.R1011

5'-most EST LIB3152-044-P1-K1-B1

Method BLASTX
NCBI GI g3924823
BLAST score 176
E value 2.0e-12



Match length 56 55 % identity (Z83113) cDNA EST yk491a11.5 comes from this gene; cDNA EST NCBI Description yk491a11.3 comes from this gene [Caenorhabditis elegans] 261508 Seq. No. 2650 4.R1011 Contig ID uC-zmflb73089a11a15'-most EST 261509 Seq. No. 2653 1.R1011 Contig ID xjt700092738.h1 5'-most EST 261510 Seq. No. 2657 1.R1011 Contig ID uC-zmflb73163d04b2 5'-most EST BLASTX Method NCBI GI q4204265 BLAST score 672 1.0e-70 E value Match length 171 70 % identity (AC005223) 45643 [Arabidopsis thaliana] NCBI Description Seq. No. 261511 2662 1.R1011 Contig ID vmt700222350.h1 5'-most EST BLASTX Method q2462828 NCBI GI 783 BLAST score E value 4.0e-88 280 Match length % identity 58 NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana] Seq. No. 261512 Contig ID 2662 2.R1011 5'-most EST rv1700456654.h1 Method BLASTX NCBI GI q2462828 BLAST score 481 E value 3.0e-48Match length 136 % identity NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 261513

Contig ID 2663_1.R1011

5'-most EST LIB148-025-Q1-E1-H9

Seq. No. 261514 Contig ID 2669 1.R1011

5'-most EST LIB3066-042-Q1-K1-G12

 Seq. No.
 261515

 Contig ID
 2669 2.R1011

 5'-most EST
 LIB148-039-Q1-E1-H1



```
Method
                  BLASTX
NCBI GI
                  q2792238
BLAST score
                   299
E value
                   9.0e-27
Match length
                  181
                   38
% identity
NCBI Description (AF032697) NBS-LRR type resistance protein [Oryza sativa]
Seq. No.
                   261516
Contig ID
                  2670 1.R1011
5'-most EST
                  uC-zmflb73256c01b1
                  BLASTN
Method
NCBI GI
                  q902585
BLAST score
                  59
E value
                   5.0e-24
Match length
                  71
                   96
% identity
NCBI Description Zea mays clone MubG9 ubiquitin gene, complete cds
Seq. No.
                   261517
Contig ID
                   2670 2.R1011
5'-most EST
                   xsy700207975.hl
Method
                  BLASTX
NCBI GI
                   q4314369
BLAST score
                   151
E value
                   4.0e-09
Match length
                   91
                   48
% identity
NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   261518
                   2671 1.R1011
Contig ID
                   LIB3075-013-Q1-K1-H9
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4455182
BLAST score
                   189
E value
                   2.0e-14
                   71
Match length
% identity
NCBI Description (AL035521) putative protein [Arabidopsis thaliana]
Seq. No.
                   261519
                   2674 1.R1011
Contig ID
5'-most EST
                   LIB148-019-Q1-E1-D12
Seq. No.
                   261520
                   2678 1.R1011
Contig ID
                   rv1700458338.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2960216
BLAST score
                   1541
E value
                   1.0e-172
```

Match length 375 78 % identity

NCBI Description (AJ223384) 26S proteasome regulatory ATPase subunit 10b

(S10b) [Manduca sexta]



```
261521
Seq. No.
                  2678 2.R1011
Contig ID
                  hbs701181082.h1
5'-most EST
                  BLASTX
Method
                  g3122625
NCBI GI
                  148
BLAST score
                  3.0e-09
E value
                  40
Match length
                  70
% identity
                  PROBABLE 26S PROTEASE REGULATORY SUBUNIT S10B >gi 2394434
NCBI Description
                   (AF024493) strong similarity to the AAA family of ATPases
                   [Caenorhabditis elegans]
                   261522
Seq. No.
                  2678 3.R1011
Contig ID
                  uC-z\overline{m}flb73278c01a2
5'-most EST
                   261523
Seq. No.
                   2681 1.R1011
Contig ID
                   uC-zmroteosinte109e02b3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4455181
                   460
BLAST score
                   1.0e-45
E value
                   150
Match length
                   57
% identity
NCBI Description
                 (AL035521) putative protein [Arabidopsis thaliana]
                   261524
Seq. No.
                   2682 1.R1011
Contig ID
                   LIB3150-032-Q1-N1-D3
5'-most EST
                   BLASTX
Method
                   g4455201
NCBI GI
BLAST score
                   601
                   6.0e-62
E value
                   260
Match length
% identity
                   51
NCBI Description (AL035440) grpE like protein [Arabidopsis thaliana]
Seq. No.
                   261525
                   2683 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73166b02b2
                   BLASTX
Method
                   q2735008
NCBI GI
                   2364
BLAST score
                   0.0e + 00
E value
Match length
                   499
% identity
NCBI Description (U81960) kinase associated protein phosphatase [Zea mays]
```

Seq. No. 261526 Contig ID 2684 1.R1011

5'-most EST xmt700264585.h1

Method BLASTX
NCBI GI g1781299
BLAST score 170
E value 3.0e-11



Match length 88 % identity 43

NCBI Description (Y09506) transformer-SR ribonucleoprotein [Nicotiana

tabacum]

Seq. No. 261527

Contig ID 2684_2.R1011

5'-most EST LIB3061-006-Q1-K1-H8

Seq. No. 261528

Contig ID 2685_1.R1011

5'-most EST LIB3067-052-Q1-K1-A10

Method BLASTX
NCBI GI g3219937
BLAST score 538
E value 1.0e-54
Match length 263
% identity 47

NCBI Description HYPOTHETICAL 35.1 KD PROTEIN C57A10.07 IN CHROMOSOME I

>gi_2058374_emb_CAB08170_ (Z94864) hypothetical protein

[Schizosaccharomyces pombe]

 Seq. No.
 261529

 Contig ID
 2686_1.R1011

 5'-most EST
 uwc700150524.h1

 Method
 BLASTX

NCBI GI g2674203 BLAST score 217 E value 2.0e-17 Match length 119 % identity 41

NCBI Description (AF036328) CLP protease regulatory subunit CLPX

[Arabidopsis thaliana]

Seq. No. 261530 Contig ID 2686 2.R1011

5'-most EST uC-zmflmo17161c10b1

Method BLASTX
NCBI GI g2674203
BLAST score 739
E value 2.0e-78
Match length 210

% identity 66

NCBI Description (AF036328) CLP protease regulatory subunit CLPX

[Arabidopsis thaliana]

Seq. No. 261531

Contig ID 2690 1.R1011

5'-most EST LIB3075-013-Q1-K1-G4

Seq. No. 261532

Contig ID 2705 1.R1011

5'-most EST uC-zmflmo17126e05b1

Seq. No. 261533

Contig ID 2705_2.R1011

5'-most EST LIB3075-013-Q1-K1-E12

Seq. No.

Contig ID

5'-most EST

261540

2710 1.R1011

LIB3069-011-Q1-K1-C5



261534 Seq. No. Contig ID 2706 1.R1011 uC-zmflb73349b01a2 5'-most EST BLASTX Method q2708737 NCBI GI BLAST score 670 6.0e-70 E value 317 Match length % identity 45 (AC003952) putative nuclear protein [Arabidopsis thaliana] NCBI Description Seq. No. 261535 2706 2.R1011 Contig ID 5'-most EST LIB3062-057-Q1-K1-E1 Method BLASTX q2708737 NCBI GI BLAST score 213 E value 1.0e-16 Match length 137 % identity 34 (AC003952) putative nuclear protein [Arabidopsis thaliana] NCBI Description 261536 Seq. No. 2706 3.R1011 Contig ID LIB143-034-Q1-E1-G4 5'-most EST Method BLASTX NCBI GI g2708737 BLAST score 232 3.0e-19E value 53 Match length 72 % identity NCBI Description (AC003952) putative nuclear protein [Arabidopsis thaliana] 261537 Seq. No. 2706 4.R1011 Contig ID 5'-most EST LIB3150-040-Q1-N1-B3 Method BLASTX q2708737 NCBI GI 254 BLAST score 9.0e-22 E value Match length 70 % identity 63 NCBI Description (AC003952) putative nuclear protein [Arabidopsis thaliana] 261538 Seq. No. Contig ID 2706 5.R1011 5'-most EST uC-zmflmo17286h01a1 261539 Seq. No. Contig ID 2707 1.R1011 5'-most EST uC-zmflb73126a09a1



261541 Seq. No. 2710 4.R1011 Contig ID LIB3062-036-Q1-K1-A3 5'-most EST 261542 Seq. No. 2722 1.R1011 Contig ID LIB3075-013-Q1-K1-C12 5'-most EST 261543 Seq. No. 2725 1.R1011 Contig ID LIB189-018-Q1-E1-A12 5'-most EST 261544 Seq. No.

2726 1.R1011 Contig ID 5'-most EST LIB3079-003-Q1-K1-D6 BLASTX Method g2462835 NCBI GI 707 BLAST score 1.0e-74E value

209 Match length 67 % identity

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

261545 Seq. No. 2727 1.R1011 Contig ID LIB3079-042-Q1-K1-B8 5'-most EST BLASTX Method NCBI GI q4558669

165 BLAST score 1.0e-10 E value 223 Match length % identity 25

NCBI Description (AC007063) putative vanadate resistance protein

[Arabidopsis thaliana]

261546 Seq. No. 2730_1.R1011 Contig ID uC-zmflmo17184c01b1 5'-most EST

261547 Seq. No. 2730 2.R1011 Contig ID 5'-most EST LIB3180-033-P2-M2-F10

261548 Seq. No. 2730 3.R1011 Contig ID 5'-most EST LIB3118-012-Q1-K1-H10

Seq. No. 261549 Contig ID 2730 4.R1011 LIB3150-108-P2-K1-A1 5'-most EST

261550 Seq. No. 2730 6.R1011 Contig ID ypc700805216.hl 5'-most EST

261551 Seq. No. Contig ID 2730 7.R1011



```
LIB3151-021-Q1-K1-B2
5'-most EST
                  261552
Seq. No.
                   2730 11.R1011
Contig ID
                  uC-z\overline{m}flb73160a08a1
5'-most EST
                   261553
Seq. No.
                   2730 12.R1011
Contig ID
                  bdu700383186.hl
5'-most EST
Seq. No.
                   261554
                   2731 1.R1011
Contig ID
                   hvj700623383.h1
5'-most EST
                   BLASTX
Method
                   q2245109
NCBI GI
BLAST score
                   486
                   1.0e-48
E value
Match length
                   159
                   58
% identity
                   (Z97343) carboxyl-terminal proteinase homolog [Arabidopsis
NCBI Description
                   thaliana]
                   261555
Seq. No.
                   2731 2.R1011
Contig ID
                   LIB3075-013-Q1-K1-D12
5'-most EST
                   BLASTX
Method
                   g136682
NCBI GI
BLAST score
                   234
E value
                   3.0e-19
Match length
                   110
                   45
% identity
                   UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L3 (UCH-L3)
NCBI Description
                   (UBIQUITIN THIOLESTERASE L3) >gi_108014_pir__A40085
                   (Human) At 1.8 Angstrom Resolution >gi_340074 (M30496)
```

ubiquitin carboxyl-terminal proteinase (EC 3.4.-.-) L3 - human >gi_2914274_pdb_1UCH_ Deubiquitinating Enzyme Uch-L3 ubiquitin carboxyl-terminal hydrolase [Homo sapiens]

261556 Seq. No. 2733 1.R1011 Contig ID $uC-z\bar{m}flb73264f03b1$ 5'-most EST BLASTN Method g2760166 NCBI GI 60 BLAST score 1.0e-24 E value 392 Match length

79 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MBK20, complete sequence [Arabidopsis thaliana]

261557 Seq. No. 2738 1.R1011 Contig ID pwr700451539.hl 5'-most EST BLASTX Method g114682 NCBI GI 567 BLAST score

E value

5.0e-58



Match length % identity

203 57

ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR NCBI Description (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)

>gi_100471_pir__A35227 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, mitochondrial - sweet potato >gi 168270 (J05397) F-1-ATPase delta subunit

precursor (EC 3.6.1.3) [Ipomoea batatas]

261558 Seq. No.

2738 2.R1011 Contig ID

5'-most EST LIB3068-053-Q1-K1-D12

BLASTX Method q114682 NCBI GI 228 BLAST score 1.0e-29 E value Match length 143 54 % identity

ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR NCBI Description

(OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)

>gi_100471_pir__A35227 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, mitochondrial - sweet potato >gi 168270 (J05397) F-1-ATPase delta subunit

precursor (EC 3.6.1.3) [Ipomoea batatas]

261559 Seq. No.

Contig ID 2738 3.R1011

uC-zmflb73361f07a2 5'-most EST

BLASTX Method g114682 NCBI GI 201 BLAST score 3.0e-15 E value 89 Match length 46

% identity

NCBI Description ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR

(OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP) >gi_100471_pir__A35227 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, mitochondrial - sweet

potato >gi_168270 (J05397) F-1-ATPase delta subunit precursor (EC 3.6.1.3) [Ipomoea batatas]

Seq. No. 261560 2738 4.R1011

Contig ID 5'-most EST LIB3059-056-Q1-K1-C6

261561 Seq. No.

Contig ID 2739 1.R1011 5'-most EST cjh700194133.hl

261562 Seq. No.

2740 1.R1011 Contig ID

5'-most EST uC-zmflb73238h07b2

Method BLASTX NCBI GI g4586045 BLAST score 746 3.0e-79 E value Match length 173



% identity 75
NCBI Description (AC007020) putative ankyrin protein [Arabidopsis thaliana]

Seq. No. 261563 Contig ID 2746_1.R1011

5'-most EST LIB3075-012-Q1-K1-H9

Seq. No. 261564

Contig ID 2751_1.R1011 5'-most EST uer700580659.h1

Method BLASTX
NCBI GI g4220483
BLAST score 456
E value 3.0e-45
Match length 142
% identity 61

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 261565

Contig ID 2752_1.R1011 5'-most EST ymt700224428.h1

Method BLASTX
NCBI GI 94115377
BLAST score 597
E value 2.0e-61
Match length 334
% identity 38

NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]

Seq. No. 261566

Contig ID 2755_1.R1011

5'-most EST uC-zmflmo17288a09b1

Seq. No. 261567

Contig ID 2755_2.R1011

Concid 10 2700_2:Riot1

5'-most EST LIB3066-045-Q1-K1-E4

Seq. No. 261568

Contig ID 2755_3.R1011

5'-most EST LIB3180-005-P2-M1-H3

Method BLASTN
NCBI GI g22212
BLAST score 38
E value 9.0e-12
Match length 50
% identity 94

NCBI Description Z.mays DNA for c1 locus

Seq. No. 261569 Contig ID 2755_4.R1011

5'-most EST LIB3066-030-Q1-K1-A5

Seq. No. 261570 Contig ID 2757 1.R1011

5'-most EST uC-zmroteosinte006d05b1

Method BLASTX NCBI GI g732189

36226



BLAST score 456 E value 6.0e-45 Match length 215 % identity 43

NCBI Description HYPOTHETICAL 49.1 KD PROTEIN IN SSB2-SPX18 INTERGENIC

REGION >gi_2131922_pir__S50724 hypothetical protein YNL207w - yeast (Saccharomyces cerevisiae) >gi_600058_emb_CAA55501_

(X78898) N1342 [Saccharomyces cerevisiae] >gi_1302211_emb_CAA96109_ (Z71483) ORF YNL207w

[Saccharomyces cerevisiae]

Seq. No. 261571

Contig ID 2758_1.R1011

5'-most EST LIB3059-028-Q1-K1-G12

Method BLASTX
NCBI GI g3738331
BLAST score 199
E value 4.0e-15
Match length 63
% identity 60

NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]

Seq. No. 261572

Contig ID 2767_1.R1011 5'-most EST wyr700236829.h1

Seq. No. 261573

Contig ID 2771_1.R1011 5'-most EST tfd700572447.h1

Seq. No. 261574

Contig ID 2774_1.R1011

5'-most EST LIB3075-012-Q1-K1-F7

Seq. No. 261575

Contig ID 2776_1.R1011 5'-most EST xyt700342875.h1

Seq. No. 261576

Contig ID 2777_1.R1011 5'-most EST ymt700222653.h1

Method BLASTX
NCBI GI g3372233
BLAST score 409
E value 8.0e-40
Match length 148
% identity 51

NCBI Description (AF019248) RNA polymerase I, II and III 24.3 kDa subunit

[Arabidopsis thaliana]

Seq. No. 261577

Contig ID 2778_1.R1011

5'-most EST uC-zmflb73296g05b2

Method BLASTX
NCBI GI g2828296
BLAST score 2822
E value 0.0e+00



```
604
Match length
                   90
% identity
                  (AL021687) RNase L inhibitor [Arabidopsis thaliana]
NCBI Description
                   261578
Sea. No.
                   2778 2.R1011
Contig ID
                   LIB3078-014-Q1-K1-E8
5'-most EST
                   BLASTX
Method
                   g1304266
NCBI GI
                   476
BLAST score
                   1.0e-47
E value
                   128
Match length
                   77
% identity
                  (D64051) HALF-1 [Triticum aestivum]
NCBI Description
                   261579
Seq. No.
                   2778 3.R1011
Contig ID
                   uC-z\overline{m}flmo17061a10b1
5'-most EST
                   BLASTX
Method
                   g2828296
NCBI GI
                   321
BLAST score
                   7.0e-41
E value
                   92
Match length
                   91
% identity
                  (AL021687) RNase L inhibitor [Arabidopsis thaliana]
NCBI Description
                   261580
Seq. No.
                   2778 4.R1011
Contig ID
                   LIB3115-003-Q1-K1-G2
5'-most EST
                   BLASTX
Method
                   g2828296
NCBI GI
BLAST score
                   279
                   1.0e-24
E value
                   57
Match length
                   91
% identity
NCBI Description (AL021687) RNase L inhibitor [Arabidopsis thaliana]
Seq. No.
                   261581
                   2778 5.R1011
Contig ID
                   LIB3137-007-Q1-K1-C12
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2828296
BLAST score
                   147
                   3.0e-09
E value
                   29
Match length
 % identity
NCBI Description (AL021687) RNase L inhibitor [Arabidopsis thaliana]
                    261582
 Seq. No.
                    2778 6.R1011
 Contig ID
                   LIB3062-021-Q1-K1-G11
 5'-most EST
```

Seq. No. 261583 Contig ID 2782_1.R1011

5'-most EST uC-zmroteosinte028c03b1

Seq. No. 261584



2784 1.R1011 Contig ID LIB3075-012-Q1-K1-D6 5'-most EST Seq. No. 261585 2787 1.R1011 Contig ID LIB3067-050-Q1-K1-F1 5'-most EST Method BLASTX g4056457 NCBI GI 406 BLAST score 3.0e-39 E value 129 Match length % identity 62 (AC005990) ESTs gb 234051 and gb F13722 come from this NCBI Description gene. [Arabidopsis thaliana] 261586 Seq. No. Contig ID 2788 1.R1011 5'-most EST uC-zmroteosinte120g02b2 Method BLASTX q3219304 NCBI GI BLAST score 493 2.0e-49 E value Match length 295 % identity 41 NCBI Description (AB009461) MUS38 [Neurospora crassa] 261587 Seq. No. Contig ID 2790 1.R1011 LIB143-043-Q1-E1-E7 5'-most EST 261588 Seq. No. 2793 1.R1011 Contig ID xmt700260526.h2 5'-most EST BLASTX Method g2583117 NCBI GI 325 BLAST score 2.0e-29 E value Match length 141 52 % identity NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana] 261589 Seq. No. 2800 1.R1011 Contig ID LIB3075-012-Q1-K1-C12 5'-most EST Method BLASTX g2911073 NCBI GI BLAST score 581 E value 7.0e-60 Match length 197 % identity NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 261590

2804 1.R1011

5'-most EST LIB3075-012-Q1-K1-C6

Seq. No. 261591

Contig ID

36229



```
2806 1.R1011
Contig ID
                    uC-zmflmo17236g06b1
5'-most EST
Method
                    BLASTX
                    g1346764
NCBI GI
                    763
BLAST score
                    3.0e-81
E value
                    150
Match length
                    95
% identity
                    SERINE/THREONINE PROTEIN PHOSPHATASE PP1
NCBI Description
                    >gi_951336_gb_AAA74625_ (U31773) protein phosphatase 1
                    [Oryza sativa]
                    261592
Seq. No.
                    2806 2.R1011
Contig ID
                    LIB3066-019-Q1-K1-D4
5'-most EST
                    BLASTX
Method
                    g1346764
NCBI GI
                    1505
BLAST score
                    1.0e-168
E value
                    301
Match length
                    93
% identity
                    SERINE/THREONINE PROTEIN PHOSPHATASE PP1
NCBI Description
                    >gi 951336 gb AAA74625_ (U31773) protein phosphatase 1
                    [Oryza sativa]
                    261593
Seq. No.
                    2806 3.R1011
Contig ID
                    uC-zmflb73018c10a1
5'-most EST
                    BLASTX
Method
                    g130697
NCBI GI
                    183
BLAST score
                    4.0e-13
E value
                    37
Match length
                    89
% identity
                    SERINE/THREONINE PROTEIN PHOSPHATASE PP1-1
NCBI Description
                    >gi_101019_pir__A32550 phosphoprotein phosphatase (EC
3.1.3.16) dis2 - fission yeast (Schizosaccharomyces pombe)
                    >gi_532664 (M27075) protein phosphatase 1
                    [Schizosaccharomyces pombe] >gi 1204254 (M27068) protein
                    phosphatase type 1 [Schizosaccharomyces pombe]
                    >gi_4176519_emb_CAA22875_ (AL035263) serine-threonine protein phosphatase ppl-1 [Schizosaccharomyces pombe]
                    261594
Seq. No.
                    2809 1.R1011
Contig ID
                    LIB148-038-Q1-E1-F8
5'-most EST
Method
                    BLASTX
NCBI GI
                    g3183979
BLAST score
                    539
                    7.0e-55
E value
                    222
Match length
% identity
NCBI Description (AJ005171) P69C protein [Lycopersicon esculentum]
```

Contig ID 2810_1.R1011 5'-most EST ntr700072549.h1

Seq. No.

261595



BLASTX Method q2997589 NCBI GI 1821 BLAST score E value 0.0e + 00387 Match length 93 % identity (AF020813) glucose-6-phosphate/phosphate-translocator NCBI Description precursor [Zea mays] 261596 Seq. No. Contig ID 2810 2.R1011 LIB3067-023-Q1-K1-D7 5'-most EST BLASTX Method NCBI GI q2997589 BLAST score 419 4.0e-41E value Match length 94 86 % identity (AF020813) glucose-6-phosphate/phosphate-translocator NCBI Description precursor [Zea mays] 261597 Seq. No. Contig ID 2810 3.R1011 5'-most EST dyk700105187.hl BLASTN Method NCBI GI q2997588 452 BLAST score 0.0e + 00E value 456 Match length 100 % identity NCBI Description Zea mays glucose-6-phosphate/phosphate-translocator precursor (gpt) mRNA, nuclear gene encoding plastid protein, complete cds Seq. No. 261598 2813 1.R1011 Contig ID uC-zmflmo17b08b1 5'-most EST BLASTX Method q1747294 NCBI GI BLAST score 2714 0.0e+00E value 575 Match length 93 % identity NCBI Description (D45383) vacuolar H+-pyrophosphatase [Oryza sativa] Seq. No. 261599 2813 2.R1011 Contig ID LIB3137-033-Q1-K1-B6 5'-most EST BLASTX Method

g1747296 NCBI GI 3534 BLAST score 0.0e+00E value 761 Match length % identity

(D45384) vacuolar H+-pyrophosphatase [Oryza sativa] NCBI Description >gi 3298476 dbj BAA31524 (AB012766) ovp2 [Oryza sativa]



```
261600
Seq. No.
                  2813 3.R1011
Contig ID
                  pmx700089774.h1
5'-most EST
Method
                  BLASTX
                  q1747296
NCBI GI
                  3624
BLAST score
                  0.0e+00
E value
                  761
Match length
                   95
% identity
                  (D45384) vacuolar H+-pyrophosphatase [Oryza sativa]
NCBI Description
                  >gi 3298476_dbj_BAA31524_ (AB012766) ovp2 [Oryza sativa]
                   261601
Seq. No.
                   2813 4.R1011
Contig ID
                   fC-zmle700428172r2
5'-most EST
                   BLASTX
Method
                   q1076627
NCBI GI
BLAST score
                   317
                   6.0e-50
E value
                   120
Match length
                   95
% identity
                   inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco
NCBI Description
                   >gi_790479_emb_CAA58701_ (X83730) inorganic pyrophosphatase
                   [Nicotiana tabacum]
                   261602
Seq. No.
                   2813 5.R1011
Contig ID
                   uC-zmflb73345a07a2
5'-most EST
Method
                   BLASTX
                   g2827755
NCBI GI
                   427
BLAST score
                   4.0e-42
E value
                   115
Match length
                   72
% identity
                   INORGANIC PYROPHOSPHATASE, VACUOLAR (PYROPHOSPHATE
NCBI Description
                   PHOSPHOHYDROLASE) (PPASE) >gi_951323 (U31467)
                   pyrophosphatase [Vigna radiata]
                   261603
Seq. No.
                   2813 6.R1011
Contig ID
                   ceu700427206.h1
5'-most EST
                   BLASTX
Method
                   g2911807
NCBI GI
                   304
BLAST score
                   7.0e-36
E value
                   111
Match length
                   83
% identity
NCBI Description (AF009568) H+-pyrophosphatase [Gossypium hirsutum]
                   261604
Seq. No.
                   2813 7.R1011
Contig ID
                   uC-zmflmo17127c10b1
 5'-most EST
Method
                   BLASTX
                   g3298474
NCBI GI
```

36232

1207

274

1.0e-133

BLAST score

Match length

E value



% identity 88 (AB012765) ovpl [Oryza sativa] NCBI Description Seq. No. 261605 2813 8.R1011 Contig ID 5'-most EST xsy700213636.h1 Method BLASTX g4191796 NCBI GI 312 BLAST score 2.0e-28 E value 151 Match length % identity 41 (AC005917) putative senescence-associated protein 5 NCBI Description [Arabidopsis thaliana] Seq. No. 261606 2813 9.R1011 Contig ID LIB3059-029-Q1-K1-A12 5'-most EST BLASTX Method q728938 NCBI GI 583 BLAST score 6.0e-72E value Match length 202 93 % identity PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP NCBI Description (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE) (H+-PPASE) >gi_322841_pir__JC1466 inorganic pyrophosphatase (EC 3.6.1.1) - barley >gi_285638_dbj_BAA02717_ (D13472) inorganic pyrophosphatse ase' [Hordeum vulgare] 261607 Seq. No. 2813 11.R1011 Contig ID uC-zmromo17114a05a1 5'-most EST Method BLASTX g1747294 NCBI GI 166 BLAST score 2.0e-11 E value Match length 55 % identity 64 NCBI Description (D45383) vacuolar H+-pyrophosphatase [Oryza sativa] 261608 Seq. No. 2813 13.R1011 Contig ID LIB3067-035-Q1-K1-H12 5'-most EST BLASTX Method g4191796 NCBI GI 210 BLAST score 6.0e - 32E value 184 Match length 46 % identity

NCBI Description (AC005917) putative senescence-associated protein 5

[Arabidopsis thaliana]

 Seq. No.
 261609

 Contig ID
 2815_1.R1011

 5'-most EST
 pmx700088183.h1



```
261610
Seq. No.
Contig ID
                   2817 1.R1011
5'-most EST
                   LIB148-034-Q1-E1-D5
Seq. No.
                   261611
Contig ID
                   2819 1.R1011
5'-most EST
                   uC-zmflb73234d12b2
                   261612
Seq. No.
                   2820 1.R1011
Contig ID
                   LIB3150-016-Q1-N1-C1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3702332
BLAST score
                   151
                   3.0e-09
E value
                   65
Match length
% identity
                   45
                  (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                   261613
Seq. No.
                   2820 2.R1011
Contig ID
                   LIB3158-006-Q1-K1-A10
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3702332
BLAST score
                   144
                   6.0e-09
E value
Match length
                   55
% identity
                   51
                  (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                   261614
Seq. No.
                   2820 3.R1011
Contig ID
                   nbm700475751.h1
5'-most EST
                   261615
Seq. No.
                   2820 4.R1011
Contig ID
                   LIB3076-026-Q1-K1-H1
5'-most EST
                   261616
Seq. No.
                   2820 5.R1011
Contig ID
                   wty700169842.h1
5'-most EST
                   261617
Seq. No.
                   2821 1.R1011
Contig ID
                   uC-z\overline{m}flb73249c11b3
5'-most EST
                   BLASTN
Method
                   g3821780
NCBI GI
BLAST score
                   34
                   2.0e-09
E value
Match length
                   34
                   100
% identity
```

NCBI Description Xenopus laevis cDNA clone 27A6-1 Seq. No. 261618

2823 1.R1011

xsy700211285.hl

Method BLASTX

Contig ID

5'-most EST



NCBI GI g3395431 BLAST score 260 E value 8.0e-22 Match length 145 % identity 40

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 261619

Contig ID 2823_2.R1011

5'-most EST uC-zmflb73137d04b1

Method BLASTN
NCBI GI g3819386
BLAST score 66
E value 2.0e-28

Match length 137 % identity 88

NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0872.rev

Seq. No. 261620

Contig ID 2823_3.R1011 5'-most EST rvt700552807.h1

Seq. No. 261621

Contig ID 2823 5.R1011

5'-most-EST LIB3060-014-Q1-K1-B3

Seq. No. 261622

Contig ID 2823_6.R1011

5'-most EST uC-zmroteosinte011e02b1

Seq. No. 261623

Contig ID 2823_7.R1011

5'-most EST uC-zmroteosinte039g05b1

Seq. No. 261624

Contig ID 2825_1.R1011

5'-most EST LIB3075-011-Q1-K1-G2

-Seq. No. 261625

Contig ID 2827_1.R1011

5'-most EST uC-zmflMo17063b09b1

Method BLASTX
NCBI GI g4502897
BLAST score 1175
E value 1.0e-129
Match length 596
% identity 43

NCBI Description cleft lip and palate associated transmembrane protein 1

>gi_4039014 (AF037338) cleft lip and palate transmembrane protein 1 [Homo sapiens] >gi_4063033 (AF037339) cleft lip

and palate transmembrane protein 1 [Homo sapiens]

Seq. No. 261626

Contig ID 2827_3.R1011 5'-most EST qmh700030284.f1

Method BLASTX NCBI GI g3879192

Match length

NCBI Description

% identity

135



```
BLAST score
                   171
                   7.0e-12
E value
Match length
                  78
                   50
% identity
                  (Z50795) weak similarity with yeast cat8 regulatory protein
NCBI Description
                   (Swiss Prot accession number P39113); cDNA EST EMBL: Z14554
                   comes from this gene; cDNA EST EMBL:T02057 comes from this
                   gene; cDNA EST EMBL: D75504 comes from this gene;
                   261627
Seq. No.
Contig ID
                   2828 1.R1011
                  LIB148-062-Q1-E1-F7
5'-most EST
                   261628
Seq. No.
Contig ID
                   2835 1.R1011
5'-most EST
                  LIB3066-004-Q1-K1-H6
                  BLASTX
Method
NCBI GI
                   g2914696
BLAST score
                   1217
                   1.0e-134
E value
Match length
                   507
                   50
% identity
                  (AC003974) putative purple acid phosphatase [Arabidopsis
NCBI Description
                   thaliana]
                   261629
Seq. No.
                   2839 1.R1011
Contig ID
5'-most EST
                   LIB3075-011-Q1-K1-E8
Method
                   BLASTX
                   q3608137
NCBI GI
BLAST score
                   180
                   6.0e-13
E value
                   89
Match length
                   37
% identity
                  (AC005314) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   261630
Contig ID
                   2846 1.R1011
5'-most EST
                   uC-zmflmo17215d09a1
Method
                   BLASTX
                   g1742951
NCBI GI
BLAST score
                   783
                   2.0e-83
E value
Match length
                   191
                   79
% identity
                  (Y09817) Ca2+-ATPase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   261631
Contig ID
                   2846 3.R1011
5'-most EST
                   xit700095954.h1
Method
                   BLASTX
NCBI GI
                   q1742951
BLAST score
                   657
E value
                   7.0e-69
```

(Y09817) Ca2+-ATPase [Arabidopsis thaliana]
36236



```
261632
Seq. No.
                   2847 1.R1011
Contig ID
                   uC-zmflb73273h07a1
5'-most EST
Method
                   BLASTX
                   q3687404
NCBI GI
BLAST score
                   314
                   9.0e-29
E value
Match length
                   73
% identity
                   82
                   (Y16126) NADP-dependent isocitrate dehydrogenase-like
NCBI Description
                  protein [Lycopersicon esculentum]
Seq. No.
                   261633
Contig ID
                   2848 1.R1011
5'-most EST
                   LIB3075-003-Q1-K1-G10
Method
                   BLASTX
NCBI GI
                   q4426964
BLAST score
                   387
                   2.0e-37
E value
Match length
                   114
% identity
                   62
NCBI Description
                   (AF126255) purple acid phosphatase precursor [Anchusa
                   officinalis]
                   261634
Seq. No.
                   2848 2.R1011
Contig ID
5'-most EST
                   LIB3075-004-Q1-K1-E6
Method
                   BLASTX
NCBI GI
                   g4160280
                   279
BLAST score
                   8.0e-25
E value
                   91
Match length
                   62
% identity
                  (AJ006224) purple acid phosphatase [Ipomoea batatas]
NCBI Description
                   261635
Seq. No.
Contig ID
                   2848 4.R1011
5'-most EST
                   uC-z\overline{m}flmo17057h01b1
                   BLASTX
Method
                   q4544387
NCBI GI
BLAST score
                   178
E value
                   3.0e-13
Match length
                   42
                   83
% identity
NCBI Description
                   (AC007047) putative purple acid phosphatase precursor
                   [Arabidopsis thaliana]
Seq. No.
                   261636
Contig ID
                   2851 1.R1011
5'-most EST
                   LIB3075-011-Q1-K1-G11
Seq. No.
                   261637
Contig ID
                   2852 1.R1011
```

Method BLASTX NCBI GI g548851

LIB3279-006-P1-K1-E8

5'-most EST



BLAST score 491 E value 2.0e-49 Match length 114 84 % identity

NCBI Description 40S RIBOSOMAL PROTEIN S20 >gi_481226_pir__S38356 ribosomal protein S20 - rice >gi_391875_dbj_BAA02157 (D12632) 40S

subunit ribosomal protein [Oryza sativa]

261638 Seq. No.

Contig ID 2852 2.R1011 5'-most EST cjh700193456.h1

Method BLASTX g1350956 NCBI GI BLAST score 198 3.0e-15E value Match length 46 87 % identity

NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)

261639 Seq. No. Contig ID 2855 1.R1011 5'-most EST $nbm7\overline{0}0477156.h1$

261640 Seq. No.

Contig ID 2860 1.R1011

5'-most EST LIB3075-011-Q1-K1-E10

Method BLASTX g466328 NCBI GI BLAST score 249 3.0e-21E value Match length 78

% identity 65

NCBI Description (L31353) hexose carrier [Ricinus communis]

Seq. No. 261641

Contig ID 2864 1.R1011

5'-most EST LIB3066-055-Q1-K1-F3

Method BLASTX NCBI GI q4455337 BLAST score 177 E value 2.0e-12 Match length 123 % identity 31

NCBI Description (AL035525) pectinesterase-like protein [Arabidopsis

thaliana]

Seq. No. 261642 Contig ID 2866 1.R1011

5'-most EST LIB3075-011-Q1-K1-E6

Seq. No. 261643

Contig ID 2870 1.R1011 5'-most EST xmt700263325.h1

Method BLASTX NCBI GI g1172043 BLAST score 163 E value 5.0e-11



Match length 53 % identity 57

NCBI Description PROBABLE POLY(A) POLYMERASE (PAP) >gi_1075158_pir__B64046

plasmid copy number control protein (pcnB) homolog - Haemophilus influenzae (strain Rd KW20) >gi 1573011

(U32691) poly(A) polymerase (pcnB) [Haemophilus influenzae

Rd]

Seq. No. 261644

Contig ID 2871 1.R1011

5'-most EST LIB3075-011-Q1-K1-C12

Seq. No. 261645

Contig ID 2873 1.R1011

5'-most EST uC-zmroteosinte038c09b1

Seq. No. 261646

Contig ID 2881 1.R1011

5'-most EST LIB3066-023-Q1-K1-B3

Method BLASTX
NCBI GI g4538993
BLAST score 298
E value 8.0e-27
Match length 111
% identity 52

NCBI Description (AL049481) putative host response protein [Arabidopsis

thaliana]

Seq. No. 261647

Contig ID 2884_1.R1011 5'-most EST fwa700099287.h1

Method BLASTX
NCBI GI g4415931
BLAST score 1533
E value 1.0e-171
Match length 565
% identity 54

NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]

>gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown

protein [Arabidopsis thaliana]

Seq. No. 261648

Contig ID 2884 3.R1011 5'-most EST xsy700213045.h1

Method BLASTX
NCBI GI g4415931
BLAST score 281
E value 3.0e-25
Match length 76
% identity 72

NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]

>gi_4559393_gb_AAD23053.1_AC006526_18 (AC006526) unknown

protein [Arabidopsis thaliana]

Seq. No. 261649 Contig ID 2888_1.R1011

5'-most EST LIB3069-051-Q1-K1-H6



Seq. No. 261650 2892 1.R1011 Contig ID LIB143-033-Q1-E1-D10 5'-most EST BLASTX Method NCBI GI q3763932 BLAST score 1290 E value 1.0e-142 366 Match length 69 % identity (AC004450) putative protein kinase [Arabidopsis thaliana] NCBI Description 261651 Seq. No. 2897 1.R1011 Contig ID 5'-most EST ymt700221167.hl Method BLASTX g1724100 NCBI GI BLAST score 714 4.0e-75E value Match length 276 % identity 48 NCBI Description (U79765) porin [Mesembryanthemum crystallinum] 261652 Seq. No. Contig ID 2897 3.R1011 5'-most EST uC-zmroB73070e10b1 261653 Seq. No. 2897 4.R1011 Contig ID 5'-most EST xjt700096659.h1Seq. No. 261654 2897_5.R1011 Contig ID 5'-most EST uC-zmroteosinte099h08b2 Seq. No. 261655 Contig ID 2897 6.R1011 5'-most EST LIB3136-049-Q1-K1-F8 Method BLASTX NCBI GI q1172558 BLAST score 149 E value 2.0e-09 Match length 49 53 % identity

NCBI Description OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT

ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)

>gi_480122_pir__S36454 porin por1 - garden pea

>gi_396819_emb_CAA80988 (Z25540) Porin [Pisum sativum]

Seq. No. 261656

Contig ID 2902 1.R1011

5'-most EST LIB3067-046-Q1-K1-E7

Method BLASTX
NCBI GI g1491710
BLAST score 274
E value 6.0e-24
Match length 114



% identity 48

NCBI Description (X96506) alpha subunit; forms heterodimer with NC2

alpha/Dr1 [Homo sapiens]

Seq. No. 261657

Contig ID 2907 1.R1011

5'-most EST LIB3067-008-Q1-K1-A2

Method BLASTX
NCBI GI g4160280
BLAST score 1513
E value 1.0e-168
Match length 428
% identity 63

NCBI Description (AJ006224) purple acid phosphatase [Ipomoea batatas]

Seq. No. 261658

Contig ID 2909 1.R1011

5'-most EST LIB3059-053-Q1-K1-F8

Method BLASTX
NCBI GI g3874563
BLAST score 391
E value 1.0e-37
Match length 184
% identity 45

NCBI Description (Z81042) similar to Yeast hypothetical protein YEY6 like;

cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ... >gi_3924825_emb_CAB05549_ (Z83113) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5

comes from this gene; cDNA

Seq. No. 261659

Contig ID 2913_1.R1011

5'-most EST LIB3088-034-Q1-K1-F9

Seq. No. 261660

Contig ID 2913 2.R1011

5'-most EST uC-zmflmo17181b05b1

Method BLASTX
NCBI GI g4432863
BLAST score 1142
E value 1.0e-125
Match length 349
% identity 66

NCBI Description (AC006300) putative phosphate/phosphoenolpyruvate

translocator protein [Arabidopsis thaliana]

Seq. No. 261661 Contig ID 2913 5.R1011

5'-most EST uC-zmflmo17132a07b1

Method BLASTX
NCBI GI g4432863
BLAST score 265
E value 2.0e-25



```
Match length
                  89
% identity
                   66
                  (AC006300) putative phosphate/phosphoenolpyruvate
NCBI Description
                  translocator protein [Arabidopsis thaliana]
                  261662
Seq. No.
Contig ID
                  2913 6.R1011
                  xmt700266057.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4049341
BLAST score
                  142
                   8.0e-09
E value
Match length
                   32
                   75
% identity
                  (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   261663
                   2914 2.R1011
Contiq ID
                  LIB3136-010-Q1-K1-B7
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2829918
BLAST score
                   1077
                   1.0e-118
E value
Match length
                   355
                   65
% identity
                  (AC002291) similar to "tub" protein gp_U82468_2072162
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   261664
                   2916 1.R1011
Contig ID
                   ceu700424703.h1
5'-most EST
                   BLASTX
Method
                   g4220484
NCBI GI
                   292
BLAST score
                   6.0e-26
E value
                   123
Match length
% identity
                   53
NCBI Description (AC006069) hypothetical protein [Arabidopsis thaliana]
                   261665
Seq. No.
                   2919 1.R1011
Contig ID
5'-most EST
                   LIB3059-018-Q1-K1-C2
Method
                   BLASTX
                   g2444180
NCBI GI
BLAST score
                   258
                   3.0e-22
E value
Match length
                   129
% identity
NCBI Description
                  (U94785) unconventional myosin [Helianthus annuus]
                   261666
Seq. No.
                   2924 1.R1011
Contig ID
5'-most EST
                   amh700026811.f1
```

36242

BLASTX

751

g3618308

1.0e-79

Method

NCBI GI BLAST score

E value



```
Match length
                  223
                  69
% identity
                  (AB001882) zinc finger protein [Oryza sativa]
NCBI Description
                  261667
Seq. No.
                  2926 1.R1011
Contig ID
                  zuv700352804.h1
5'-most EST
                  BLASTX
Method
                  g3641839
NCBI GI
                  402
BLAST score
                  6.0e-66
E value
                  193
Match length
                  59
% identity
                  (AL023094) isoflavone reductase - like protein [Arabidopsis
NCBI Description
                  thaliana]
                  261668
Seq. No.
                  2930 1.R1011
Contig ID
                  LIB3150-039-Q1-N1-B11
5'-most EST
                  BLASTX
Method
                  g2191141
NCBI GI
                   451
BLAST score
                   7.0e-45
E value
                   118
Match length
                   73
% identity
                  (AF007269) A_IG002N01.21 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   261669
Seq. No.
                   2934 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73147f01b1
                   261670
Seq. No.
                   2935_1.R1011
Contig ID
                   uC-zmflb73160e05a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1370180
                   332
BLAST score
                   9.0e-31
E value
                   92
Match length
                   74
% identity
NCBI Description (Z73939) RAB5B [Lotus japonicus]
Seq. No.
                   261671
                   2948 1.R1011
Contig ID
                   LIB3079-023-Q1-K1-B2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4115918
BLAST score
                   518
E value
                   3.0e-52
Match length
                   135
% identity
                   77
                  (AF118222) similar to nascent polypeptide associated
NCBI Description
                   complex alpha chain [Arabidopsis thaliana]
```

36243

261672

2948_2.R1011

Seq. No.

Contig ID



LIB36-012-Q1-E1-C7 5'-most EST BLASTX Method q4115918 NCBI GI 446 BLAST score 6.0e-44E value 136 Match length % identity 68 (AF118222) similar to nascent polypeptide associated NCBI Description complex alpha chain [Arabidopsis thaliana] 261673 Seq. No.

Contig ID 2948_3.R1011
5'-most EST LIB3069-020-Q1-K1-D1
Method BLASTX
NCBI GI g4115918
BLAST score 230
E value 4.0e-19
Match length 50

Seq. No. 261674 Contig ID 2952 1.R1011 5'-most EST LIB3069-002-

5'-most EST LIB3069-002-Q1-K1-G6

Method BLASTX
NCBI GI g3746059
BLAST score 153
E value 1.0e-09
Match length 60
% identity 53

NCBI Description (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis

thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative

cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 261675

Contig ID 2952_2.R1011

5'-most EST uC-zmflmo17041c02b1

Method BLASTX
NCBI GI g3746059
BLAST score 1354
E value 1.0e-150
Match length 525
% identity 53

NCBI Description (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis

thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative

cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 261676

Contig ID 2952_3.R1011 5'-most EST xsy700217845.h1

Method BLASTX
NCBI GI g1652649
BLAST score 520
E value 2.0e-57
Match length 183
% identity 62



```
(D90907) hypothetical protein [Synechocystis sp.]
NCBI Description
                   261677
Seq. No.
                   2952 4.R1011
Contiq ID
                  LIB3<del>1</del>37-038-Q1-K1-B4
5'-most EST
                  BLASTX
Method
                   q1652649
NCBI GI
                   288
BLAST score
                   1.0e-25
E value
                   84
Match length
                   62
% identity
                  (D90907) hypothetical protein [Synechocystis sp.]
NCBI Description
                   261678
Seq. No.
                   2952 5.R1011
Contig ID
                   uer700581779.h1
5'-most EST
                   BLASTX
Method
                   g3746059
NCBI GI
                   254
BLAST score
                   1.0e-21
E value
                   94
Match length
                   56
% identity
                  (AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis
NCBI Description
                   thaliana] >gi_4432812_gb_AAD20662_ (AC006593) putative
                   cysteinyl-tRNA synthetase [Arabidopsis thaliana]
                   261679
Seq. No.
Contig ID
                   2954 1.R1011
                   LIB3066-028-Q1-K1-B9
5'-most EST
                   BLASTX
Method
                   g1621440
NCBI GI
BLAST score
                   558
                   5.0e-57
E value
                   208
Match length
                   56
% identity
                  (U72148) plasma membrane H+-ATPase [Lycopersicon
NCBI Description
                   esculentum]
                   261680
Seq. No.
                   2956 1.R1011
Contig ID
                   ymt700221821.h1
5'-most EST
Method
                   BLASTX
                   g2895945
NCBI GI
BLAST score
                   300
E value
                   7.0e-27
Match length
                   206
                   39
% identity
                  (AF045888) putative DNA cytosine methyltransferase DNMT2
NCBI Description
                   [Homo sapiens]
                   261681
Seq. No.
                   2957 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73096q03b1
                   261682
Seq. No.
```

2957 2.R1011

LIB3150-034-Q1-N1-E11

Contig ID 5'-most EST



```
      Seq. No.
      261683

      Contig ID
      2957_3.R1011

      5'-most EST
      xdb700340188.h1
```

Seq. No. 261684

Contig ID 2957_5.R1011

5'-most EST uC-zmflb73161b09b2

Seq. No. 261685 Contig ID 2957_7.R1011

5'-most EST uC-zmflmo17204g10b1

Method BLASTX
NCBI GI g3551838
BLAST score 423
E value 3.0e-41
Match length 140

% identity 61

NCBI Description (AF070967) SKP1-like protein [Nicotiana clevelandii]

Seq. No. 261686

Contig ID 2958_1.R1011

5'-most EST LIB3060-020-Q1-K1-D9

Seq. No. 261687

Contig ID 2959_1.R1011

5'-most EST LIB3066-001-Q1-K1-A12

Seq. No. 261688 Contig ID 2960_3.R1011

5'-most EST uC-zmrob73076h04b1

Seq. No. 261689

Contig ID 2964_1.R1011

5'-most EST LIB3279-015-P1-K1-G1

Seq. No. 261690

Contig ID 2965_1.R1011 5'-most EST uC-zmflmo17103c09a1

Seq. No. 261691

Contig ID 2965_2.R1011 5'-most EST gwl700618130.h1

Method BLASTX
NCBI GI g462680
BLAST score 152
E value 2.0e-09
Match length 102
% identity 33

NCBI Description MYOSIN ID HEAVY CHAIN >gi_422294_pir__A47106 myosin heavy

chain ID - slime mold (Dictyostelium discoideum)

Seq. No. 261692

Contig ID 2966_1.R1011 5'-most EST uwc700155616.h1

Method BLASTX NCBI GI g1279876



```
BLAST score
                      994
                      1.0e-108
E value
Match length
                      250
% identity
                      79
                      (U52867) high affinity sulfate transporter HVST1 [Hordeum
NCBI Description
                      261693
Seq. No.
Contig ID
                      2970 1.R1011
                      LIB3150-047-Q1-N1-A9
5'-most EST
Method
                      BLASTX
NCBI GI
                      q135159
BLAST score
                      929
                      1.0e-100
E value
Match length
                      279
                      62
% identity
                      ASPARAGINYL-TRNA SYNTHETASE (ASPARAGINE--TRNA LIGASE)
NCBI Description
                      (ASNRS) >gi_68529_pir__SYECNT asparagine--tRNA ligase (EC 6.1.1.22) precursor - Escherichia coli
                      >gi_41000_emb_CAA48274_ (X68192) Asparaginyl-tRNA
synthetase [Escherichia coli] >gi_147935 (M33145)
asparaginyl-tRNA synthetase (asnS) [Escherichia coli]
                      >gi_1651455_dbj_BAA35682_ (D90731) Asparaginyl-tRNA synthetase (EC 6.1.1.22) (asparagine-tRNA ligase) (asnRS).
                      [Escherichia coli] >gi 1787161 (AE000195) asparagine tRNA
                      synthetase [Escherichia coli]
                      261694
Seq. No.
                      2972 1.R1011
Contig ID
                      wty700166589.h1
5'-most EST
Method
                      BLASTN
NCBI GI
                      g3821780
BLAST score
                      36
                      2.0e-10
E value
Match length
                      48
% identity
                      67
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                      261695
                      2972 2.R1011
Contig ID
5'-most EST
                      LIB3062-033-Q1-K1-H12
                      261696
Seq. No.
                      2975 1.R1011
Contig ID
5'-most EST
                      pmx700089014.h1
Seq. No.
                      261697
                      2978 1.R1011
Contig ID
                      LIB3075-009-Q1-K1-H10
5'-most EST
Method
                      BLASTX
```

Method BLASTX
NCBI GI g4263787
BLAST score 218
E value 1.0e-17
Match length 58
% identity 69

NCBI Description (AC006068) unknown protein [Arabidopsis thaliana]



261698 Seq. No. Contig ID 2979 1.R1011 . 5'-most EST LIB3068-056-Q1-K1-D4 Method BLASTX NCBI GI g1173638 BLAST score 982 1.0e-107 E value Match length 217 87 % identity (U35779) 1-aminocyclopropane-1-carboxylate synthase NCBI Description [Triticum aestivum] Seq. No. 261699 2980 1.R1011 Contig ID uC-zmflb73163c12b2 5'-most EST BLASTX Method NCBI GI q1575595 1784 BLAST score E value 0.0e + 00374 Match length 93 % identity (U67717) fimbrin/plastin-like [Triticum aestivum] NCBI Description Seq. No. 261700 2980 2.R1011 Contig ID uC-zmflb73192a11a1 5'-most EST 261701 Seq. No. Contig ID 2982 1.R1011 5'-most EST uC-zmflb73071b08b3 BLASTX Method q3738291 NCBI GI BLAST score 376 2.0e-35 E value Match length 243 36 % identity (AC005309) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 261702 Contig ID 2982 2.R1011 5'-most EST wyr700240590.h1 Method BLASTX g3738291 NCBI GI 167 BLAST score 2.0e-11 E value Match length 112 35 % identity (AC005309) unknown protein [Arabidopsis thaliana] NCBI Description 261703 Seq. No. 2983 1.R1011 Contig ID nbm700468166.h15'-most EST

5'-most EST nbm7004681
Method BLASTX
NCBI GI g231536
BLAST score 1602
E value 1.0e-179
Match length 357



% identity NCBI Description CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase (EC 3.4.11.1) - Arabidopsis thaliana >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase
[Arabidopsis thaliana] >gi_4115380 (AC005967) putative leucine aminopeptidase [Arabidopsis thaliana] 261704 Seq. No. Contig ID 2983 3.R1011 tfd700574706.hl 5'-most EST BLASTX Method NCBI GI a1483563 BLAST score 256 6.0e-22 E value Match length 61 % identity NCBI Description (X99825) leucine aminopeptidase [Petroselinum crispum] 261705

Seq. No.

Contig ID 2985 1.R1011 5'-most EST LIB3075-009-Q1-K1-F3

Method BLASTX NCBI GI g3513744 BLAST score 263 7.0e-23 E value

Match length 93 53 % identity

NCBI Description (AF080118) contains similarity to Medicago truncatula MtN3

(GB:Y08726) [Arabidopsis thaliana]

Seq. No. 261706 Contig ID 2987 1.R1011

5'-most EST LIB3075-009-Q1-K1-F6

Method BLASTX NCBI GI g3047101 BLAST score 253 E value 2.0e-21 Match length 107 % identity 45

NCBI Description (AF058919) Similar to protein kinase; coded for by A.

thaliana cDNA H36947; coded for by A. thaliana cDNA H37158

[Arabidopsis thaliana]

Seq. No. 261707 Contig ID 2992 2.R1011

LIB3075-009-Q1-K1-G2 5'-most EST

261708 Seq. No.

2995 1.R1011 Contig ID LIB84-015-Q1-E1-G3 5'-most EST

BLASTX Method NCBI GI g132724 BLAST score 389 E value 3.0e-37 Match length 114

36249



% identity 68 50S RIBOSOMAL PROTEIN L18 >gi 71259 pir R5BS8F ribosomal NCBI Description

protein L18 - Bacillus stearothermophilus

261709 Seq. No.

3003 1.R1011 Contig ID

uC-zmflmo17271h05b1 5'-most EST

Method BLASTX g1345587 NCBI GI BLAST score 1230 1.0e-138 E value Match length 261 % identity 100

14-3-3-LIKE PROTEIN GF14-6 >gi 998430 bbs 164522 (S77133) NCBI Description

GF14-6=14-3-3 protein homolog [Zea mays, XL80, Peptide, 261

aa] [Zea mays]

261710 Seq. No. Contig ID 3003 2.R1011

5'-most EST uC-zmflb73124a02b1

BLASTX Method NCBI GI g4204309 BLAST score 343 E value 4.0e-32 Match length 160 49 % identity

(AC003027) lcl prt seq No definition line found NCBI Description

[Arabidopsis thaliana]

261711 Seq. No. 3003 3.R1011 Contig ID

LIB3076-003-Q1-K1-F11 5'-most EST

Method BLASTX NCBI GI g1345588 572 BLAST score 4.0e-59 E value 116 Match length 100 % identity

14-3-3-LIKE PROTEIN GF14-12 >gi 998432 bbs_164524 NCBI Description

GF14-12=GRF2 product/14-3-3 protein homolog [Zea mays,

XL80, Peptide, 261 aa]

261712 Seq. No.

3003 6.R1011 Contig ID

LIB3068-038-Q1-K1-B12 5'-most EST

BLASTX Method NCBI GI q1345587 BLAST score 171 6.0e-12 E value Match length 49 73 % identity

14-3-3-LIKE PROTEIN GF14-6 >gi 998430 bbs 164522 (S77133) NCBI Description

GF14-6=14-3-3 protein homolog [Zea mays, XL80, Peptide, 261

aa] [Zea mays]

261713 Seq. No. 3003 9.R1011 Contig ID

36250



```
uC-zmflb73224h10a1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q168602
                  343
BLAST score
E value
                  0.0e + 00
                  387
Match length
                   97
% identity
                  Zea mays regulatory protein GF14-12 mRNA, complete cds
NCBI Description
                  261714
Seq. No.
                  3003 14.R1011
Contig ID
                  uC-zmflb73052c12b1
5'-most EST
                  BLASTX
Method
                  g1345587
NCBI GI
                  149
BLAST score
                  1.0e-09
E value
                   44
Match length
                   77
% identity
                  14-3-3-LIKE PROTEIN GF14-6 >gi 998430 bbs 164522 (S77133)
NCBI Description
                   GF14-6=14-3-3 protein homolog [Zea mays, XL80, Peptide, 261
                   aa] [Zea mays]
                   261715
Seq. No.
                   3004 1.R1011
Contig ID
5'-most EST
                   LIB3068-006-Q1-K1-C5
Method
                   BLASTX
                   g4049502
NCBI GI
BLAST score
                   205
E value
                   8.0e-16
Match length
                   174
                   32
% identity
                  (AL034563) transcription initiation factor iif, beta
NCBI Description
                   subunit [Schizosaccharomyces pombe]
                   261716
Seq. No.
Contig ID
                   3004 2.R1011
5'-most EST
                   LIB3067-028-Q1-K1-B5
Seq. No.
                   261717
Contig ID
                   3005 1.R1011
5'-most EST
                   uC-zmroteosinte019g05b1
Method
                   BLASTX
NCBI GI
                   q2493053
BLAST score
                   365
E value
                   1.0e-34
Match length
                   70
% identity
                   99
                   ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL >gi 639793
NCBI Description
                   (L39120) mitochondrial F1F0 ATP synthase epsilon subunit
                   [Zea mays]
```

Seq. No. 261718

Contig ID 3005_2.R1011

5'-most EST LIB143-047-Q1-E1-H6

Method BLASTX
NCBI GI g2493053
BLAST score 369



4.0e-35 E value Match length 70 100 % identity

ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL >gi 639793 NCBI Description

(L39120) mitochondrial F1F0 ATP synthase epsilon subunit

[Zea mays]

261719 Seq. No.

Contig ID 3009 1.R1011

5'-most EST LIB3116-007-Q1-K1-D11

Seq. No. 261720

3012 1.R1011 Contig ID

5'-most EST LIB36-016-Q2-E2-D5

261721 Seq. No.

3015 1.R1011 Contig ID

LIB189-001-Q1-E1-C5 5'-most EST

Method BLASTX NCBI GI g2529707 1130 BLAST score E value 1.0e-124 Match length 395

% identity 53

NCBI Description (AF001434) Hpast [Homo sapiens]

261722 Seq. No.

3019 1.R1011 Contig ID

5'-most EST LIB3075-009-Q1-K1-B6

Seq. No. 261723

Contig ID 3021 1.R1011

uC-zmflb73136e12b15'-most EST

Seq. No. 261724

Contig ID 3022 1.R1011

5'-most EST uC-zmflb73039g06b1

Method BLASTX NCBI GI g3426038 BLAST score 1341 1.0e-148 E value Match length 370

73 % identity

NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

Seq. No. 261725

Contig ID 3024 1.R1011

LIB3150-020-Q1-N1-B1 5'-most EST

Method BLASTX NCBI GI g3130051 BLAST score 529 E value 7.0e-54145 Match length 66 % identity

(AL023518) conserved hypothetical protein NCBI Description

[Schizosaccharomyces pombe]



261726 Seq. No. 3025 1.R1011 Contig ID 5'-most EST LIB3075-009-Q1-K1-C11 Seq. No. 261727 Contig ID 3027 1.R1011 LIB3075-009-Q1-K1-B1 5'-most EST 261728 Seq. No. Contig ID 3028_1.R1011 5'-most EST LIB3075-008-Q1-K1-H3 BLASTX Method NCBI GI g2982432 BLAST score 268 2.0e-23 E value Match length 75 68 % identity NCBI Description (AL022224) putative protein [Arabidopsis thaliana] 261729 Seq. No. 3028 3.R1011 Contig ID tzu700204775.h1 5'-most EST Method BLASTX NCBI GI q2982432 BLAST score 265 E value 5.0e-23Match length 75 67 % identity (AL022224) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 261730 3031_1.R1011 Contig ID 5'-most EST LIB3075-008-Q1-K1-G9 BLASTX Method NCBI GI q4093165 BLAST score 344 E value 5.0e - 32Match length 161 % identity 45 NCBI Description (AF095931) p34-Arc [Dictyostelium discoideum] Seq. No. 261731 Contig ID 3036 1.R1011 LIB3062-038-Q1-K1-C5 5'-most EST Method BLASTX NCBI GI g4587610

BLAST score 1023 1.0e-111 E value Match length 395 % identity 55

(AC006951) putative indole-3-glycerol phosphate synthase NCBI Description

precursor [Arabidopsis thaliana]

Seq. No. 261732 3036 2.R1011 Contig ID

5'-most EST uC-zmflb73022a01b1



```
261733
Seq. No.
Contig ID
                  3036 4.R1011
                  uC-zmflmo17362g12a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1351303
                  187
BLAST score
E value
                  5.0e-14
Match length
                  51
                  71
% identity
NCBI Description
                  INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE PRECURSOR (IGPS)
                  >gi 619732 (U18770) indole-3-glycerol phosphate synthase
                   [Arabidopsis thaliana]
                   261734
Seq. No.
Contig ID
                  3043 2.R1011
5'-most EST
                  uC-zmflb73075b09a1
Method
                  BLASTN
NCBI GI
                  q3420038
                  57
BLAST score
E value
                   4.0e-23
Match length
                  103
                   56
% identity
                  Zea mays gypsy/Ty3-type retrotransposon Tekay, complete
NCBI Description
                  sequence
                   261735
Seq. No.
Contig ID
                   3043 4.R1011
5'-most EST
                  uC-zmflmo17300e01a1
Method
                  BLASTN
                  q3420038
NCBI GI
BLAST score
                   44
                   2.0e-15
E value
Match length
                   64
                   47
% identity
NCBI Description
                  Zea mays gypsy/Ty3-type retrotransposon Tekay, complete
                   sequence
Seq. No.
                   261736
Contig ID
                   3046 1.R1011
                  LIB3075-008-Q1-K1-G10
5'-most EST
                   261737
Seq. No.
```

3053 1.R1011 Contig ID fwa700101064.hl 5'-most EST

Seq. No. 261738 Contig ID 3057 1.R1011 wty700164206.h1 5'-most EST

Method BLASTX NCBI GI q4587524 BLAST score 232 E value 3.0e-1969 Match length % identity 61

(AC007060) T518.13 [Arabidopsis thaliana] NCBI Description

Seq. No. 261739

E value

Match length

8.0e-77

147



```
3059 1.R1011
Contig ID
                   uC-zmflb73178c07b1
5'-most EST
Method
                   BLASTX
                   g2230757
NCBI GI
BLAST score
                   1143
                   1.0e-125
E value
Match length
                   383
                   62
% identity
NCBI Description
                   (Y11969) dnaJ-like protein [Arabidopsis thaliana]
                   261740
Seq. No.
                   3059 2.R1011
Contig ID
                   xyt7\overline{0}0343372.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g4220643
                   36
BLAST score
E value
                   1.0e-10
Match length
                   60
                   90
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MWD22, complete sequence [Arabidopsis thaliana]
                   261741
Seq. No.
Contig ID
                   3059 4.R1011
5'-most EST
                   LIB84-021-Q1-E1-A7
Seq. No.
                   261742
                   3060 1.R1011
Contig ID
                   LIB3075-008-Q1-K1-E9
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4468817
                   472
BLAST score
                   5.0e-47
E value
Match length
                   106
                   79
% identity
NCBI Description
                  (AL035601) putative protein [Arabidopsis thaliana]
                   261743
Seq. No.
Contig ID
                   3063 1.R1011
5'-most EST
                   LIB3079-056-Q1-K1-B11
Method
                   BLASTX
NCBI GI
                   g3204108
BLAST score
                   628
E value
                   3.0e-87
Match length
                   181
% identity
NCBI Description
                   (AJ006764) putative deoxycytidylate deaminase [Cicer
                   arietinum]
                   261744
Seq. No.
Contig ID
                   3076 1.R1011
                   ceu7\overline{0}0430074.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1321661
BLAST score
                   729
```



```
% identity
                  93
                  (D45423) ascorbate peroxidase [Oryza sativa]
NCBI Description
                  261745
Seq. No.
                  3076 2.R1011
Contig ID
                  LIB3067-006-Q1-K1-A11
5'-most EST
                  BLASTX
Method
                  g1321661
NCBI GI
                  1209
BLAST score
                  1.0e-133
E value
                  250
Match length
                  91
% identity
                  (D45423) ascorbate peroxidase [Oryza sativa]
NCBI Description
                  261746
Seq. No.
                   3076 3.R1011
Contig ID
                  LIB143-046-Q1-E1-B4
5'-most EST
Method
                   BLASTX
                   q1321661
NCBI GI
BLAST score
                   1194
                   1.0e-131
E value
                   250
Match length
                   90
% identity
                  (D45423) ascorbate peroxidase [Oryza sativa]
NCBI Description
                   261747
Seq. No.
                   3076 4.R1011
Contig ID
                   LIB3067-002-Q1-K1-E5
5'-most EST
Method
                   BLASTX
                   q1321661
NCBI GI
                   241
BLAST score
                   4.0e-20
E value
                   50
Match length
                   92
% identity
NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]
                   261748
Seq. No.
                   3076 6.R1011
Contig ID
                   uC-zmflmo17320c06b1
5'-most EST
                   BLASTX
Method
                   g3688398
NCBI GI
                   525
BLAST score
                   2.0e-53
E value
                   108
Match length
                   92
% identity
NCBI Description (AJ006358) ascorbate peroxidase [Hordeum vulgare]
                   261749
Seq. No.
                   3076 10.R1011
Contig ID
                   uC-zmrob73036g01b1
 5'-most EST
                   BLASTN
Method
                   q287829
NCBI GI
BLAST score
                   47
                   7.0e-17
E value
                   59
Match length
                   97
 % identity
```

NCBI Description Z.mays gene for polygalacturonase



```
261750
Seq. No.
Contig ID
                  3076 11.R1011
5'-most EST
                  LIB3075-008-Q1-K1-D7
                  261751
Seq. No.
                  3076 12.R1011
Contig ID
                  LIB3067-060-Q1-K1-B10
5'-most EST
Method
                  BLASTX
                   q3688398
NCBI GI
BLAST score
                   644
                   3.0e-67
E value
                   131
Match length
                   92
% identity
                  (AJ006358) ascorbate peroxidase [Hordeum vulgare]
NCBI Description
                   261752
Seq. No.
                   3076 15.R1011
Contig ID
                   uer700578164.h1
5'-most EST
Method
                   BLASTN
                   q1321660
NCBI GI
                   49
BLAST score
E value
                   1.0e-18
Match length
                   81
% identity
                   91
NCBI Description Rice mRNA for ascorbate peroxidase, complete cds
                   261753
Seq. No.
                   3080 1.R1011
Contig ID
                   xsy700210945.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1345881
BLAST score
                   630
                   1.0e-65
E value
Match length
                   131
% identity
                   88
                   CYTOCHROME B5 >gi 1076743 pir S46307 cytochrome b5 - rice
NCBI Description
                   >gi 414705 emb CAA53366 (X75670) cytochrome b5 [Oryza
                   sativa]
                   261754
Seq. No.
                   3080 2.R1011
Contig ID
                   uC\text{-}zmroteosinte048e09b1\\
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1345881
BLAST score
                   611
E value
                   3.0e-63
Match length
                   127
                   87
% identity
                   CYTOCHROME B5 >gi 1076743 pir S46307 cytochrome b5 - rice
NCBI Description
                   >qi 414705 emb CAA53366 (X75670) cytochrome b5 [Oryza
```

Seq. No. 261755

Contig ID 3082_1.R1011

5'-most EST uC-zmroteosinte098h03b2

sativa]

Method BLASTX

36257



```
g3023500
NCBI GI
                  308
BLAST score
                  8.0e-28
E value
Match length
                  86
% identity
                  67
                  ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 2
NCBI Description
                  (ENDOPEPTIDASE CLP 2) >gi 2351823 (U92039) ATP-dependent
                  Clp protease, proteolytic subunit [Synechococcus PCC7942]
                  261756
Seq. No.
                  3082_2.R1011
Contig ID
                  uC-zmrob73059g11a1
5'-most EST
Method
                  BLASTX
                  q3023500
NCBI GI
BLAST score
                  207
                  5.0e-16
E value
Match length
                  63
                  62
% identity
                  ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 2
NCBI Description
                  (ENDOPEPTIDASE CLP 2) >gi 2351823 (U92039) ATP-dependent
                  Clp protease, proteolytic subunit [Synechococcus PCC7942]
Seq. No.
                  261757
                  3083 1.R1011
Contig ID
                  LIB3075-008-Q1-K1-B6
5'-most EST
Method
                  BLASTX
                  g4376158
NCBI GI
BLAST score
                  232
                  3.0e-19
E value
                  83
Match length
                  63
% identity
NCBI Description (X98873) aspartate kinase [Arabidopsis thaliana]
Seq. No.
                  261758
                  3084 1.R1011
Contig ID
                  LIB3075-035-Q1-K1-A7
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1076668
BLAST score
                  1309
                   0.0e + 00
E value
Match length
                   389
                   95
% identity
                  NADH dehydrogenase (EC 1.6.99.3) - potato
NCBI Description
                   >gi 639834_emb_CAA58823_ (X83999) NADH dehydrogenase
                   [Solanum tuberosum]
                   261759
Seq. No.
Contig ID
                   3084 2.R1011
5'-most EST
                   LIB3150-094-P1-N1-C12
                  BLASTX
Method
NCBI GI
                   q1076668
BLAST score
                   253
```

E value 1.0e-21 Match length 50 96 % identity

NCBI Description NADH dehydrogenase (EC 1.6.99.3) - potato

>gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase



[Solanum tuberosum]

```
Seq. No.
                   261760
                   3084 3.R1011
Contig ID
                   yyf700351854.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4581156
                   2009
BLAST score
                   0.0e + 00
E value
Match length
                   474
                   84
% identity
                  (AC006919) putative pyruvate kinase [Arabidopsis thaliana]
NCBI Description
                   261761
Seq. No.
Contig ID
                   3084 4.R1011
                   uC-zmflmo17257h06b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3550985
BLAST score
                   1366
                   1.0e-151
E value
Match length
                   384
                   75
% identity
NCBI Description (AB010740) OsS5a [Oryza sativa]
                   261762
Seq. No.
                   3084 5.R1011
Contig ID
                   uC-zmflb73345b01a2
5'-most EST
Method
                   BLASTN
NCBI GI
                   q1213276
                   196
BLAST score
                   1.0e-106
E value
                   216
Match length
                   98
% identity
NCBI Description Z.mays ZEMa gene
                   261763
Seq. No.
                   3084 7.R1011
Contig ID
5'-most EST
                   ceu700422108.h1
                   BLASTX
Method
                   g4581156
NCBI GI
                   307
BLAST score
                   5.0e-28
E value
Match length
                   66
                   92
% identity
NCBI Description (AC006919) putative pyruvate kinase [Arabidopsis thaliana]
                   261764
Seq. No.
Contig ID
                   3084_8.R1011
                   uC-zmflmo17201f02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1076668
                   503
BLAST score
E value
                   8.0e-51
                   96
Match length
                   94
 % identity
```

>gi 639834 emb CAA58823_ (X83999) NADH dehydrogenase

NCBI Description NADH dehydrogenase (EC 1.6.99.3) - potato



[Solanum tuberosum]

261765 Seq. No. 3084 9.R1011 Contig ID uC-zmflmo17021a11b1 5'-most EST BLASTX Method g2586087 NCBI GI 221 BLAST score 2.0e-17 E value 164 Match length

13

% identity (U72724) receptor kinase-like protein [Oryza sativa] NCBI Description

261766 Seq. No. 3084 10.R1011 Contig ID pmx700088503.h1 5'-most EST Method BLASTN NCBI GI g1213276

BLAST score 110 2.0e-54 E value 130 Match length 96 % identity

NCBI Description Z.mays ZEMa gene

261767 Seq. No. 3084 11.R1011 Contig ID

5!-most EST LIB3136-040-P1-K1-B11

Method BLASTX q4503521 NCBI GI BLAST score 909 4.0e-98 E value 306

Match length 56 % identity

murine mammary tumor integration site 6 (oncogene homolog) NCBI Description

>gi_2498490_sp_Q64252_INT6_MOUSE VIRAL INTEGRATION SITE PROTEIN INT-6 >gi_1854579 (L35556) Int-6 [Mus musculus] >gi_2114363 (U629 $\overline{6}$ 2) similar to mouse Int-6 [Homo sapiens] >gi 2351382 (U54562) eIF3-p48 [Homo sapiens] >gi 2688818 (U85947) Int-6 [Homo sapiens] >gi 2695701 (U94175) mammary

tumor-associated protein INT6 [Homo sapiens]

Seq. No. 261768

Contig ID 3084 12.R1011

5'-most EST fC-zmfl1700337559d1

Method BLASTN NCBI GI q1213278 BLAST score 91 E value 1.0e-43 Match length 153 98 % identity

NCBI Description Z.mays ZEMb gene

Seq. No. 261769

3084 13.R1011 Contig ID uC-zmflb73139c01b1 5'-most EST

Method BLASTX NCBI GI g4220480



```
BLAST score 1260
E value 1.0e-139
Match length 399
% identity 64
NCBI Description (AC006069
```

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 261770

Contig ID 3084_14.R1011

5'-most EST LIB3088-003-Q1-K1-A5

Method BLASTN
NCBI GI g793901
BLAST score 110
E value 1.0e-54
Match length 122
% identity 98

NCBI Description Z.mays mRNA for ZEMa protein (ZEM1 gene)

Seq. No. 261771

Contig ID 3084_15.R1011

5'-most EST LIB143-065-Q1-E1-F7

Method BLASTX
NCBI GI g1076668
BLAST score 244
E value 8.0e-35
Match length 92
% identity 83

NCBI Description NADH dehydrogenase (EC 1.6.99.3) - potato

>gi 639834 emb CAA58823 (X83999) NADH dehydrogenase

[Solanum tuberosum]

Seq. No. 261772

Contig ID 3084 16.R1011

5'-most EST LIB3079-006-Q1-K1-B11

Method BLASTX
NCBI GI g4503521
BLAST score 539
E value 7.0e-55
Match length 193
% identity 55

NCBI Description murine mammary tumor integration site 6 (oncogene homolog)

>gi 2498490 sp Q64252 INT6 MOUSE VIRAL INTEGRATION SITE
PROTEIN INT-6 >gi 1854579 (L35556) Int-6 [Mus musculus]
>gi 2114363 (U62962) similar to mouse Int-6 [Homo sapiens]
>gi 2351382 (U54562) eIF3-p48 [Homo sapiens] >gi 2688818
(U85947) Int-6 [Homo sapiens] >gi 2695701 (U94175) mammary

tumor-associated protein INT6 [Homo sapiens]

Seq. No. 261773

Contig ID 3084_17.R1011 5'-most EST mwy700441495.h1 Method BLASTN

Method BLASTN
NCBI GI g1213278
BLAST score 85
E value 1.0e-39

Match length 97 % identity 98

NCBI Description Z.mays ZEMb gene

Match length

96



```
261774
Seq. No.
                   3084 18.R1011
Contig ID
                  xdb7\overline{0}0341194.h1
5'-most EST
                  BLASTN
Method
                   g1213276
NCBI GI
BLAST score
                   361
                   0.0e+00
E value
                   436
Match length
                   98
% identity
NCBI Description Z.mays ZEMa gene
                   261775
Seq. No.
                   3084 19.R1011
Contig ID
                   LIB3116-004-Q1-K1-H9
5'-most EST
                   BLASTN
Method
                   g1213278
NCBI GI
                   41
BLAST score
                   1.0e-13
E value
Match length
                   41
                   100
% identity
NCBI Description Z.mays ZEMb gene
                   261776
Seq. No.
                   3084 20.R1011
Contig ID
                   uC-zmflb73117b09b2
5'-most EST
Method
                   BLASTN
                   g1213276
NCBI GI
                   75
BLAST score
                   1.0e-33
E value
                   79
Match length
% identity
                   99
NCBI Description Z.mays ZEMa gene
                   261777
Seq. No.
Contig ID
                   3084 21.R1011
5'-most EST
                   LIB3069-054-Q1-K1-D10
                   BLASTN
Method
NCBI GI
                   g1213276
BLAST score
                   145
E value
                   2.0e-75
Match length
                   153
% identity
                   99
NCBI Description Z.mays ZEMa gene
Seq. No.
                   261778
Contig ID
                   3084 22.R1011
5'-most EST
                   uC-zmflMo17019f03b1
Method
                   BLASTN
NCBI GI
                   q21634
BLAST score
                   44
E value
                   3.0e-15
```



```
261779
Seq. No.
Contig ID
                  3084 23.R1011
5'-most EST
                  pmx700082157.h1
Method
                  BLASTX
NCBI GI
                  g1076668
BLAST score
                  188
                  4.0e-14
E value
Match length
                  36
% identity
                  89
                  NADH dehydrogenase (EC 1.6.99.3) - potato
NCBI Description
                  >gi 639834 emb CAA58823 (X83999) NADH dehydrogenase
                  [Solanum tuberosum]
                  261780
Seq. No.
Contig ID
                  3084 24.R1011
5'-most EST
                  uC-zmflmo17157a08a1
Method
                  BLASTX
NCBI GI
                  q4503521
BLAST score
                  204
E value
                  6.0e-16
Match length
                  83
                  47
% identity
                  murine mammary tumor integration site 6 (oncogene homolog)
NCBI Description
                  >gi_2498490_sp_Q64252_INT6_MOUSE VIRAL INTEGRATION SITE
                  PROTEIN INT-6 >gi_1854579 (L35556) Int-6 [Mus musculus]
                  >gi_2114363 (U62962) similar to mouse Int-6 [Homo sapiens]
                  >gi_2351382 (U54562) eIF3-p48 [Homo sapiens] >gi_2688818
                   (U85947) Int-6 [Homo sapiens] >gi_2695701 (U94175) mammary
                  tumor-associated protein INT6 [Homo sapiens]
Seq. No.
                  261781
Contig ID
                   3084 26.R1011
5'-most EST
                  xyt700344338.h1
Seg. No.
                   261782
Contig ID
                  3084 27.R1011
                  ntr700076239.h1
5'-most EST
Method
                  BLASTN
                  q3821780
NCBI GI
BLAST score
                  36
E value
                   2.0e-10
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  261783
                  3084 28.R1011
Contig ID
5'-most EST
                  LIB3180-013-P2-M1-D11
Method
                  BLASTX
NCBI GI
                  q125606
BLAST score
                   222
```

E value 5.0e-18 Match length 68 % identity 65

NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 100463 pir S12248

pyruvate kinase (EC 2.7.1.40) - potato

>gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum



tuberosum]

Seq. No. 261784

Contig ID 3084 29.R1011 5'-most EST clt700044108.rl

261785 Seq. No.

Contig ID 3084_30.R1011 5'-most EST uC-zmflb73301f01a1

Method BLASTX NCBI GI q3688634 BLAST score 261 1.0e-22 E value Match length 72 % identity 68

NCBI Description (U89162) similar to mouse mammary tumor associated gene

Int-6 product [Drosophila melanogaster]

261786 Seq. No.

Contig ID 3084 32.R1011

LIB3069-057-Q1-K1-F6 5'-most EST

Method BLASTX NCBI GI g1168817 BLAST score 351 E value 5.0e-66 Match length 206 % identity 62

pombe) >gi_521099_emb_CAA55382_ (X78799) cdc7 [Schizosaccharomyces pombe] >gi_4455770_emb_CAB36886_

(AL035537) cell division control protein 7

[Schizosaccharomyces pombe]

Seq. No. 261787

Contig ID 3084 33.R1011

5'-most EST uC-zmflmo17053d11b1

Method BLASTX NCBI GI g4503521 BLAST score 543 E value 3.0e-55

Match length 160 % identity 64

NCBI Description murine mammary tumor integration site 6 (oncogene homolog)

>gi 2498490 sp Q64252 INT6 MOUSE VIRAL INTEGRATION SITE PROTEIN INT-6 >gi 1854579 (L35556) Int-6 [Mus musculus] >gi 2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >gi_2351382 (U54562) eIF3-p48 [Homo sapiens] >gi_2688818 (U85947) Int-6 [Homo sapiens] >gi 2695701 (U94175) mammary

tumor-associated protein INT6 [Homo sapiens]

Seq. No. 261788

3084 34.R1011 Contig ID 5'-most EST uC-zmflb73325e01a1

Method BLASTN NCBI GI g1213276

BLAST score 77



E value 3.0e-35
Match length 81
% identity 99

NCBI Description Z.mays ZEMa gene

Seq. No. 261789

Contig ID 3084_35.R1011

5'-most EST LIB3061-032-Q1-K1-B4

Method BLASTX
NCBI GI g4220480
BLAST score 381
E value 2.0e-36
Match length 104
% identity 37

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 261790

Contig ID 3084 36.R1011

5'-most EST uC-zmflmo17375b09a1

Method BLASTN
NCBI GI g793901
BLAST score 81
E value 1.0e-37

Match length 97 % identity 96

NCBI Description Z.mays mRNA for ZEMa protein (ZEM1 gene)

Seq. No. 261791

Contig ID 3084_37.R1011 5'-most EST uC-zmflb73020f01b1

Seq. No. 261792

Contig ID 3084_38.R1011

5'-most EST LIB3 $\overline{07}6-014-Q1-K1-H6$

Method BLASTX
NCBI GI g3550985
BLAST score 226
E value 2.0e-18
Match length 49
% identity 90

NCBI Description (AB010740) OsS5a [Oryza sativa]

Seq. No. 261793

Contig ID 3084_39.R1011 5'-most EST ypc700802822.h1

Seq. No. 261794

Contig ID 3084_40.R1011

5'-most EST LIB3067-049-Q1-K1-H10

Method BLASTX
NCBI GI g3550985
BLAST score 492
E value 1.0e-49
Match length 117
% identity 85

NCBI Description (AB010740) OsS5a [Oryza sativa]



Seq. No. 261795 3084 42.R1011 Contig ID 5'-most EST uC-zmflb73097b07b1 Method BLASTN NCBI GI g1213276 BLAST score 82 6.0e-38

% identity NCBI Description Z.mays ZEMa gene

94

97

261796 Seq. No.

E value Match length

3084 43.R1011 Contig ID vmt700219978.h15'-most EST

Method BLASTX NCBI GI q3549652 146 BLAST score 4.0e-09 E value Match length 30 % identity 93

(AJ224982) MAP3K epsilon protein kinase [Arabidopsis NCBI Description

thaliana]

261797 Seq. No.

3084 44.R1011 Contig ID uC-zmrob73011e04b1 5'-most EST

261798 Seq. No.

3084 45.R1011 Contig ID

5'-most EST LIB3076-033-Q1-K1-B7

Method BLASTN NCBI GI g1906603 BLAST score 65 E value 6.0e-28 Match length 142

% identity 87

Zea mays ACCase gene, intron containing colonist1 and NCBI Description colonist2 retrotransposons and reverse transcriptase

pseudogene, complete sequence

Seq. No. 261799

3084 46.R1011 Contig ID

LIB3059-032-Q1-K1-A4 5'-most EST

Method BLASTN g793901 NCBI GI BLAST score 86 2.0e-40 E value 94 Match length 98 % identity

NCBI Description Z.mays mRNA for ZEMa protein (ZEM1 gene)

Seq. No. 261800

Contig ID 3084 47.R1011

5'-most EST uC-zmflmo17268e04b1

Seq. No. 261801

3084 48.R1011 Contig ID



5'-most EST LIB3079-014-Q1-K1-A12

261802 Seq. No. Contig ID 3084 51.R1011

zuv700356879.h1 5'-most EST

261803 Seq. No.

3084 57.R1011 Contig ID 5'-most EST ceu700433582.h1

261804 Seq. No.

3084_60.R1011 Contig ID

LIB3067-001-Q1-K1-D1 5'-most EST

261805 Seq. No.

3084_64.R1011 Contig ID ypc700801222.hl 5'-most EST

Seq. No. 261806

Contig ID 3097 1.R1011 ypc700801625.h1 5'-most EST

Method BLASTX g1350720 NCBI GI BLAST score 431 E value 3.0e-42 Match length 111 76 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L32

261807 Seq. No.

Contig ID 3097 2.R1011

5'-most EST LIB3150-019-Q1-N1-H12

Method BLASTX NCBI GI q1350720 BLAST score 475 E value 2.0e-47 Match length 111

% identity 81

NCBI Description 60S RIBOSOMAL PROTEIN L32

Seq. No. 261808 3097 3.R1011 Contig ID

5'-most EST LIB3059-047-Q1-K1-C7

Method BLASTX g1350720 NCBI GI BLAST score 478 6.0e-48 E value Match length 111 82 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L32

Seq. No. 261809

3097 4.R1011 Contig ID

5'-most EST LIB3150-028-Q1-N1-C2

Method BLASTX NCBI GI g1350720 BLAST score 425



1.0e-41 E value Match length 111 74 % identity

60S RIBOSOMAL PROTEIN L32 NCBI Description

261810 Seq. No.

3097 5.R1011 Contig ID

LIB36-019-Q1-E1-C8 5'-most EST

BLASTX Method NCBI GI g1350720 431 BLAST score 2.0e-42E value 111 Match length 76 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L32

261811 Seq. No.

3097 6.R1011 Contig ID pmx700088054.h1 5'-most EST

BLASTX Method NCBI GI g1350720 413 BLAST score 3.0e-40E value Match length 111 73 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L32

261812 Seq. No.

3097 9.R1011 Contig ID

5'-most EST LIB3069-035-01-K1-C11

BLASTX Method g4506635 NCBI GI BLAST score 239 3.0e-20 E value 68 Match length 71 % identity

ribosomal protein L32 >gi_132886_sp_P02433_RL32_HUMAN 60S RIBOSOMAL PROTEIN L32 >gi_71335_pir_R5HU32 ribosomal NCBI Description

protein L32 - human >gi_71336_pir__R5MS32 ribosomal protein L32 - mouse >gi_71337_pir__R5RT32 ribosomal protein L32 - rat >gi_36132_emb_CAA27048 (X03342) rpL32 (aa 1-135) [Homo sapiens] >gi_57117_emb_CAA29777 (X06483) ribosomal protein L32 [Rattus norvegicus] >gi_200781 (K02060) ribosomal

protein L32-3A [Mus musculus] >gi 226004 prf 1405339A

ribosomal protein L32 [Rattus norvegicus]

Seq. No. 261813 3098 2.R1011 Contig ID

5'-most EST LIB3075-008-Q1-K1-A12

261814 Seq. No.

3102 1.R1011 Contig ID 5'-most EST ymt700223129.h1

BLASTX Method NCBI GI g3334320 BLAST score 999 E value 1.0e-108



Match length 200 94 % identity

NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)

ribosome-associated protein p40 [Glycine max]

Seq. No. 261815 3102 2.R1011 Contig ID

5'-most EST LIB3115-024-P1-K1-A2

Seq. No. 261816

Contig ID 3103 1.R1011 5'-most EST xjt700095589.h1

261817 Seq. No.

Contig ID 3105 1.R1011 yyf700351258.h1 5'-most EST

Method BLASTX NCBI GI q4586111 BLAST score 506 E value 7.0e-51 190 Match length % identity 58

NCBI Description (AL049638) putative protein [Arabidopsis thaliana]

261818 Seq. No.

Contig ID 3109 1.R1011

5'-most EST LIB3066-001-Q1-K1-C8

261819 Seq. No. 3110 1.R1011 Contig ID

xjt700095305.h1 5'-most EST

Method BLASTX NCBI GI q2058273 BLAST score 841 E value 3.0e-90 Match length 189

% identity 87

NCBI Description (D83527) YK426 [Oryza sativa]

Seq. No. 261820

Contig ID 3110 2.R1011

5'-most EST LIB3181-003-P1-M1-H4

Method BLASTX NCBI GI g2058273 BLAST score 539 E value 9.0e-78 179 Match length % identity 85

NCBI Description (D83527) YK426 [Oryza sativa]

Seq. No. 261821

3110 3.R1011 Contig ID

5'-most EST LIB189-021-Q1-E1-E3

Method BLASTX NCBI GI g2058273 BLAST score 826 E value 2.0e-88



Match length 189 % identity 85

NCBI Description (D83527) YK426 [Oryza sativa]

Seq. No. 261822

Contig ID 3110_10.R1011 5'-most EST uer700580107.h1

Seq. No. 261823

Contig ID 3111 1.R1011

5'-most EST LIB3075-007-Q1-K1-G8

Method BLASTX
NCBI GI g2370312
BLAST score 457
E value 9.0e-80
Match length 202
% identity 70

NCBI Description (AJ000995) DnaJ-like protein [Medicago sativa] >gi_3202020

(AF069507) DnaJ-like protein MsJ1 [Medicago sativa]

Seq. No. 261824

Contig ID 3112_1.R1011 5'-most EST uwc700151904.h1

Method BLASTX
NCBI GI g4539371
BLAST score 227
E value 4.0e-18
Match length 153
% identity 40

NCBI Description (AL049525) putative protein [Arabidopsis thaliana]

Seq. No. 261825

Contig ID 3112_2.R1011

5'-most EST LIB3150-004-Q1-N1-G1

Seq. No. 261826

Contig ID 3115 1.R1011

5'-most EST LIB3068-031-Q1-K1-F9

Method BLASTX
NCBI GI g3560264
BLAST score 331
E value 3.0e-30
Match length 248
% identity 35

NCBI Description (AL031535) soll family protein [Schizosaccharomyces pombe]

Seq. No. 261827

Contig ID 3117_1.R1011

5'-most EST LIB3075-007-Q1-K1-H3

Method BLASTX
NCBI GI g3668091
BLAST score 149
E value 2.0e-09
Match length 118
% identity 28

NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]



```
261828
Seq. No.
                  3120 1.R1011
Contig ID
                  xsy700212006.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4455158
BLAST score
                  883
                  7.0e-95
E value
                  217
Match length
                  73
% identity
                  (AL021687) kinase-like protein [Arabidopsis thaliana]
NCBI Description
                  261829
Seq. No.
                   3124_1.R1011
Contig ID
                  uC-z\overline{m}flb73063d04b1
5'-most EST
                  BLASTX
Method
                   g2688830
NCBI GI
BLAST score
                   1679
                   0.0e+00
E value
                   458
Match length
                   73
% identity
                  (AF000952) putative sugar transporter [Prunus armeniaca]
NCBI Description
                   261830
Seq. No.
                   3124 2.R1011
Contig ID
                   uC-zmrob73019f04b1
5'-most EST
Seq. No.
                   261831
                   3124 4.R1011
Contig ID
                   LIB3279-050-P1-K1-C12
5'-most EST
                   BLASTX
Method
                   g2688830
NCBI GI
BLAST score
                   539
                   7.0e-55
E value
                   197
Match length
                   59
% identity
                  (AF000952) putative sugar transporter [Prunus armeniaca]
NCBI Description
Seq. No.
                   261832
                   3124_5.R1011
Contig ID
                   uC-zmflmo17327e11a1
5'-most EST
                   261833
Seq. No.
                   3124 9.R1011
Contig ID
                   uC-zmflb73239a09a1
5'-most EST
                   BLASTX
Method
                   q2688830
NCBI GI
BLAST score
                   192
E value
                   2.0e-14
Match length
                   46
% identity
                  (AF000952) putative sugar transporter [Prunus armeniaca]
NCBI Description
```

Seq. No. 261834 Contig ID 3126 1.R1011

5'-most EST LIB3137-027-Q1-K1-F1

Seq. No. 261835



```
Contig ID
                   3126 3.R1011
                  LIB3075-007-Q1-K1-F4
5'-most EST
                   261836
Seq. No.
Contig ID
                   3129 1.R1011
                   tzu700203381.h1
5'-most EST
                   BLASTX
Method
                   g1871177
NCBI GI
                   298
BLAST score
                   1.0e-26
E value
Match length
                   83
                   73
% identity
                  (U90439) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   261837
                   3129 2.R1011
Contig ID
                   wen7\overline{0}0334590.h1
5'-most EST
                   261838
Seq. No.
                   3129 3.R1011
Contig ID
                   wty700170349.h1
5'-most EST
                   BLASTX
Method
                   g1871177
NCBI GI
BLAST score
                   192
                   5.0e-15
E value
Match length
                   85
                   51
% identity
                  (U90439) unknown protein [Arabidopsis thaliana]
NCBI Description
                   261839
Seq. No.
                   3134 1.R1011
Contig ID
                   tzu700204341.hl
5'-most EST
                   BLASTX
Method
                   g3341681
NCBI GI
                   710
BLAST score
                   1.0e-80
E value
                   204
Match length
% identity
                   82
                   (AC003672) small GTP-binding protein [Arabidopsis thaliana]
NCBI Description
                   >qi 741994 prf 2008312A GTP-binding protein [Arabidopsis
                   thaliana]
                   261840
Seq. No.
                   3148 1.R1011
Contig ID
                   bdu700382959.h1
5'-most EST
                   261841
Seq. No.
Contig ID
                   3152 1.R1011
5'-most EST
                   vmt700221264.h1
                   BLASTX
Method
                   q1213460
NCBI GI
                   677
BLAST score
E value
                   1.0e-70
```

NCBI Description (U03374) C subunit of V-ATPase [Amblyomma americanum]

364

40

Match length

% identity



261842 Seq. No. 3152 2.R1011 Contig ID

uC-zmf1b73030c05b15'-most EST

BLASTX Method NCBI GI g2245679 BLAST score 240 E value 7.0e-20 Match length 126

% identity (AF006655) V-ATPase C subunit [Drosophila melanogaster] NCBI Description

261843 Seq. No.

3152 3.R1011 Contig ID

uC-zmflMo17089c12b1 5'-most EST

41

BLASTX Method NCBI GI q4502315 257 BLAST score 7.0e-22 E value 160 Match length 36 % identity

ATPase, H+ transporting, lysosomal (vacuolar proton pump) NCBI Description

42kD >gi 401329 sp P21283_VATC_HUMAN VACUOLAR ATP SYNTHASE SUBUNIT C (V-ATPASE C SUBUNIT) >gi 542836_pir__JN0907 H+-transporting ATPase (EC 3.6.1.35) chain C, vacuolar -

human >gi 37643 emb CAA48903 (X69151) vacuolar

proton-ATPase [Homo sapiens]

261844 Seq. No.

3152 6.R1011 Contig ID ntr700072430.h2 5'-most EST

Seq. No. 261845

3156 1.R1011 Contig ID

LIB3075-007-Q1-K1-C6 5'-most EST

261846 Seq. No.

Contig ID 3158 1.R1011 5'-most EST pmx700085919.h1

Method BLASTX g585322 NCBI GI BLAST score 607 E value 1.0e-62 223 Match length % identity

NCBI Description INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE)

(PPASE) >gi_539751_pir__A45153 inorganic pyrophosphatase (EC 3.6.1.1) - bovine

261847 Seq. No.

3160 1.R1011 Contig ID

5'-most EST LIB3075-007-Q1-K1-D1

Method BLASTX NCBI GI g3461828 BLAST score 208 2.0e-16 E value Match length 108 % identity 40



```
(AC004138) unknown protein [Arabidopsis thaliana]
NCBI Description
                  261848
Seq. No.
                  3163 1.R1011
Contig ID
5'-most EST
                  uC-zmroteosinte098f09b2
                  261849
Seq. No.
                  3163 2.R1011
Contig ID
                  dyk700103482.h1
5'-most EST
Seq. No.
                  261850
                  3168 1.R1011
Contig ID
5'-most EST
                  gct701169356.hl
Seq. No.
                  261851
                  3170 1.R1011
Contig ID
                  LIB3088-022-Q1-K1-C3
5'-most EST
                  261852
Seq. No.
                  3170 2.R1011
Contig ID
5'-most EST
                  uC-zmflmo17201f10a1
                  261853
Seq. No.
                  3170 3.R1011
Contig ID
5'-most EST
                  xjt700092001.h1
Seq. No.
                   261854
                   3172 1.R1011
Contig ID
                  LIB3078-057-Q1-K1-B12
5'-most EST
                  BLASTX
Method
NCBI GI
                  g554565
BLAST score
                   1109
                   1.0e-121
E value
                   214
Match length
                   100
% identity
NCBI Description (M24889) glutathione S-transferase [Artificial gene]
                   261855
Seq. No.
Contig ID
                   3172 2.R1011
5'-most EST
                   uC-zmroteosintel18c11b1
Method
                   BLASTX
NCBI GI
                   g554565
BLAST score
                   215
E value
                   4.0e-17
Match length
                   46
% identity
NCBI Description (M24889) glutathione S-transferase [Artificial gene]
Seq. No.
                   261856
                   3172 3.R1011
Contig ID
                   ntr700073513.h1
5'-most EST
```

 Seq. No.
 261856

 Contig ID
 3172_3.R1011

 5'-most EST
 ntr700073513.h1

 Method
 BLASTN

 NCBI GI
 g168487

 BLAST score
 253

 E value
 1.0e-140

Match length 299 % identity 97



```
NCBI Description Maize glutathione S-transferase gene (GST-I), exons 2 and 3
                   261857
Seq. No.
Contig ID
                   3172 8.R1011
                   yyf7\overline{0}0350139.h1
5'-most EST
Method
                   BLASTN
                   q168486
NCBI GI
                   97
BLAST score
E value
                   2.0e-47
Match length
                   185
                   99
% identity
NCBI Description Maize glutathione S-transferase gene (GST-I), exon 1
                   261858
Seq. No.
Contig ID
                   3173 1.R1011
                   uC-zmflmo17202b07b1
5'-most EST
Method
                   BLASTX
                   g4539324
NCBI GI
                   290
BLAST score
E value
                   1.0e-25
Match length
                   227
                   34
% identity
                  (AL035679) kinesin like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   261859
Contig ID
                   3173 2.R1011
5'-most EST
                   LIB3088-042-Q1-K1-G1
                   261860
Seq. No.
                   3173 5.R1011
Contig ID
5'-most EST
                   uC-zmflb73283f07b2
                   261861
Seq. No.
Contig ID
                   3173 8.R1011
5'-most EST
                   tzu700206552.h1
Method
                   BLASTX
NCBI GI
                   g4539324
BLAST score
                   181
E value
                   4.0e-13
Match length
                   107
% identity
                   49
                  (AL035679) kinesin like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   261862
                   3177 1.R1011
Contig ID
5'-most EST
                   uC-zmflMo17086g11b1
Method
                   BLASTX
                   g4512667
NCBI GI
BLAST score
                   1916
E value
                   0.0e + 00
Match length
                   568
% identity
                   68
                  (AC006931) putative MAP kinase [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 261863 3177 4.R1011 Contig ID

5'-most EST LIB36-006-Q1-E1-C12



Method BLASTX
NCBI GI g4512667
BLAST score 491
E value 1.0e-49
Match length 111
% identity 83

NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No. 261864

Contig ID 3178_1.R1011

5'-most EST LIB3075-006-Q1-K1-G3

Method BLASTX
NCBI GI g3600058
BLAST score 553
E value 6.0e-63
Match length 224
% identity 58

NCBI Description (AF080120) similar to vacuolar ATPases [Arabidopsis

thaliana]

Seq. No. 261865

Contig ID 3181_1.R1011

5'-most EST uC-zmflmo17077c01b1

 Seq. No.
 261866

 Contig ID
 3182_1.R1011

 5'-most EST
 uwc700152674.h1

Method BLASTX
NCBI GI g2695861
BLAST score 1001
E value 1.0e-109
Match length 217
% identity 87

NCBI Description (Y14272) 3-deoxy-D-manno-2-octulosonate-8-phosphate

synthase [Pisum sativum] >gi_2695863_emb_CAA74645_ (Y14273)
3-deoxy-D-manno-2-octulosonate-8-phosphate synthase [Pisum

sativum]

Seq. No. 261867

Contig ID 3185_1.R1011

5'-most EST uC-zmflmo17061c04b1

Method BLASTX
NCBI GI g3355486
BLAST score 773
E value 5.0e-82
Match length 289
% identity 58

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 261868

Contig ID 3185_2.R1011

5'-most EST uC-zmflmo17017b03b1

Method BLASTX
NCBI GI g3355486
BLAST score 317
E value 5.0e-29
Match length 200

% identity (AC004218) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 261869 Contig ID 3188 1.R1011 LIB3075-006-Q1-K1-H6 5'-most EST Seq. No. 261870 3190 1.R1011 Contig ID 5'-most EST ypc700799210.h1 261871 Seq. No. Contig ID 3190 2.R1011 5'-most EST wty700168763.h1 261872 Seq. No. 3192 1.R1011 Contig ID clt700044424.fl 5'-most EST Method BLASTX g2623310 NCBI GI BLAST score 221 2.0e-17 E value

186 Match length % identity 37

(AC002409) unknown protein [Arabidopsis thaliana] NCBI Description

>qi 3402721 (AC004261) unknown protein [Arabidopsis

thaliana]

Seq. No. 261873 3193 1.R1011 Contig ID

LIB3075-005-Q1-K1-A3 5'-most EST

261874 Seq. No. 3194 1.R1011 Contig ID

LIB3067-022-Q1-K1-G6 5'-most EST

BLASTX Method g2493852 NCBI GI 326 BLAST score 6.0e-30 E value Match length 63 97 % identity

CYTOCHROME C OXIDASE POLYPEPTIDE VC NCBI Description

>gi_1070356_emb_CAA92107_ (Z68091) cytochrome c oxidase, Vc

subunit [Hordeum vulgare]

261875 Seq. No. 3194 2.R1011 Contig ID 5'-most EST wty700170067.hl

BLASTX Method g2493852 NCBI GI 326 BLAST score 4.0e-30 E value 63 Match length 97 % identity

NCBI Description CYTOCHROME C OXIDASE POLYPEPTIDE VC

>gi_1070356_emb_CAA92107_ (Z68091) cytochrome c oxidase, Vc subunit [Hordeum vulgare]



```
261876
Seq. No.
Contig ID
                  3194 3.R1011
                  LIB3078-036-Q1-K1-D12
5'-most EST
Method
                  BLASTX
                  g2493852
NCBI GI
BLAST score
                  227
                  2.0e-18
E value
Match length
                  56
                  75
% identity
                  CYTOCHROME C OXIDASE POLYPEPTIDE VC
NCBI Description
                  >gi_1070356_emb_CAA92107_ (Z68091) cytochrome c oxidase, Vc
                  subunit [Hordeum vulgare]
                  261877
Seq. No.
                  3195 1.R1011
Contig ID
                  fdz701158412.h1
5'-most EST
                  BLASTX
Method
                  q4406764
NCBI GI
BLAST score
                   254
                   6.0e-22
E value
Match length
                   112
                   42
% identity
                  (AC006836) putative uridylyl transferase [Arabidopsis
NCBI Description
                  thaliana]
                   261878
Seq. No.
                   3198 1.R1011
Contig ID
                   LIB3075-006-Q1-K1-F2
5'-most EST
Method
                   BLASTX
                   q2245120
NCBI GI
                   289
BLAST score
                   6.0e-26
E value
                   115
Match length
                   49
% identity
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   261879
Seq. No.
                   3199 1.R1011
Contig ID
5'-most EST
                   LIB3069-055-Q1-K1-H10
                   BLASTX
Method
                   g4587518
NCBI GI
BLAST score
                   494
                   1.0e-49
E value
                   118
Match length
                   78
% identity
                  (AC007060) Strong similarity to F19I3.8 gi_3033381 putative
NCBI Description
                   UDP-galactose-4-epimerase from Arabidopsis thaliana BAC
                   gb AC004238 and is a member of PF 01370 the NAD dependent
                   epimerase/dehydratase family. EST gb AA59
```

Seq. No. 261880 Contig ID 3200 1.R1011

5'-most EST uC-zmflb73060b05b1

Method BLASTX
NCBI GI g3063708
BLAST score 409



9.0e-40 E value 212 Match length 40 % identity

(AL022537) putative protein [Arabidopsis thaliana] NCBI Description

261881 Seq. No.

3200 2.R1011 Contig ID

LIB3078-047-Q1-K1-F6 5'-most EST

BLASTX Method NCBI GI g3063708 171 BLAST score 7.0e-12 E value Match length 121 % identity 38

(AL022537) putative protein [Arabidopsis thaliana] NCBI Description

261882 Seq. No.

3202 1.R1011 Contig ID

LIB36-015-Q1-E1-B5 5'-most EST

BLASTX Method g3355617 NCBI GI BLAST score 415 2.0e-40 E value 84

Match length 92 % identity

(AJ000229) unnamed protein product [Hordeum vulgare] NCBI Description

261883 Seq. No.

3203 1.R1011 Contig ID $xmt7\overline{0}0263755.h1$ 5'-most EST

Method BLASTX NCBI GI q4406775 BLAST score 484 4.0e-48 E value 427 Match length % identity 33

NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]

261884 Seq. No.

3203 2.R1011 Contig ID

5'-most EST uC-zmflmo17197b04b1

Method BLASTX NCBI GI q1749546 BLAST score 253 E value 8.0e-21 Match length 217 % identity 40

(D89169) similar to Saccharomyces cerevisiae SCD6 protein, NCBI Description

SWISS-PROT Accession Number P45978 [Schizosaccharomyces

pombe]

Seq. No. 261885

3203 3.R1011 Contig ID

5'-most EST uC-zmflmo17321h04b1

261886 Seq. No.

3209_1.R1011 Contig ID

Match length

NCBI Description

% identity

240 77

thaliana]



5'-most EST uC-zmflb73194b11b2 Method BLASTX NCBI GI g2088656 BLAST score 145 8.0e-09 E value Match length 59 % identity 41 (AF002109) DNA-directed RNA polymerase II isolog NCBI Description [Arabidopsis thaliana] 261887 Seq. No. 3211 1.R1011 Contig ID LIB3150-043-Q1-N1-E1 5'-most EST BLASTX Method NCBI GI g4325324 BLAST score 2199 0.0e+00E value Match length 536 % identity 76 NCBI Description (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis thaliana] 261888 Seq. No. 3211_2.R1011 Contig ID 5'-most EST uC-zmflmo17341c07b1 BLASTX Method NCBI GI q4325324 239 BLAST score 6.0e-20 E value Match length 77 % identity 60 NCBI Description (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis thaliana] Seq. No. 261889 Contig ID 3211 3.R1011 5'-most EST LIB3156-007-Q1-K1-E2 Method BLASTX NCBI GI q4325324 BLAST score 297 E value 2.0e-26 Match length 69 % identity 83 (AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis NCBI Description thaliana] 261890 Seq. No. 3219 1.R1011 Contig ID wen700332553.h1 5'-most EST Method BLASTX NCBI GI q3386615 BLAST score 1015 E value 1.0e-110

36280

(AC004665) putative phosphomannomutase [Arabidopsis

E value

Match length

% identity

6.0e-23

106

56



```
261891
Seq. No.
                   3219 2.R1011
Contig ID
5'-most EST
                  bdu700382725.h1
Method
                  BLASTX
NCBI GI
                  g3386615
                   233
BLAST score
                  2.0e-19
E value
Match length
                   65
% identity
                   69
NCBI Description
                  (AC004665) putative phosphomannomutase [Arabidopsis
                   thaliana]
                   261892
Seq. No.
Contig ID
                   3221 1.R1011
5'-most EST
                  LIB3180-005-P2-M1-E10
Method
                  BLASTX
NCBI GI
                  q4503515
BLAST score
                   549
E value
                   8.0e-56
Match length
                   315
                   38
% identity
                  UNKNOWN >gi 2351380 (U54559) translation initiation factor
NCBI Description
                   eIF3 p40 subunit [Homo sapiens]
Seq. No.
                   261893
Contig ID
                   3221 2.R1011
                   tzu700204776.h1
5'-most EST
Seq. No.
                   261894
Contig ID
                   3221 3.R1011
5'-most EST
                  xyt700343404.h1
                   261895
Seq. No.
Contig ID
                   3222 1.R1011
5'-most EST
                  LIB3115-017-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   q4455332
BLAST score
                   211
E value
                   2.0e-16
Match length
                   97
% identity
                   48
NCBI Description
                  (AL035525) putative protein [Arabidopsis thaliana]
Seq. No.
                   261896
Contig ID
                   3223 1.R1011
5'-most EST
                   ntr700073416.hl
Seq. No.
                   261897
Contig ID
                   3226 1.R1011
5'-most EST
                  LIB3066-016-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                   g2262166
BLAST score
                   267
```



NCBI Description (AC002329) hypothetical protein [Arabidopsis thaliana]

Seq. No. 261898

Contig ID 3237 1.R1011

5'-most EST uC-zmflmo17053f07b1

Method BLASTX
NCBI GI g3763916
BLAST score 1355
E value 1.0e-150
Match length 493
% identity 55

NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]

>gi 4531439 gb AAD22124.1 AC006224 6 (AC006224) unknown

protein [Arabidopsis thaliana]

Seq. No. 261899

Contig ID 3244 1.R1011

5'-most EST uC-zmflb73224b10b2

Seq. No. 261900

Contig ID 3246_1.R1011

5'-most EST LIB3079-024-Q1-K1-E7

Method BLASTX
NCBI GI g3687235
BLAST score 553
E value 3.0e-56
Match length 150
% identity 75

NCBI Description (AC005169) putative copia-like transposable element

[Arabidopsis thaliana]

Seq. No. 261901

Contig ID 3246 2.R1011

5'-most EST LIB3279-017-P1-K1-E4

 Seq. No.
 261902

 Contig ID
 3246_3.R1011

 5'-most EST
 ymt700220735.h1

Method BLASTX
NCBI GI g3687235
BLAST score 246
E value 8.0e-21
Match length 79
% identity 66

NCBI Description (AC005169) putative copia-like transposable element

[Arabidopsis thaliana]

Seq. No. 261903

Contig ID 3246_5.R1011 5'-most EST clt700043172.f1

Method BLASTX
NCBI GI g3687235
BLAST score 201
E value 2.0e-15
Match length 60
% identity 68

NCBI Description (AC005169) putative copia-like transposable element



[Arabidopsis thaliana]

Seq. No. 261904 Contig ID 3246_8.R1011 5'-most EST xyt700343571.h1

Seq. No. 261905

Contig ID 3246_11.R1011 5'-most EST dyk700103089.h1

Seq. No. 261906

Contig ID 3248_1.R1011 5'-most EST zuv700353831.h1

Method BLASTX
NCBI GI g4455222
BLAST score 166
E value 7.0e-11
Match length 164
% identity 30

NCBI Description (AL035440) hypothetical protein [Arabidopsis thaliana]

Seq. No. 261907

Contig ID 3248_2.R1011

5'-most EST uC-zmflb73391d01a1

Seq. No. 261908

Contig ID 3252_1.R1011 5'-most EST wyr700236805.h1

Method BLASTX
NCBI GI g4103987
BLAST score 879
E value 1.0e-94
Match length 217
% identity 78

NCBI Description (AF030516) 5,10-methylenetetrahydrofolate

dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase

[Pisum sativum]

Seq. No. 261909 Contig ID 3252 2.R1011

5'-most EST uC-zmflmo17055a08b1

Method BLASTX
NCBI GI g4103987
BLAST score 450
E value 9.0e-45
Match length 143
% identity 62

NCBI Description (AF030516) 5,10-methylenetetrahydrofolate

dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase

[Pisum sativum]

Seq. No. 261910

Contig ID 3253_1.R1011

5'-most EST LIB3156-008-Q1-K1-E5

Method BLASTX NCBI GI g134102 BLAST score 2066



E value 0.0e+00 Match length 524 79

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60

KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA)

>gi_72959_pir__ HHWTBA ribulose-bisphosphate carboxylase
subunit-binding protein alpha chain - wheat (fragment)
>gi_1345582_emb_CAA30699_ (X07851) rubisco subunit
binding-protein alpha subunit (543 AA) [Triticum

aestivum]

Seq. No. 261911 Contig ID 3253 2.R1011

5'-most EST uC-zmflb73059g12b1

Method BLASTX
NCBI GI g3063448
BLAST score 738
E value 3.0e-78
Match length 203
% identity 70

NCBI Description (AC003981) F22013.10 [Arabidopsis thaliana]

Seq. No. 261912
Contig ID 3253_3.R1011

5'-most EST uC-zmflb73252a07b3

Method BLASTX
NCBI GI g134102
BLAST score 288
E value 9.0e-26
Match length 64
% identity 84

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60

KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA)

>gi_72959_pir__HHWTBA ribulose-bisphosphate carboxylase
subunit-binding protein alpha chain - wheat (fragment)
>gi_1345582_emb_CAA30699_ (X07851) rubisco subunit
binding-protein alpha subunit (543 AA) [Triticum

aestivum]

Seq. No. 261913

Contig ID 3261 1.R1011

5'-most EST LIB3075-005-Q1-K1-H11

Seq. No. 261914

Contig ID 3265 1.R1011

5'-most EST uC-zmflmo17161a12b1

Seq. No. 261915

Contig ID 3266_1.R1011 5'-most EST fwa700101089.h1

Method BLASTX
NCBI GI g132659
BLAST score 690
E value 1.0e-72
Match length 188
% identity 72

NCBI Description 50S RIBOSOMAL PROTEIN L13, CHLOROPLAST PRECURSOR (CL13)



>gi_81483_pir__A32033 ribosomal protein L13 precursor, chloroplast - spinach >gi 170133 (J04461) ribosomal protein L13 [Spinacia oleracea]

Seq. No. 261916 Contig ID 3274 1.R1011 5'-most EST LIB3150-014-Q1-N1-F10 Method BLASTX NCBI GI q4176527 BLAST score 170 E value 1.0e-11 Match length 182

% identity NCBI Description (AL035263) hypothetical protein [Schizosaccharomyces pombe]

261917 Seq. No. Contig ID 3285 1.R1011

5'-most EST LIB3116-010-Q1-K1-D9

26

Seq. No. 261918

Contig ID 3286 1.R1011

5'-most EST LIB3059-002-Q1-K2-C3

Method BLASTX NCBI GI q3264605 BLAST score 459 E value 2.0e-45 Match length 109 % identity

NCBI Description (AF061508) ribosomal protein L25 [Zea mays]

Seq. No. 261919

Contig ID 3286 2.R1011

5'-most EST uC-zmflmo17021h09b1

Method BLASTX NCBI GI q3176687 BLAST score 1875 E value 0.0e+00Match length 591 % identity 59

(AC003671) Strong similarity to trehalose-6-phosphate NCBI Description

synthase homolog from A. thaliana chromosome 4 contig gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and gb_R64855 come from this gene. [Arabidopsis thaliana]

Seq. No. 261920 Contig ID 3286 3.R1011 5'-most EST fwa700100725.h1

261921 Seq. No.

3286 4.R1011 Contig ID LIB3279-051-P1-K1-D10 5'-most EST

Method BLASTX NCBI GI g585876 BLAST score 453

E value 9.0e-45Match length 117 % identity 78



60S RIBOSOMAL PROTEIN L23A (L25) >gi 1084424_pir_ S48026 NCBI Description ribosomal protein L25 - common tobacco >gi 310935 (L18908) 60S ribosomal protein L25 [Nicotiana tabacum]

261922 Seq. No.

3286 5.R1011 Contig ID

LIB3078-033-Q1-K1-E7 5'-most EST

Method BLASTX NCBI GI g585876 455 BLAST score 5.0e-45 E value 155 Match length 64 % identity

60S RIBOSOMAL PROTEIN L23A (L25) >gi_1084424_pir__S48026 NCBI Description

ribosomal protein L25 - common tobacco >gi_310935 (L18908)

60S ribosomal protein L25 [Nicotiana tabacum]

261923 Seq. No.

3289 1.R1011 Contig ID

LIB3136-007-Q1-K1-H10 5'-most EST

BLASTX Method g1709358 NCBI GI BLAST score 1094 1.0e-119 E value 400 Match length 53 % identity

NCBI Description NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE

PHOSPHOHYDROLASE) (NTPASE) >gi_629638_pir__S48859

nucleoside triphosphatase - garden pea

>gi_2129890_pir__S65147 nucleoside triphosphatase

precursor, chromatin-associated - garden pea >gi_563612_emb_CAA83655_ (Z32743) nucleoside triphosphatase

[Pisum sativum] >gi_4519173_dbj_BAA75506.1_ (AB022319) nucleoside triphosphatase (NTPase) [Pisum sativum]

261924 Seq. No.

Contig ID 3292 1.R1011

LIB3075-005-Q1-K1-B11 5'-most EST

261925 Seq. No.

3294 1.R1011 Contig ID

5'-most EST uC-zmflmo17072f03b1

261926 Seq. No.

3294 2.R1011 Contig ID

uC-zmroteosinte041a05b1 5'-most EST

Method BLASTX NCBI GI q730461 BLAST score 215 3.0e-17 E value Match length 56 % identity

40S RIBOSOMAL PROTEIN YS29A >gi 626904 pir S48503 NCBI Description

ribosomal protein S29.e.A, cytosolic - yeast (Saccharomyces cerevisiae) >gi_287628_dbj_BAA03507_ (D14676) ribosomal protein YS29 [Saccharomyces cerevisiae] >gi 625108 (U19729)

Ylr388wp [Saccharomyces cerevisiae]



Seq. No. 261927

Contig ID 3294 3.R1011

5'-most EST LIB3059-031-Q1-K1-C2

Method BLASTX
NCBI GI g730461
BLAST score 215
E value 4.0e-17
Match length 56
% identity 68

NCBI Description 40S RIBOSOMAL PROTEIN YS29A >gi_626904_pir__S48503

ribosomal protein S29.e.A, cytosolic - yeast (Saccharomyces cerevisiae) >gi_287628_dbj_BAA03507_ (D14676) ribosomal protein YS29 [Saccharomyces cerevisiae] >gi_625108 (U19729)

Ylr388wp [Saccharomyces cerevisiae]

Seq. No. 261928

Contig ID 3294_4.R1011

5'-most EST LIB3067-029-Q1-K1-E8

Method BLASTX
NCBI GI g730461
BLAST score 215
E value 5.0e-17
Match length 56
% identity 68

NCBI Description 40S RIBOSOMAL PROTEIN YS29A >gi 626904 pir__S48503

ribosomal protein S29.e.A, cytosolic - yeast (Saccharomyces cerevisiae) >gi 287628 dbj BAA03507 (D14676) ribosomal protein YS29 [Saccharomyces cerevisiae] >gi 625108 (U19729)

Ylr388wp [Saccharomyces cerevisiae]

Seq. No. 261929

5'-most EST

Contig ID 3294 5.R1011

LIB3069-049-Q1-K1-A8

Method BLASTX
NCBI GI g730461
BLAST score 215
E value 4.0e-17
Match length 56
% identity 68

NCBI Description 40S RIBOSOMAL PROTEIN YS29A >gi 626904_pir__S48503

ribosomal protein S29.e.A, cytosolic - yeast (Saccharomyces cerevisiae) >gi_287628_dbj_BAA03507_ (D14676) ribosomal protein YS29 [Saccharomyces cerevisiae] >gi_625108 (U19729)

Ylr388wp [Saccharomyces cerevisiae]

Seq. No. 261930

Contig ID 3294_11.R1011 5'-most EST cat700017904.r1

Method BLASTX
NCBI GI 9730461
BLAST score 151
E value 1.0e-09
Match length 45
% identity 67

NCBI Description 40S RIBOSOMAL PROTEIN YS29A >gi_626904_pir__S48503

ribosomal protein S29.e.A, cytosolic - yeast (Saccharomyces



cerevisiae) >gi_287628_dbj_BAA03507_ (D14676) ribosomal
protein YS29 [Saccharomyces cerevisiae] >gi_625108 (U19729)
Ylr388wp [Saccharomyces cerevisiae]

Seq. No. 261931

Contig ID 3294_12.R1011 5'-most EST wty700172403.h1

Method BLASTN
NCBI GI g3687405
BLAST score 49

E value 2.0e-18
Match length 73
% identity 92

NCBI Description Lycopersicon esculentum mRNA for hypothetical protein

Seq. No. 261932

Contig ID 3295_1.R1011 5'-most EST clt700043919.f1

Method BLASTX
NCBI GI g3831441
BLAST score 181
E value 8.0e-13
Match length 83
% identity 60~

NCBI Description (AC005819) hypothetical protein [Arabidopsis thaliana]

Seq. No. 261933

Contig ID 3296 1.R1011

5'-most EST LIB3075-005-Q1-K1-B6

Seq. No. 261934 Contig ID 3297 1.R1011

5'-most EST LIB3078-012-Q1-K1-G7

Method BLASTN
NCBI GI g2739216
BLAST score 62
E value 3.0e-26

Match length 86 % identity 93

NCBI Description Hordeum vulgare L41 ribosomal protein

Seq. No. 261935

Contig ID 3297_2.R1011

5'-most EST LIB3075-005-Q1-K1-B7

Method BLASTN
NCBI GI g2739216
BLAST score 55
E value 4.0e-22
Match length 75
% identity 93

NCBI Description Hordeum vulgare L41 ribosomal protein

Seq. No. 261936 Contig ID 3297 3.R1011

5'-most EST LIB3156-020-Q1-K1-F1

Method BLASTN NCBI GI q2739216



BLAST score 52 E value 4.0e-20 Match length 72 % identity 93

NCBI Description Hordeum vulgare L41 ribosomal protein

Seq. No. 261937

Contig ID 3307_1.R1011 5'-most EST fdz701161754.h1

Seq. No. 261938

Contig ID 3309_1.R1011

5'-most EST LIB3066-030-Q1-K1-D2

Seq. No. 261939

Contig ID 3312_1.R1011

5'-most EST LIB3075-011-Q1-K1-A5

Seq. No. 261940

Contig ID 3320 1.R1011

5'-most EST LIB143-014-Q1-E1-D11

Method BLASTX
NCBI GI g2500345
BLAST score 444
E value 1.0e-43

E value 1.0e Match length 126 % identity 71

NCBI Description NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG (HIGH MOBILITY

GROUP-LIKE NUCLEAR PROTEIN 2 HOMOLOG)

>gi_2618578_dbj_BAA23363_ (D50420) OTK27 [Homo sapiens]

>gi_3859990 (AF091076) OTK27 [Homo sapiens]

>gi_1589072_prf__2210268A nuclear protein-NHP2-like protein

[Homo sapiens]

Seq. No. 261941

Contig ID 3320_2.R1011

5'-most EST LIB3075-004-Q1-K1-F8

Method BLASTX
NCBI GI g2500345
BLAST score 379
E value 4.0e-36
Match length 121
% identity 63

NCBI Description NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG (HIGH MOBILITY

GROUP-LIKE NUCLEAR PROTEIN 2 HOMOLOG)

>gi_2618578_dbj_BAA23363_ (D50420) OTK27 [Homo sapiens]

gi_3859990 (AF091076) OTK27 [Homo sapiens]

>gi_1589072_prf__2210268A nuclear protein-NHP2-like protein

[Homo sapiens]

Seq. No. 261942

Contig ID 3320 3.R1011

5'-most EST uC-zmflmo17053h08a1

Seq. No. 261943

Contig ID 3320_6.R1011 5'-most EST hbs701184279.h1

E value



```
BLASTX
Method
                   g2500345
NCBI GI
BLAST score
                   164
                   7.0e-15
E value
                   56
Match length
                   79
% identity
                  NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG (HIGH MOBILITY
NCBI Description
                   GROUP-LIKE NUCLEAR PROTEIN 2 HOMOLOG)
                   >gi 2618578_dbj_BAA23363_ (D50420) OTK27 [Homo sapiens]
                   >gi 3859990 (AF091076) OTK27 [Homo sapiens]
                   >gi 1589072 prf 2210268A nuclear protein-NHP2-like protein
                   [Homo sapiens]
Seq. No.
                   261944
                   3320 9.R1011
Contig ID
5'-most EST
                   LIB3156-010-Q1-K1-C7
                   {\tt BLASTX}
Method
NCBI GI
                   q2500345
BLAST score
                   200
                   1.0e-17
```

Match length 74 % identity NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG (HIGH MOBILITY NCBI Description

GROUP-LIKE NUCLEAR PROTEIN 2 HOMOLOG) >gi_2618578_dbj_BAA23363 (D50420) OTK27 [Homo sapiens]

>gi_3859990 (AF091076) OTK27 [Homo sapiens]

>gi 1589072 prf 2210268A nuclear protein-NHP2-like protein

[Homo sapiens]

261945 Seq. No. Contig ID 3323 1.R1011 5'-most EST LIB3150-036-Q1-N1-C2 BLASTX Method NCBI GI q4586056

66

BLAST score 154 E value 1.0e-09 Match length 210 % identity

NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]

Seq. No. 261946

Contig ID 3331 1.R1011

5'-most EST LIB3075-004-Q1-K1-E3

Method BLASTX NCBI GI q4468814 BLAST score 296 E value 1.0e-26 Match length 127 % identity 53

NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seq. No. 261947

3332 1.R1011 Contiq ID

5'-most EST uC-zmflmo17125a10b1

BLASTX Method NCBI GI g640023 BLAST score 1442



E value 1.0e-160 Match length 291

% identity 98

NCBI Description (X83696) gamma-tubulin 3 [Zea mays]

Seq. No. 261948

Contig ID 3332_2.R1011 5'-most EST rvt700552226.h1

Method BLASTN
NCBI GI g640022
BLAST score 188
E value 1.0e-101
Match length 196
% identity 99

NCBI Description Z.mays mRNA for gamma-tubulin

Seq. No. 261949

Contig ID 3338 1.R1011

5'-most EST uC-zmflmo17103f12b1

Method BLASTX
NCBI GI g3182996
BLAST score 492
E value 5.0e-49
Match length 231
% identity 46

NCBI Description TRANSLATION INITIATION FACTOR EIF-2B BETA SUBUNIT (EIF-2B

GDP-GTP EXCHANGE FACTOR) (S20I15) >gi 1117954 (U40756)

S20i15 [Fugu rubripes]

Seq. No. 261950

Contig ID 3340 1.R1011

5'-most EST uC-zmflMo17009a10b1

Seq. No. 261951

Contig ID 3344 1.R1011

5'-most EST LIB148-003-Q1-E1-A1

Method BLASTX
NCBI GI g2245138
BLAST score 868
E value 3.0e-93
Match length 233
% identity 72

NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 261952 Contig ID 3344_2.R1011 5'-most EST nwy700446707.h1

Seq. No. 261953

Contig ID 3344_4.R1011 5'-most EST nbm700475518.h1

Seq. No. 261954

Contig ID 3345_1.R1011 5'-most EST cyk700049676.f1

Seq. No. 261955



Contig ID 3346_1.R1011 5'-most EST hvj700619136.h1

Method BLASTX
NCBI GI g2347098
BLAST score 192
E value 2.0e-14
Match length 36
% identity 94

NCBI Description (U76845) ubiquitin-specific protease [Arabidopsis thaliana] >gi 4490742 emb_CAB38904.1_ (AL035708) ubiquitin-specific

protease (AtUBP3) [Arabidopsis thaliana]

Seq. No. 261956

Contig ID 3346 2.R1011

5'-most EST uC-zmflb73114b07b1

Seq. No. 261957

Contig ID 3355 1.R1011

5'-most EST uC-zmflb73166g04b2

Seq. No. 261958

Contig ID 3355 2.R1011

5'-most EST LIB3075-004-Q1-K1-B2

Seq. No. 261959

Contig ID 3359 1.R1011

5'-most EST LIB189-023-Q1-E1-A11

Method BLASTX
NCBI GI g2702273
BLAST score 159
E value 4.0e-10
Match length 299
% identity 29

NCBI Description (AC003033) carrot B2 protein-like [Arabidopsis thaliana]

Seq. No. 261960

Contig ID 3359_2.R1011

5'-most EST uC-zmflb73194f04b2

Method BLASTX
NCBI GI g2702273
BLAST score 301
E value 1.0e-26
Match length 173
% identity 41

NCBI Description (AC003033) carrot B2 protein-like [Arabidopsis thaliana]

Seq. No. 261961

Contig ID 3359_4.R1011

5'-most EST LIB3067-054-Q1-K1-A3

Seq. No. 261962 Contig ID 3361_1.R1011

5'-most EST LIB3066-017-Q1-K1-E1

Seq. No. 261963 Contig ID 3362 1.R1011

5'-most EST LIB3075-004-Q1-K1-B9

5'-most EST

BLAST score

Method

NCBI GI



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BLASTX
Method
NCBI GI
                   q4505495
                   277
BLAST score
                   4.0e-24
E value
Match length
                   166
                   40
% identity
NCBI Description
                   8-oxoguanine DNA glycosylase >gi_1890182_emb_CAA72414_
                   (Y11731) DNA glycosylase/AP lyase [Homo sapiens]
                   >gi_1903206_emb_CAA72536_ (Y11838) 8-oxoguanine DNA
                   glycosylase homolog 1 [Homo sapiens]
                   >gi_1906757_dbj_BAA19103_ (AB000410) hOGG1 [Homo sapiens]
                   >gi_2197083 (AF003595) 8-oxoguanine DNA glycosylase 1 [Homo
                   sapiens] >gi 2351704 (U88527) 8-hydroxyguanine
                   glycosylase/Tyase [Homo sapiens]
Seq. No.
                   261964
Contig ID
                   3365 1.R1011
                   clt700045652.f1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g585565
BLAST score
                   508
                   5.0e-51
E value
                   138
Match length
                   72
% identity
                  RIBOSOME RECYCLING FACTOR HOMOLOG (NUCLEAR LOCATED PROTEIN
NCBI Description
                   D2) >gi_629661_pir__S32716 nuclear protein - carrot
                   >gi 297891 emb CAA51077 (X72384) nuclear located protein
                   [Daucus carota]
                   261965
Seq. No.
Contig ID
                   3367 1.R1011
                   LIB3075-003-Q1-K1-H3
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2104951
BLAST score
                   189
E value
                   3.0e-19
Match length
                   81
% identity
NCBI Description (U96717) MAP kinase-like protein [Selaginella lepidophylla]
Seq. No.
                   261966
Contig ID
                   3368 1.R1011
                   LIB3180-018-P2-M1-A2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3928099
BLAST score
                   596
E value
                   3.0e-84
                   385
Match length
                   27
% identity
NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]
Seq. No.
                   261967
                   3373 1.R1011
Contig ID
```

uC-zmflb73264d09b1

BLASTX

899

g3882211

```
1 0e-96
```

E value 1.0e-96
Match length 433
% identity 45
NCBI Description (AB018288) KIAA0745 protein [Homo sapiens]
Seq. No. 261968

Contig ID 3373_2.R1011
5'-most EST LIB3069-004-Q1-K1-E9
Method BLASTX
NCBI GI g3882211

NCBI GI g3882211
BLAST score 189
E value 9.0e-24
Match length 105
% identity 53

NCBI Description (AB018288) KIAA0745 protein [Homo sapiens]

 Seq. No.
 261969

 Contig ID
 3374_1.R1011

 5'-most EST
 hvj700622535.h1

 Method
 BLASTX

Method BLASTX
NCBI GI g2895578
BLAST score 589
E value 2.0e-60
Match length 433
% identity 30

NCBI Description (AF041338) vacuolar proton pump subunit SFD alpha isoform

[Bos taurus]

Seq. No. 261970 Contig ID 3374_5.R1011 5'-most EST wyr700241325.h1

Seq. No. 261971 Contig ID 3383 1.E

Contig ID 3383_1.R1011 5'-most EST fdz701158994.h2

Method BLASTX
NCBI GI 94376915
BLAST score 151
E value 1.0e-09
Match length 104
% identity 35

NCBI Description (AE001646) Lipoate-Protein Ligase A [Chlamydia pneumoniae]

Seq. No. 261972

Contig ID 3396 1.R1011

5'-most EST LIB3075-003-Q1-K1-F11

Method BLASTX
NCBI GI g530088
BLAST score 283
E value 4.0e-25
Match length 84
% identity 64

NCBI Description (U12735) aminoalcoholphosphotransferase [Glycine max]

Seq. No. 261973 Contig ID 3399 1.R1011

5'-most EST LIB148-035-Q1-E1-A2

E value

Match length

% identity

4.0e-47

175

57



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Seq. No.
                  261974
Contig ID
                   3402 1.R1011
                  LIB3078-046-Q1-K1-C9
5'-most EST
Method
                  BLASTX
NCBI GI
                   g1350986
BLAST score
                  1129
E value
                   1.0e-124
Match length
                   241
                   93
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                  >gi_483431_dbj_BAA05059_ (D26060) cýc07 [Oryza sativa]
                   261975
Seq. No.
Contig ID
                  3402 2.R1011
5'-most EST
                  uC-zmflB73010d08b1
Method
                  BLASTX
NCBI GI
                  q4432841
BLAST score
                   164
E value
                   7.0e-11
Match length
                  82
% identity
                   44
NCBI Description
                  (AC006283) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   261976
Contig ID
                   3402 6.R1011
5'-most EST
                  uC-zmflb73061c09b1
Method
                  BLASTX
NCBI GI
                  g1350986
BLAST score
                   430
E value
                   3.0e-42
Match length
                  94
% identity
                   90
NCBI Description
                  40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                  >gi_483431_dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]
                   261977
Seq. No.
                   3402 7.R1011
Contig ID
5'-most EST
                  LIB3150-103-P2-K1-E3
Method
                  BLASTX
                  g4079800
NCBI GI
BLAST score
                  402
E value
                   4.0e-39
Match length
                  92
% identity
                   90
NCBI Description
                  (AF052503) S-phase-specific ribosomal protein [Oryza
                  sativa]
                   261978
Seq. No.
Contig ID
                  3402 10.R1011
5'-most EST
                  uC-zmroteosinte067h07b1
Method
                  BLASTX
NCBI GI
                  g4309744
BLAST score
                  473
```



NCBI Description (AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No. 261979

Contig ID 3402_11.R1011

5'-most EST LIB3180-038-P2-M2-H5

Method BLASTX
NCBI GI g4079800
BLAST score 453
E value 4.0e-45
Match length 93
% identity 92

NCBI Description (AF052503) S-phase-specific ribosomal protein [Oryza

sativa]

Seq. No. 261980

Contig ID 3402 12.R1011

5'-most EST LIB3076-028-Q1-K1-G6

Method BLASTX
NCBI GI 94309744
BLAST score 231
E value 2.0e-19
Match length 99
% identity 48

NCBI Description (AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No. 261981

Contig ID 3402_14.R1011 5'-most EST LIB189-032-Q1-E1-H4

Method BLASTX
NCBI GI g1350986
BLAST score 514
E value 2.0e-52
Match length 120
% identity 83

NCBI Description 40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)

>gi_483431_dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]

Seq. No. 261982

Contig ID 3402_16.R1011 5'-most EST uC-zmrob73033g07b1

Method BLASTX
NCBI GI g4079800
BLAST score 270
E value 1.0e-23
Match length 67
% identity 84

NCBI Description (AF052503) S-phase-specific ribosomal protein [Oryza

sativa]

Seq. No. 261983

Contig ID 3402_20.R1011 5'-most EST hvj700621167.h1

Seq. No. 261984 Contig ID 3408_1.R1011

5'-most EST uC-zmflb73200g02b1



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261985
Seq. No.
Contig ID
                   3408 2.R1011
5'-most EST
                  cjh700195163.h1
                  261986
Seq. No.
                  3410 1.R1011
Contig ID
                  uC-zmflb73067d07b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4185499
BLAST score
                  206
E value
                   2.0e-15
Match length
                  189
                   30
% identity
NCBI Description
                  (AF096095) fertilization-independent seed 2 protein
                   [Arabidopsis thaliana] >gi 4185501 (AF096096)
                   fertilization-independent seed 2 protein [Arabidopsis
                  thaliana]
                  261987
Seq. No.
Contig ID
                  3412 1.R1011
5'-most EST
                  gct701173680.h1
Method
                  BLASTX
NCBI GI
                  g4314371
BLAST score
                   523
E value
                   3.0e-53
Match length
                  192
% identity
                   54
                  (AC006340) putative G9a protein [Arabidopsis thaliana]
NCBI Description
                  261988
Seq. No.
Contig ID
                   3414 1.R1011
5'-most EST
                  LIB3066-014-Q1-K1-F2
                   261989
Seq. No.
Contig ID
                   3417 1.R1011
5'-most EST
                  LIB3078-023-Q1-K1-E1
Seq. No.
                   261990
Contig ID
                   3420 1.R1011
5'-most EST
                  uC-zmflmo17158b11a1
Method
                  BLASTX
NCBI GI
                   g4584957
BLAST score
                   3307
E value
                   0.0e+00
                   667
Match length
% identity
                   100
NCBI Description
                  (AF077337) heat shock protein 101; 101 kDa heat shock
                  protein [Zea mays]
```

Seq. No. 261991

Contig ID 3421_1.R1011

5'-most EST LIB3079-016-Q1-K1-G6

Method BLASTX
NCBI GI g2960101
BLAST score 191
E value 7.0e-14
Match length 227



% identity 26

NCBI Description (AL022121) hypothetical protein Rv3677c [Mycobacterium

tuberculosis]

Seq. No. 261992

Contig ID 3428_1.R1011

5'-most EST LIB3075-003-Q1-K1-A4

Seq. No. 261993

Contig ID 3439 1.R1011

5'-most EST LIB3079-003-Q1-K1-F4

Method BLASTX
NCBI GI g1172818
BLAST score 698
E value 2.0e-73
Match length 149
% identity 91

% identity 91
NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal

protein S16 [Oryza sativa] >gi_1096552_prf__2111468A

ribosomal protein S16 [Oryza sativa]

Seq. No. 261994

Contig ID 3439 2.R1011

5'-most EST LIB84-024-Q1-E1-F5

Method BLASTX
NCBI GI g1172818
BLAST score 686
E value 3.0e-72
Match length 149

Match length 149 % identity 89

NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal

protein S16 [Oryza sativa] >gi_1096552_prf__2111468A

ribosomal protein S16 [Oryza sativa]

Seq. No. 261995

Contig ID 3439 3.R1011

5'-most EST uC-zmflmo17039g03b1

Method BLASTX
NCBI GI g3549665
BLAST score 612
E value 6.0e-63
Match length 512
% identity 36

NCBI Description (AL031394) hypothetical protein [Arabidopsis thaliana]

Seq. No. 261996

Contig ID 3450_1.R1011 5'-most EST LIB148-015-Q1-E1-H3

Seq. No. 261997

Contig ID 3452 1.R1011

5'-most EST uC-zmflmo17017a03b1

Seq. No. 261998

Contig ID 3452_2.R1011

5'-most EST LIB3075-001-Q1-K1-G12



```
261999
Seq. No.
Contig ID
                  3452 3.R1011
                  xyt700343544.h1
5'-most EST
                  262000
Seq. No.
Contig ID
                  3461 1.R1011
5'-most EST
                  pmx700086844.hl
                  BLASTX
Method
NCBI GI
                  g1658193
BLAST score
                  1795
E value
                  0.0e+00
Match length
                  355
                  99
% identity
                  (U74319) obtusifoliol 14-alpha demethylase CYP51 [Sorghum
NCBI Description
                  bicolor]
Seq. No.
                  262001
                  3461 2.R1011
Contig ID
                  fdz701166238.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1658193
BLAST score
                   208
                  2.0e-16
E value
Match length
                   40
                  97
% identity
                  (U74319) obtusifoliol 14-alpha demethylase CYP51 [Sorghum
NCBI Description
                  bicolor]
Seq. No.
                  262002
                  3468 1.R1011
Contig ID
5'-most EST
                  LIB3075-001-Q1-K1-D12
                  BLASTX
Method
NCBI GI
                  g3913808
BLAST score
                  1111
                  1.0e-121
E value
Match length
                   231
% identity
                   91
                  FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME
NCBI Description
                   SYNTHETASE) >gi_2429618_dbj_BAA22284_ (AB007120)
                   ferrochelatase [Oryza sativa]
Seq. No.
                   262003
Contig ID
                   3469 1.R1011
5'-most EST
                  cjh700193427.h1
Method
                  BLASTX
NCBI GI
                  q4337001
BLAST score
                   368
E value
                   5.0e-35
Match length
                  106
% identity
```

NCBI Description (AF118129) Tsil-interacting protein TSIP1 [Nicotiana

tabacum]

262004 Seq. No.

3469 2.R1011 Contig ID

5'-most EST LIB3066-019-Q1-K1-C10

Method BLASTX



q3879119 NCBI GI BLAST score 223 E value 9.0e-18 Match length 114 41 % identity NCBI Description (Z70310) similar to Glutathione S-transferases. [Caenorhabditis elegans] Seq. No. 262005 Contig ID 3469 3.R1011 5'-most EST LIB143-004-Q1-E1-F12 Method BLASTX NCBI GI q3879119 BLAST score 332 E value 2.0e-30 Match length 155 48 % identity NCBI Description (Z70310) similar to Glutathione S-transferases. [Caenorhabditis elegans] Seq. No. 262006 Contig ID 3469 4.R1011 5'-most EST clt700042822.f1 Seq. No. 262007 Contig ID 3471 1.R1011 5'-most EST LIB3062-041-Q1-K1-A10 Method BLASTX NCBI GI q3063449 BLAST score 369 E value 5.0e-35 Match length 106 % identity 67 NCBI Description (AC003981) F22013.11 [Arabidopsis thaliana] Seq. No. 262008 3472 1.R1011 Contig ID 5'-most EST LIB3066-038-Q1-K1-C6 Seq. No. 262009 Contig ID 3473 1.R1011 5'-most EST LIB148-034-Q1-E1-F12 BLASTX g3281853 810 3.0e-86 258 % identity

Method NCBI GI BLAST score E value Match length

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 262010 Contig ID 3473 2.R1011 5'-most EST uC-zmflb73222b09b1

Seq. No. 262011 Contig ID 3473 3.R1011 uC-zmflb73222b09a1 5'-most EST



Method BLASTX
NCBI GI g3281853
BLAST score 205
E value 4.0e-16
Match length 69
% identity 58

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No.
Contig ID
5'-most EST

3475_1.R1011 wty700164129.h1

262012

Method BLASTX
NCBI GI g1352186
BLAST score 1330
E value 1.0e-147
Match length 504
% identity 52

NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE)

(CYTOCHROME P450 74) >gi_404866 (U00428) allene oxide

synthase [Linum usitatissimum]

Seq. No. 262013

Contig ID 3475 2.R1011

5'-most EST uC-zmflb73346f04a2

Method BLASTX
NCBI GI g2244749
BLAST score 2101
E value 0.0e+00
Match length 471
% identity 84

% identity 84

NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 262014

Contig ID 3475_5.R1011

5'-most EST LIB3060-024-Q1-K1-D5

Method BLASTX
NCBI GI g1352186
BLAST score 345
E value 1.0e-32
Match length 93
% identity 63

NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE)

(CYTOCHROME P450 74) >gi_404866 (U00428) allene oxide

synthase [Linum usitatissimum]

Seq. No. 262015

Contig ID 3475 7.R1011

5'-most EST LIB3180-030-P2-M2-A5

Method BLASTX
NCBI GI g2244749
BLAST score 385
E value 3.0e-37
Match length 91
% identity 80

NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 262016



Contig ID 3475_8.R1011 5'-most EST wty700166008.h1

Method BLASTX
NCBI GI g2244749
BLAST score 166
E value 3.0e-11
Match length 35
% identity 91

NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No. 262017

Contig ID 3475_13.R1011

5'-most EST uC-zmflmo17332e08a1

Seq. No. 262018

Contig ID 3483_1.R1011 5'-most EST fwa700101142.h1

Method BLASTX
NCBI GI g3413700
BLAST score 428
E value 4.0e-42
Match length 131
% identity 63

NCBI Description (AC004747) putative YME1 protein [Arabidopsis thaliana]

Seq. No. 262019

Contig ID 3485 1.R1011

5'-most EST uC-zmflb73049a06b1

Method BLASTX
NCBI GI g2500408
BLAST score 245
E value 4.0e-20
Match length 150

Match length 150 % identity 38

NCBI Description 30S RIBOSOMAL PROTEIN S5 >gi_2314466_gb_AAD08343.1_

(AE000633) ribosomal protein S5 (rps5) [Helicobacter pylori

26695] >gi 4155832 (AE001547) 30S RIBOSOMAL PROTEIN S5

[Helicobacter pylori J99]

Seq. No. 262020 Contig ID 3488 1.R1011

5'-most EST dyk700103253.h1

Method BLASTX
NCBI GI g4587571
BLAST score 857
E value 5.0e-92
Match length 226
% identity 72

NCBI Description (AC006550) Belongs to the PF_01027 Uncharacterized protein

family UPF0005 with 7 transmembrane domains. [Arabidopsis

thaliana]

Seq. No. 262021

Contig ID 3488_3.R1011 5'-most EST xsy700207390.h1

Method BLASTX NCBI GI g4587571



```
BLAST score
E value
                  8.0e-36
Match length
                  94
% identity
                  72
                  (AC006550) Belongs to the PF 01027 Uncharacterized protein
NCBI Description
                  family UPF0005 with 7 transmembrane domains. [Arabidopsis
                  thaliana]
Seq. No.
                  262022
                  3501 1.R1011
Contig ID
5'-most EST
                  xsy700217790.hl
Method
                  BLASTX
NCBI GI
                  q1710780
                  648
BLAST score
E value
                  1.0e-67
                  175
Match length
% identity
                  72
                  40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433
NCBI Description
                   (X96613) cytoplasmic ribosomal protein S7 [Podospora
                  anserina]
                  262023
Seq. No.
Contig ID
                  3501 2.R1011
5'-most EST
                  LIB3059-003-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  a168664
BLAST score
                  160
                  1.0e-10
E value
Match length
                  29
                  100
% identity
NCBI Description (M13507) zein protein precursor [Zea mays]
Seq. No.
                  262024
Contig ID
                  3501 3.R1011
5'-most EST
                  LIB3150-039-Q1-N1-F4
Method
                  BLASTX
NCBI GI
                  q1710780
BLAST score
                  340
E value
                  9.0e-32
Match length
                  96
                  71
% identity
                  40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433
NCBI Description
                   (X96613) cytoplasmic ribosomal protein S7 [Podospora
                  anserina]
Seq. No.
                  262025
Contig ID
                  3501 4.R1011
5'-most EST
                  pmx700091406.h1
                  BLASTX
Method
NCBI GI
                  g1710780
BLAST score
                  157
```

E value 2.0e-10 Match length 41 % identity 78

NCBI Description 40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_

(X96613) cytoplasmic ribosomal protein S7 [Podospora

anserina]



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262026
Seq. No.
Contig ID
                  3501 5.R1011
5'-most EST
                  LIB3069-052-Q1-K1-G1
                  262027
Seq. No.
Contig ID
                  3508 1.R1011
                  LIB3075-004-Q1-K1-F10
5'-most EST
Seq. No.
                  262028
Contig ID
                  3514 1.R1011
5'-most EST
                  LIB3075-004-Q1-K1-H2
                  262029
Seq. No.
Contig ID
                  3515 1.R1011
5'-most EST
                  LIB3078-040-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g133867
BLAST score
                  679
                  3.0e-71
E value
Match length
                  145
                  90
% identity
                  40S RIBOSOMAL PROTEIN S11 >gi 82722 pir S16577 ribosomal
NCBI Description
                  protein S11 - maize >gi 22470 emb_CAA39438_ (X55967)
                  ribosomal protein S11 [Zea mays]
Seq. No.
                  262030
Contig ID
                  3515 2.R1011
5'-most EST
                  LIB3075-004-Q1-K1-H9
Method
                  BLASTX
                  q133867
NCBI GI
                   602
BLAST score
                  2.0e-62
E value
                  113
Match length
                   99
% identity
                 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal
NCBI Description
                  protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)
                  ribosomal protein S11 [Zea mays]
                   262031
Seq. No.
                  3515 3.R1011
Contig ID
5'-most EST
                  LIB3088-022-Q1-K1-F10
                  BLASTX
Method
NCBI GI
                   g133867
BLAST score
                   286
                   2.0e-25
E value
                   56
Match length
% identity
                   95
```

NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)

ribosomal protein S11 [Zea mays]

 Seq. No.
 262032

 Contig ID
 3515_5.R1011

 5'-most EST
 hrx700703927.h1

 Method
 BLASTX

 NCBI GI
 g133867



BLAST score 394 E value 4.0e-38 Match length 95 % identity 82

NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir_S16577 ribosomal

protein S11 - maize >gi 22470 emb CAA39438 (X55967)

ribosomal protein S11 [Zea mays]

Seq. No. 262033 Contig ID 3517 1.R1011

5'-most EST ypc700804539.h1

Seq. No. 262034

Contig ID 3519_1.R1011 5'-most EST qmh700030315.f1

Method BLASTX
NCBI GI g3367534
BLAST score 1216
E value 1.0e-134
Match length 325
% identity 70

NCBI Description (AC004392) Strong similarity to coatamer alpha subunit

(HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis

thaliana]

Seq. No. 262035

Contig ID 3519 2.R1011

5'-most EST uC-zmflmo17426h04a1

Seq. No. 262036

Contig ID 3519_3.R1011 5'-most EST wty700170418.h1

Method BLASTX
NCBI GI g3367534
BLAST score 256
E value 7.0e-22
Match length 59
% identity 68

NCBI Description (AC004392) Strong similarity to coatamer alpha subunit

(HEPCOP) homolog gb_U24105 from Homo sapiens. [Arabidopsis

thaliana]

Seq. No. 262037

Contig ID 3519 4.R1011 5'-most EST qmh700026735.f1

Method BLASTX
NCBI GI g4567286
BLAST score 354
E value 2.0e-35
Match length 117
% identity 62

NCBI Description (AC006841) putative coatomer alpha subunit [Arabidopsis

thaliana]

Seq. No. 262038 Contig ID 3522 1.R1011

5'-most EST fC-zmse700614547a1



```
Method
                   BLASTX
NCBI GI
                   q3482933
BLAST score
                   986
E value
                   1.0e-116
Match length
                   336
% identity
                   64
NCBI Description
                  (AC003970) Similar to cdc2 protein kinases [Arabidopsis
Seq. No.
                  262039
Contig ID
                   3523 1.R1011
5'-most EST
                  xmt700266505.h1
Seq. No.
                  262040
Contig ID
                  3523 2.R1011
5'-most EST
                  LIB143-006-Q1-E1-C5
                  262041
Seq. No.
Contig ID
                  3528_1.R1011
5'-most EST
                  uC-zmroteosinte013e05b1
Method
                  BLASTX
NCBI GI
                  q1076670
BLAST score
                  846
```

E value 1.0e-90 Match length 179 % identity

NADH dehydrogenase (EC 1.6.99.3) - potato NCBI Description

>gi_668985_emb_CAA59062_ (X84319) NADH dehydrogenase

[Solanum tuberosum]

Seq. No. 262042 Contig ID 3528 2.R1011 5'-most EST uC-zmflb73039h09b1 Method BLASTX NCBI GI g3929358 BLAST score 157

E value 3.0e-10 Match length 43 72 % identity

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR

(COMPLEX I-23KD) (CI-23KD) >gi_1666177_emb_CAA70326_

(Y09109) NADH dehydrogenase [Nicotiana tabacum]

Seq. No. 262043

Contig ID 3530 1.R1011

5'-most EST uC-zmflb73345b03a2

Method BLASTX NCBI GI g2464901 BLAST score 174 E value 2.0e-12 Match length 55 % identity

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 262044 Contig ID

3533_1.R1011

5'-most EST LIB3075-006-Q1-K1-G10

E value

Match length

% identity

4.0e-66

NCBI Description Z.mays mRNA for glycine-rich protein

145



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262045
Seq. No.
Contig ID
                   3537 1.R1011
5'-most EST
                   gct701173419.h2
                   262046
Seq. No.
Contig ID
                   3539 1.R1011
5'-most EST
                   xdb7\overline{0}0339312.h1
Method
                   BLASTX
NCBI GI
                   q82696
BLAST score
                   307
E value
                   1.0e-27
Match length
                   63
                   97
% identity
NCBI Description glycine-rich protein - maize >gi_22293 emb CAA43431_
                    (X61121) glycine-rich protein [Zea mays]
                   262047
Seq. No.
Contig ID
                   3539 2.R1011
5'-most EST
                   xdb7\overline{0}0337903.h1
                   262048
Seq. No.
Contig ID
                   3539_3.R1011
5'-most EST
                  - uC-zmflmo17262d08a1
Method
                   BLASTX
NCBI GI
                   a544421
BLAST score
                   209
E value
                   3.0e-16
Match length
                   43
% identity
NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN 1 >gi_485420_pir__S12311
                   glycine-rich RNA-binding protein (clone S1) - sorghum
                   (fragment) >gi_21623_emb_CAA40863_ (X57663) glycine-rich RNA-binding protein [Sorghum bicolor]
Seq. No.
                   262049
                   3539 4.R1011
Contig ID
5'-most EST
                   uC-zmflb73018d04b1
Method
                   BLASTX
NCBI GI
                   q1592812
BLAST score
                   325
E value
                   7.0e-30
Match length
                   132
% identity
NCBI Description (X95957) 22 kDa polypeptide [Nicotiana tabacum]
Seq. No.
                   262050
Contig ID
                   3539 5.R1011
5'-most EST
                   uC-zmflb73168e07a1
Method
                   BLASTN
NCBI GI
                   q22292
BLAST score
                   129
```



Seq. No. 262051

Contig ID 3539_6.R1011

5'-most EST LIB3152-005-P1-K1-H3

Method BLASTN
NCBI GI g22292
BLAST score 281
E value 1.0e-157
Match length 308
% identity 98

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 262052

Contig ID 3539 7.R1011

5'-most EST LIB3150-084-P2-N2-E4

Method BLASTN
NCBI GI g22292
BLAST score 229
E value 1.0e-126
Match length 273
% identity 96

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 262053

Contig ID 3539_8.R1011

5'-most EST LIB3066-047-Q1-K1-D4

Method BLASTN
NCBI GI g22292
BLAST score 298
E value 1.0e-167
Match length 390

Match length 390 % identity 94

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 262054

Contig ID 3539_10.R1011

5'-most EST LIB3\overline{1}36-015-Q1-K1-D3

Seq. No. 262055

Contig ID 3539_12.R1011 5'-most EST uC-zmflmo17076f02a1

Method BLASTN
NCBI GI g22292
BLAST score 207
E value 1.0e-112
Match length 248
% identity 96

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 262056

Contig ID 3539_16.R1011 5'-most EST rv1700456130.h1

Method BLASTN
NCBI GI g22292
BLAST score 109
E value 2.0e-54
Match length 155
% identity 93



```
NCBI Description Z.mays mRNA for glycine-rich protein
```

Seq. No. 262057

Contig ID 3539_19.R1011 5'-most EST fdz701164562.h1

Method BLASTN
NCBI GI g22292
BLAST score 249
E value 1.0e-137
Match length 330
% identity 94

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 262058

Contig ID 3539_20.R1011 5'-most EST xdb700337006.h1

Method BLASTN
NCBI GI g22292
BLAST score 151
E value 2.0e-79
Match length 174
% identity 97

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 262059

Contig ID 3544 1.R1011

5'-most EST LIB3075-007-Q1-K1-G1

Method BLASTX
NCBI GI g2801701
BLAST score 225
E value 7.0e-18
Match length 274

% identity 20

NCBI Description (AF042379) spindle pole body protein spc97 homolog GCP2

[Homo sapiens]

Seq. No. 262060

Contig ID 3545 1.R1011

5'-most EST LIB3075-007-Q1-K1-G3

Method BLASTX
NCBI GI g2500107
BLAST score 274
E value 3.0e-24
Match length 63
% identity 83

NCBI Description DNA REPAIR PROTEIN RAD51 HOMOLOG >gi 1143810 (U22441)

LeRAD51 [Solanum lycopersicum]

Seq. No. 262061

Contig ID 3547 2.R1011

5'-most EST uC-zmflmo17090d04a1

Seq. No. 262062

Contig ID 3551_3.R1011 5'-most EST nbm700469951.h1

Method BLASTX NCBI GI g2244816



BLAST score 188 2.0e-14 E value 79 Match length 58 % identity (Z97336) hypothetical protein [Arabidopsis thaliana] NCBI Description 262063 Seq. No. 3556 1.R1011 Contig ID LIB3\overline{151}-031-Q1-K1-A2 5'-most EST BLASTX Method NCBI GI g1362066 856 BLAST score 6.0e-92 E value Match length 204 82 % identity small GTP-binding protein - garden pea NCBI Description >qi 871510 emb CAA90080 (Z49900) small GTP-binding protein [Pisum satīvum] 262064 Seq. No. 3558_1.R1011 Contig ID 5'-most EST LIB3075-008-Q1-K1-E3 Method BLASTX g2245068 NCBI GI 386 BLAST score 7.0e-37 E value 146 Match length % identity 54 (Z97342) serine protease homolog [Arabidopsis thaliana] NCBI Description 262065 Seq. No. Contig ID 3560 1.R1011 5'-most EST LIB3075-008-Q1-K1-F2 262066 Seq. No. Contig ID 3564 1.R1011 5'-most EST LIB3059-041-Q1-K1-D3 262067 Seq. No. Contig ID 3568 1.R1011 LIB148-040-Q1-E1-D3 5'-most EST 262068 Seq. No. Contig ID 3575 1.R1011 5'-most EST dyk700105004.hl 262069

Seq. No.

Contig ID 3576 1.R1011 5'-most EST ymt700219372.h1

Method BLASTX NCBI GI q2369714 BLAST score 4007 E value 0.0e + 00Match length 843 % identity 90

NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]



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262070
Seq. No.
Contig ID
                   3576_2.R1011
                   uC-z\overline{m}flmo17122f07b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2369714
                   555
BLAST score
                   5.0e-57
E value
Match length
                   120
                   93
% identity
NCBI Description
                  (Z97178) elongation factor 2 [Beta vulgaris]
                   262071
Seq. No.
                   3576 3.R1011
Contig ID
5'-most EST
                   tfd700569719.h1
                   BLASTX
Method
                   g2369714
NCBI GI
BLAST score
                   392
E value
                   6.0e-38
                   86
Match length
                   87
% identity
                  (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                   262072
Seq. No.
                   3576 5.R1011
Contig ID
5'-most EST
                   uC-zmromo17111e12a1
Method
                   BLASTX
                   g2369714
NCBI GI
BLAST score
                   243
                   2.0e-20
E value
Match length
                   55
                   87
% identity
                  (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                   262073
Seq. No.
                   3576_6.R1011
Contig ID
5'-most EST
                   uC-zmflmo17092d11a1
Method
                   BLASTX
NCBI GI
                   q2369714
BLAST score
                   401
E value
                   8.0e-39
Match length
                   90
% identity
                   87
NCBI Description
                  (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                   262074
Contig ID
                   3576 18.R1011
5'-most EST
                   uC-zmflMo17092d11b1
Method
                   BLASTX
NCBI GI
                   g2369714
BLAST score
                   287
```

NCBI GI g2369714
BLAST score 287
E value 8.0e-39
Match length 99
% identity 90

NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No. 262075 Contig ID 3577 1.R1011



5'-most EST nbm700473493.h1 BLASTX Method NCBI GI q2760084 BLAST score 778 E value 7.0e-83 263 Match length 14 % identity (Y16045) leucine-rich repeat protein [Arabidopsis thaliana] NCBI Description 262076 Seq. No. 3577 2.R1011 Contig ID 5'-most EST uC-zmflb73185f07a1 BLASTX Method q2760084 NCBI GI BLAST score 643 E value 3.0e-82 353 Match length 22 % identity (Y16045) leucine-rich repeat protein [Arabidopsis thaliana] NCBI Description Seq. No. 262077 Contig ID 3580 1.R1011 5'-most EST ymt700223409.h1 BLASTX Method " NCBI GI g3023819 BLAST score 157 E value 2.0e-10 Match length 55 49 % identity CELL DIVISION PROTEIN FTSJ HOMOLOG >gi_2127806_pir__G64471 NCBI Description cell division protein J - Methanococcus jannaschii >gi_1592021 (U67577) cell division protein FtsJ [Methanococcus jannaschii] Seq. No. 262078 Contig ID 3582 1.R1011 5'-most EST uC-zmflmo17017f03b1 Method BLASTX NCBI GI g3786007 BLAST score 654 E value 3.0e-70 Match length 329 % identity 47 NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana] Seq. No. 262079 Contig ID 3588 1.R1011 tzu700201559.h1 5'-most EST Method BLASTX NCBI GI q4538911 BLAST score 429 E value 1.0e-41 265 Match length

Seq. No. 262080

% identity

NCBI Description

35

(AL049482) hypothetical protein [Arabidopsis thaliana]



```
3588 2.R1011
Contig ID
                  pmx700084678.hl
5'-most EST
Seq. No.
                  262081
                  3596 1.R1011
Contig ID
5'-most EST
                  LIB3066-021-Q1-K1-A7
                  BLASTX
Method
                  g4580398
NCBI GI
BLAST score
                  714
                  2.0e-75
E value
```

% identity 54 NCBI Description (AC007171) putative protein kinase APK1A [Arabidopsis

thaliana]

249

 Seq. No.
 262082

 Contig ID
 3603_1.R1011

 5'-most EST
 LIB148-015-Q1-E1-B9

 Method
 BLASTX

 NCBI GI
 q2582800

NCBI GI g2582800 BLAST score 782 E value 3.0e-83 Match length 246 % identity 59

Match length

NCBI Description (Y11607) protein phosphatase 2C [Medicago sativa]

5'-most EST LIB3076-043-Q1-K1-E7

Method BLASTX
NCBI GI g2582800
BLAST score 347
E value 1.0e-32
Match length 121
% identity 58

NCBI Description (Y11607) protein phosphatase 2C [Medicago sativa]

 Seq. No.
 262084

 Contig ID
 3609_1.R1011

 5'-most EST
 xsy700208148.h1

 Method
 BLASTA

NCBI GI g3719211 BLAST score 521 E value 1.0e-52 Match length 169 % identity 62

NCBI Description (U97021) UIP2 [Arabidopsis thaliana]

Seq. No. 262085

Contig ID 3609_2.R1011 5'-most EST uC-zmflb73199g04b1

Seq. No. 262087



```
3610 1.R1011
Contig ID
                  uC-z\overline{m}flmo17306f01a1
5'-most EST
                  BLASTX
Method
                  q1001135
NCBI GI
BLAST score
                   476
                   4.0e-47
E value
                   318
Match length
                   57
% identity
                  (D64001) acetolactate synthase [Synechocystis sp.]
NCBI Description
                   262088
Seq. No.
                   3610 5.R1011
Contig ID
5'-most EST
                   ypc700799479.h1
                   262089
Seq. No.
                   3614 1.R1011
Contig ID
                   uC-zmflb73160a10b2
5'-most EST
                   262090
Seq. No.
                   3622 1.R1011
Contig ID
5'-most EST
                   LIB3075-014-Q1-K1-B1
Method
                   BLASTX
                   g4240303
NCBI GI
                   160
BLAST score
                   8.0e-11
E value
                   105
Match length
% identity
                   38
                  (AB020714) KIAA0907 protein [Homo sapiens]
NCBI Description
                   262091
Seq. No.
Contig ID
                   3623 1.R1011
                   LIB3066-043-Q1-K1-H12
5'-most EST
                   262092
Seq. No.
                   3626 1.R1011
Contig ID
5'-most EST
                   LIB3136-014-Q1-K1-C9
Method
                   BLASTX
NCBI GI
                   q3617770
BLAST score
                   1122
                   1.0e-123
E value
Match length
                   300
% identity
                   70
NCBI Description (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]
                   262093
Seq. No.
Contig ID
                   3626 2.R1011
5'-most EST
                   dyk700103982.h1
Method
                   BLASTX
NCBI GI
                   g3617770
BLAST score
                   478
                   8.0e-48
E value
Match length
                   128
                   71
% identity
NCBI Description (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]
```

262094

3627_1.R1011

Seq. No.

Contig ID



5'-most EST LIB3115-013-P1-K1-B1 Method BLASTX NCBI GI q549732

BLAST score 227 E value 2.0e-18 Match length 72

% identity 51

NCBI Description HYPOTHETICAL 16.2 KD PROTEIN IN PIR3-APE2 INTERGENIC REGION

>gi_481110_pir__S37791 hypothetical protein YKL160w - yeast

(Saccharomyces cerevisiae) >gi_407488_emb_CAA81494_

(Z26877) unknown [Saccharomyces cerevisiae] >gi_486279_emb_CAA82002_ (Z28160) ORF YKL160w

[Saccharomyces cerevisiae] >gi_1582545_prf__2118404F ORF

[Saccharomyces cerevisiae]

Seq. No. 262095

Contig ID 3627_2.R1011 5'-most EST yyf700349445.h1

Seq. No. 262096

Contig ID 3627 3.R1011

5'-most EST LIB3079-035-Q1-K1-D2

Method BLASTX
NCBI GI g549732
BLAST score 195
E value 2.0e-14
Match length 67
% identity 49

NCBI Description HYPOTHETICAL 16.2 KD PROTEIN IN PIR3-APE2 INTERGENIC REGION

>gi_481110_pir__S37791 hypothetical protein YKL160w - yeast

(Saccharomyces cerevisiae) >gi_407488_emb_CAA81494_

(Z26877) unknown [Saccharomyces cerevisiae] >gi_486279_emb_CAA82002_ (Z28160) ORF YKL160w

[Saccharomyces cerevisiae] >gi 1582545 prf 2118404F ORF

[Saccharomyces cerevisiae]

Seq. No. 262097

Contig ID 3627_8.R1011 5'-most EST hvj700619794.h1

Seq. No. 262098

Contig ID 3627_9.R1011 5'-most EST hvj700619860.h1

Seq. No. 262099

Contig ID 3630 1.R1011

5'-most EST LIB143-059-Q1-E1-A2

Method BLASTX
NCBI GI g107350
BLAST score 407
E value 3.0e-39
Match length 315
% identity 31

NCBI Description Pm5 protein - human >gi_1335273_emb_CAA40655_ (X57398) pm5

protein [Homo sapiens]

Seq. No. 262100



Contig ID 3631 1.R1011 5'-most EST vux700159991.h1 262101 Seq. No. Contig ID 3637 1.R1011 5'-most EST $xmt7\overline{0}0262127.h1$

262102 Seq. No. 3645 1.R1011 Contig ID 5'-most EST LIB3075-015-Q1-K1-F4

Method BLASTX g1373017 NCBI GI BLAST score 226

E value 2.0e-18 Match length 118 44 % identity

NCBI Description (U26266) deoxyhypusine synthase [Homo sapiens]

262103 Seq. No. 3652 1.R1011 Contig ID

5'-most EST uC-zmflb73256b08b1

Method BLASTX NCBI GI g4325345 BLAST score 611 E value 2.0e-63 Match length 186 % identity 28

NCBI Description (AF128393) similar to thioredoxin-like proteins (Pfam:

PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42,

N=1) [Arabidopsis thaliana]

Seq. No. 262104 Contig ID 3652_2.R1011

5'-most EST uC-zmflmo17329b05a1

Method BLASTX NCBI GI q4325345 BLAST score 1114 1.0e-122 E value Match length 303 30 % identity

(AF128393) similar to thioredoxin-like proteins (Pfam: NCBI Description

PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42,

N=1) [Arabidopsis thaliana]

Seq. No. 262105

Contig ID 3652 3.R1011 5'-most EST xsy700217124.h1

Method BLASTX NCBI GI q2501555 BLAST score 1510 E value 1.0e-168 Match length 312 % identity 91

POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi 549984 (U13148) NCBI Description



Seq. No. 262106 Contig ID 3652_5.R1011

5'-most EST LIB3070-014-Q1-N1-E12

Seq. No. 262107

Contig ID 3655_1.R1011

5'-most EST LIB3075-017-Q1-K1-B11

Seq. No. 262109

Contig ID 3657 1.R1011

5'-most EST LIB3062-004-Q1-K1-E10

Method BLASTX
NCBI GI g3913427
BLAST score 1253
E value 1.0e-138
Match length 340
% identity 71

NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

(SAMDC) >gi_1532073_emb_CAA69075_ (Y07767) S-adenosylmethionine decarboxylase [Zea mays]

Seq. No. 262110 Contig ID 3657_2.R1011 5'-most EST uwc700150172.h1

Seq. No. 262111

Contig ID 3660 1.R1011

5'-most EST uC-zmflmo17289b10b1

Method BLASTX
NCBI GI g4584255
BLAST score 1214
E value 1.0e-134
Match length 235
% identity 90

NCBI Description (Y18471) SINAlp [Vitis vinifera]

Seq. No. 262112

Contig ID 3662_1.R1011

5'-most EST uC-zmflb73201a11b1

Method BLASTX
NCBI GI g3183217
BLAST score 424
E value 4.0e-41
Match length 242
% identity 43

NCBI Description HYPOTHETICAL PROTEIN KIAA0103 >gi_285943_dbj BAA03493

(D14659) KIAA0103 [Homo sapiens]

Seq. No. 262113

Contig ID 3662_2.R1011

5'-most EST LIB3075-018-Q1-K1-D3



262114 Seq. No. Contig ID 3662 3.R1011 5'-most EST xsy700210046.hl Seq. No. 262115 Contig ID 3662 5.R1011 5'-most EST gct701173963.h1 262116 Seq. No. 3663 1.R1011 Contig ID LIB3075-018-Q1-K1-E3 5'-most EST BLASTX Method

g3935150 NCBI GI BLAST score 485 2.0e-48 E value 129 Match length % identity 44

(AC005106) T25N20.14 [Arabidopsis thaliana] NCBI Description

Seq. No. 262117 3663 2.R1011 Contig ID

5'-most EST uC-zmflmo17289a03b1

Method BLASTX NCBI GI g3935150 560 BLAST score 2.0e-80 E value Match length 260 % identity 61

NCBI Description (AC005106) T25N20.14 [Arabidopsis thaliana]

262118 Seq. No. Contig ID 3671 1.R1011

LIB3066-046-Q1-K1-C5 5'-most EST

Method BLASTX NCBI GI q2244835 BLAST score 694 E value 4.0e-73Match length 204 % identity 64

NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No. 262119

Contig ID 3672 1.R1011

5'-most EST LIB3075-019-Q1-K1-A12

Method BLASTX NCBI GI q4262239 BLAST score 787 E value 5.0e-84 Match length 213 % identity

NCBI Description (AC006200) putative membrane transporter [Arabidopsis

thaliana]

Seq. No. 262120 Contig ID 3673 2.R1011

5'-most EST LIB3067-044-Q1-K1-E6



Seq. No. 262121

Contig ID 3673_4.R1011

5'-most EST uC-zmrob73002f04a1

Seq. No. 262122

Contig ID 3675 1.R1011

5'-most EST LIB3066-053-Q1-K1-E4

Seq. No. 262123

Contig ID 3683_1.R1011 5'-most EST zuv700354335.h1

Method BLASTX
NCBI GI g130720
BLAST score 451
E value 2.0e-44
Match length 160
% identity 53

NCBI Description PROTEOLIPID PROTEIN PPA1 >gi_101508_pir_A34633 probable

H+-transporting ATPase (EC 3.6.1.35) lipid-binding protein - yeast (Saccharomyces cerevisiae) >gi_172221 (M35294) proteolipid protein of proton ATPase [Saccharomyces

cerevisiae] >gi 500700 (U10399) Ppa1p: Proteolipid protein

of proton ATPase [Saccharomyces cerevisiae]

Seq. No. 262124

Contig ID 3683_2.R1011

5'-most EST uC-zmromo17011g03a1

Method BLASTX
NCBI GI g2414624
BLAST score 208
E value 2.0e-16
Match length 55
% identity 69

NCBI Description (Z99259) ATP synthase subunit [Schizosaccharomyces pombe]

Seq. No. 262125

Contig ID 3692 1.R1011

5'-most EST LIB148-032-Q1-E1-E3

Seq. No. 262126

Contig ID 3698_1.R1011 5'-most EST wyr700240853.h1

Method BLASTX
NCBI GI g543867
BLAST score 1259
E value 1.0e-139
Match length 330
% identity 77

NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR

>gi_1076684_pir__A47493 H+-transporting ATP synthase (EC

3.6.1.34) gamma chain precursor - sweet potato

>gi 303626_dbj_BAA03526_ (D14699) F1-ATPase gammma subunit

[Ipomoea batatas]

Seq. No. 262127

Contig ID 3698 2.R1011

5'-most EST uC-zmroteosinte083e07b1



Method BLASTX
NCBI GI g543867
BLAST score 184
E value 2.0e-13
Match length 46
% identity 76

NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR

>gi_1076684_pir__A47493 H+-transporting ATP synthase (EC

3.6.1.34) gamma chain precursor - sweet potato

>gi_303626_dbj_BAA03526_ (D14699) F1-ATPase gammma subunit

[Ipomoea batatas]

Seq. No. 262128

Contig ID 3698 3.R1011

5'-most EST uC-zmflb73034e06b2

Seq. No. 262129

Contig ID 3699 1.R1011

5'-most EST LIB3069-024-Q1-K1-D6

Method BLASTN
NCBI GI g168406
BLAST score 84
E value 7.0e-39
Match length 128
% identity 91

NCBI Description Z.mays alcohol dehydrogenase (ADH-1 C-m allele) gene,

complete cds

Seq. No. 262130 Contig ID 3699 2.R1011

5'-most EST LIB3062-033-Q1-K1-C6

Method BLASTX
NCBI GI g2529662
BLAST score 474
E value 3.0e-47
Match length 99
% identity 92

NCBI Description (AC002535) putative small nuclear ribonucleoprotein, Sm D2

[Arabidopsis thaliana] >gi_3738278 (AC005309) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis

thaliana]

Seq. No. 262131

Contig ID 3699 3.R1011

5'-most EST uC-zmflmo17324e10a1

Method BLASTN
NCBI GI g168406
BLAST score 88
E value 1.0e-41
Match length 124
% identity 93

NCBI Description Z.mays alcohol dehydrogenase (ADH-1 C-m allele) gene,

complete cds

Seq. No. 262132 Contig ID 3699 4

Contig ID 3699_4.R1011

5'-most EST LIB84-006-Q1-E1-D5

Seq. No.

Contig ID



```
Seq. No.
                   262133
                   3699 5.R1011
Contig ID
5'-most EST
                   uC-zmflmo17049d08a1
Seq. No.
                   262134
                   3699 9.R1011
Contig ID
5'-most EST
                   zuv700353164.h1
                   BLASTN
Method
NCBI GI
                   g168406
BLAST score
                   74
E value
                   3.0e-33
                   130
Match length
                   89
% identity
                   Z.mays alcohol dehydrogenase (ADH-1 C-m allele) gene,
NCBI Description
                   complete cds
                   262135
Seq. No.
                   3699 10.R1011
Contig ID
5'-most EST
                   uC-zmflmo17127h06b1
Method
                   BLASTN
NCBI GI
                   g22118
BLAST score
                   68
                   1.0e-29
E value
Match length
                   128
% identity
                   88
NCBI Description Z.mays DNA for Adhl-Cm allele
                   262136
Seq. No.
Contig ID
                   3699 12.R1011
                   uC-z\overline{m}flb73108f04a1
5'-most EST
Method
                   BLASTN
                   g168406
NCBI GI
BLAST score
                   84
                   2.0e-39
E value
Match length
                   108
% identity
                   94
NCBI Description Z.mays alcohol dehydrogenase (ADH-1 C-m allele) gene,
                   complete cds
Seq. No.
                   262137
Contig ID
                   3699 13.R1011
5'-most EST
                   uC-zmflb73120d11a1
Seq. No.
                   262138
Contig ID
                   3699 14.R1011
5'-most EST
                   uC-zmromo17037e11a1
Method
                   BLASTN
NCBI GI
                   g22118
BLAST score
                   73
E value
                   1.0e-32
Match length
                   109
                   93
% identity
```

36321

NCBI Description Z.mays DNA for Adhl-Cm allele

3699_15.R1011



5'-most EST uC-zmflb73164g06a1 Method BLASTN NCBI GI g168406

BLAST score 67
E value 4.0e-29
Match length 95
% identity 93

NCBI Description Z.mays alcohol dehydrogenase (ADH-1 C-m allele) gene,

complete cds

Seq. No. 262140

Contig ID 3699_16.R1011 5'-most EST nbm700477428.h1

Seq. No. 262141

Contig ID 3699 18.R1011

5'-most EST LIB3075-021-Q1-K1-E1

Method BLASTN
NCBI GI g168406
BLAST score 76
E value 2.0e-34
Match length 128
% identity 90

NCBI Description Z.mays alcohol dehydrogenase (ADH-1 C-m allele) gene,

complete cds

Seq. No. 262142

Contig ID 3699_19.R1011

5'-most EST LIB3115-032-P1-K1-H7

Method BLASTN
NCBI GI g168406
BLAST score 98
E value 2.0e-47
Match length 130
% identity 94

NCBI Description Z.mays alcohol dehydrogenase (ADH-1 C-m allele) gene,

complete cds

Seq. No. 262143

Contig ID 3699_20.R1011 5'-most EST uC-zmromo17113b01a1

Method BLASTN
NCBI GI g168406
BLAST score 77
E value 3.0e-35

Match length 133 % identity 90

NCBI Description Z.mays alcohol dehydrogenase (ADH-1 C-m allele) gene,

complete cds

Seq. No. 262144

Contig ID 3703_1.R1011

5'-most EST LIB3061-045-Q1-K1-A6

Method BLASTX
NCBI GI g2668744
BLAST score 780
E value 5.0e-83

```
Match length
                  148
% identity
                   97
NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]
Seq. No.
                  262145
Contig ID
                  3703 2.R1011
5'-most EST
                  LIB3150-054-Q1-N1-F3
Method
                  BLASTX
NCBI GI
                  q464981
BLAST score
                  249
E value
                  4.0e-21
Match length
                  48
% identity
                  96
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762)
                  ubiquitin carrier protein [Lycopersicon esculentum]
Seq. No.
                  262146
Contig ID
                  3704_1.R1011
5'-most EST
                  uC-zmrob73068g09b1
Method
                  BLASTX
NCBI GI
                  q1350969
BLAST score
                  350
E value
                  8.0e-33
Match length
                  66
% identity
                  95
NCBI Description 40S RIBOSOMAL PROTEIN S26 (S31) >gi 971284 dbj BAA07208
                  (D38011) ribosomal protein S31 [Oryza sativa]
Seq. No.
                  262147
Contig ID
                  3704 3.R1011
5'-most EST
                  LIB3157-021-Q1-K1-D6
```

Seq. No. 262148
Contig ID 3704 4.R1011
5'-most EST LIB3059-038-Q1-K1-E6

~ ...

 Seq. No.
 262149

 Contig ID
 3705_2.R1011

 5'-most EST
 fdz701165375.h1

 Method
 BLASTX

 NCBI GI
 g1524370

 RLAST score
 531

BLAST score 531 E value 8.0e-54 Match length 192 % identity 55

NCBI Description (X92491) TOM20 [Solanum tuberosum]

 Seq. No.
 262150

 Contig ID
 3705_3.R1011

 5'-most EST
 LIB3067-033-Q1-K1-A2

 Method
 BLASTX

NCBI GI g1524370 BLAST score 158 E value 1.0e-10 Match length 50 % identity 52

Seq. No.

Contig ID

262156

3713 1.R1011



```
NCBI Description
                  (X92491) TOM20 [Solanum tuberosum]
                  262151
Seq. No.
Contig ID
                  3705 5.R1011
5'-most EST
                  LIB3059-005-Q1-K1-F12
                  BLASTX
Method
                  g1524370
NCBI GI
BLAST score
                  291
                  3.0e-26
E value
Match length
                  90
                  61
% identity
NCBI Description
                  (X92491) TOM20 [Solanum tuberosum]
Seq. No.
                  262152
                  3705 6.R1011
Contig ID
5'-most EST
                  uC-zmflb73416c07a1
                  262153
Seq. No.
                  3709 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17197a07b1
Method
                  BLASTX
                  g4586242
NCBI GI
BLAST score
                  346
                  2.0e-32
E value
Match length
                  91
                  71
% identity
NCBI Description
                  (AL049640) putative protein (fragment) [Arabidopsis
                  thaliana]
                  262154
Seq. No.
Contig ID
                  3712 1.R1011
5'-most EST
                  uC-zmflmo17341g06b1
Method
                  BLASTX
NCBI GI
                  q4104933
BLAST score
                  1442
E value
                  1.0e-160
Match length
                  594
                  49
% identity
NCBI Description
                  (AF042346) putative phenylalanyl-tRNA synthetase
                  beta-subunit; PheHB [Homo sapiens]
Seq. No.
                  262155
Contig ID
                  3712 2.R1011
5'-most EST
                  LIB3158-012-Q1-K1-D12
Method
                  BLASTX
NCBI GI
                  g3876233
BLAST score
                  260
E value
                  2.0e-22
Match length
                  134
% identity
                  45
                  (Z50044) similar to phenylalanyl-tRNA synthetase; cDNA EST
NCBI Description
                  EMBL:T01401 comes from this gene; cDNA EST yk303c5.3 comes
                  from this gene; cDNA EST yk303c5.5 comes from this gene;
                  cDNA EST yk452d5.3 comes from this gene; cDNA EST yk
```



```
5'-most EST
                   fwa700101532.h1
                   262157
Seq. No.
                   3714 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73008c10b1
Method
                   BLASTX
                   q3915029
NCBI GI
BLAST score
                   1735
                   0.0e + 00
E value
                   358
Match length
                   91
% identity
                  ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
NCBI Description
                   (STEAROYL-ACP DESATURASE) >gi 976257 dbj BAA07631 (D38753)
                   stearyl-ACP desaturase [Oryza sativa]
                   262158
Seq. No.
                   3718 1.R1011
Contig ID
5'-most EST
                   nbm7\overline{0}0470308.h1
Method
                   BLASTX
NCBI GI
                   q1665777
                   252
BLAST score
                   8.0e-33
E value
Match length
                   170
                   43
% identity
                  (D87444) Similar to S.cerevisiae EMP70 protein precursor
NCBI Description
                   (S25110) [Homo sapiens]
                   262159
Seq. No.
Contig ID
                   3724 1.R1011
5'-most EST
                   wyr700243458.h1
                   BLASTX
Method
                   g118104
NCBI GI
BLAST score
                   824
                   3.0e-88
E value
Match length
                   172
                   92
% identity
NCBI Description
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                   >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                   maize >gi 168461 (M55021) cyclophilin [Zea mays]
                   >gi 829148 emb CAA48638 (X68678) cyclophilin [Zea mays]
                   262160
Seq. No.
                   3724 2.R1011
Contig ID
5'-most EST
                   LIB3079-018-Q1-K1-H10
Method
                   BLASTX
                   g1041815
NCBI GI
                   211
BLAST score
                   1.0e-16
E value
Match length
                   61
                   57
% identity
NCBI Description (U16721) lipid transfer protein [Oryza sativa]
                   262161
Seq. No.
                   3724 3.R1011
```

5'-most EST LIB3079-045-Q1-K1-E12

Method BLASTX

Contig ID



```
g1041815
NCBI GI
BLAST score
                  226
                  2.0e-18
E value
Match length
                  66
                  56
% identity
NCBI Description
                  (U16721) lipid transfer protein [Oryza sativa]
                  262162
Seq. No.
                  3724 4.R1011
Contig ID
                  LIB3088-025-Q1-K1-H6
5'-most EST
                  BLASTX
Method
NCBI GI
                  g118104
BLAST score
                  272
                  7.0e-24
E value
                  56
Match length
% identity
                  95
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                  (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi 68408 pir CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi 168461 (M55021) cyclophilin [Zea mays]
                  >qi 829148 emb CAA48638 (X68678) cyclophilin [Zea mays]
Seq. No.
                  262163
                  3724 5.R1011
Contig ID
5'-most EST
                  LIB3059-025-Q1-K1-B6
Method
                  BLASTX
                  g118104
NCBI GI
BLAST score
                  744
E value
                  6.0e-79
Match length
                  169
                  85
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                  (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi 168461 (M55021) cyclophilin [Zea mays]
                  >gi 829148 emb CAA48638 (X68678) cyclophilin [Zea mays]
Seq. No.
                  262164
Contig ID
                  3724 7.R1011
5'-most EST
                  LIB3079-033-Q1-K1-H9
                  BLASTX
Method
NCBI GI
                  q118104
BLAST score
                  427
E value
                  7.0e-42
Match length
                  84
                  98
% identity
NCBI Description
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
                  (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi_168461 (M55021) cyclophilin [Zea mays]
                  >gi_829148_emb_CAA48638 (X68678) cyclophilin [Zea mays]
```

 Seq. No.
 262165

 Contig ID
 3736_1.R1011

 5'-most EST
 uC-zmflb73120e12b1

 Method
 BLASTX

 NCBI GI
 q3309082



```
BLAST score
                      882
   E value
                      7.0e - 95
   Match length
                      213
   % identity
                      77
   NCBI Description
                     (AF076251) calcineurin B-like protein 1 [Arabidopsis
                      thaliana]
   Seq. No.
                      262166
   Contig ID
                      3736 2.R1011
   5'-most EST
                      tfd700571303.h1
   Seq. No.
                      262167
   Contig ID
                      3737_1.R1011
   5'-most EST
                      xmt700264344.h1
   Method
                      BLASTX
   NCBI GI
                      g2244806
   BLAST score
                      800
   E value
                      4.0e-85
   Match length
                      393
   % identity
                      46
   NCBI Description
                     (Z97336) hypothetical protein [Arabidopsis thaliana]
   Seq. No.
                      262168
   Contig ID
                      3737 2.R1011
   5'-most EST
                      LIB3069-018-Q1-K1-D6
Seq. No.
                      262169
   Contig ID
                      3737 3.R1011
   5'-most EST
                      uC-zmflb73094b10a1
   Seq. No.
                      262170
   Contig ID
                      3738 1.R1011
   5'-most EST
                      LIB148-020-Q1-E1-E1
   Seq. No.
                      262171
   Contig ID
                      3740 1.R1011
   5'-most EST
                      LIB3075-027-Q1-K1-F2
   Method
                      BLASTX
   NCBI GI
                      q1653667
   BLAST score
                      181
   E value
                      3.0e-13
   Match length
                      61
   % identity
                      56
   NCBI Description (D90915) hypothetical protein [Synechocystis sp.]
   Seq. No.
                      262172
                      3743 1.R1011
   Contig ID
   5'-most EST
                      LIB3075-027-Q1-K1-H2
   Method
                      BLASTX
   NCBI GI
                      g4582459
   BLAST score
                      649
```

E value 5.0e-68 Match length 167

74 % identity

NCBI Description (AC007071) putative RanBP7/importin protein [Arabidopsis

thaliana]



Seq. No. 262173

Contig ID 3749_1.R1011 5'-most EST xmt700259322.h1

Method BLASTX
NCBI GI g509810
BLAST score 777
E value 1.0e-82
Match length 363
% identity 49

NCBI Description (L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No. 262174

Contig ID 3753_1.R1011 5'-most EST nbm700469023.h1

Method BLASTX
NCBI GI g2582351
BLAST score 349
E value 7.0e-33
Match length 137
% identity 50

NCBI Description (AF018639) unknown [Dictyostelium discoideum]

Seq. No. 262175

Contig ID 3754_1.R1011 5'-most EST xsy700207823.h1

Method BLASTX
NCBI GI g2983997
BLAST score 440
E value 5.0e-43
Match length 159
% identity 54

NCBI Description (AE000749) hypothetical protein [Aquifex aeolicus]

Seq. No. 262176

Contig ID 3761_1.R1011

5'-most EST uC-zmflb73144g03b1

Seq. No. 262177

Contig ID 3764 1.R1011

5'-most EST LIB3079-052-Q1-K1-B9

Method BLASTX
NCBI GI g1711512
BLAST score 1931
E value 0.0e+00
Match length 479
% identity 80

NCBI Description SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 2 (SRP54)

>gi_1076577_pir__S51598 signal recognition particle 54K
protein - tomato (cv. UC82-B) >gi_556902_emb_CAA84288_
(Z34527) 54-kD signal recognition particle (SRP) specific

protein [Lycopersicon esculentum]

Seq. No. 262178 Contig ID 3764 2.R1011

5'-most EST uC-zmroteosinte063c05b1

Method BLASTX NCBI GI g1711512



BLAST score 355 E value 2.0e-68 Match length 175 % identity 83

NCBI Description SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 2 (SRP54)
>gi_1076577_pir__S51598 signal recognition particle 54K
protein - tomato (cv. UC82-B) >gi_556902_emb_CAA84288_
(Z34527) 54-kD signal recognition particle (SRP) specific

protein [Lycopersicon esculentum]

Seq. No. 262179

Contig ID 3764 3.R1011

5'-most EST LIB36-001-Q1-E1-H9

Method BLASTX
NCBI GI g1711512
BLAST score 358
E value 5.0e-34
Match length 79
% identity 87

NCBI Description SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 2 (SRP54)

>gi_1076577_pir__S51598 signal recognition particle 54K
protein - tomato (cv. UC82-B) >gi_556902_emb_CAA84288_
(Z34527) 54-kD signal recognition particle (SRP) specific

protein [Lycopersicon esculentum]

Seq. No. 262180

Contig ID 3764 4.R1011

5'-most EST LIB3079-049-Q1-K1-B9

Method BLASTX
NCBI GI g1711511
BLAST score 286
E value 1.0e-34
Match length 116
% identity 71

NCBI Description SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 2 (SRP54)

>gi 1020002 (L48285) signal recognition particle 54 kDa

subunit [Hordeum vulgare]

Seq. No. 262181

Contig ID 3764_5.R1011 5'-most EST xmt700263377.h1

Method BLASTX
NCBI GI g1711511
BLAST score 252
E value 1.0e-21
Match length 65
% identity 85

NCBI Description SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 2 (SRP54)

>gi 1020002 (L48285) signal recognition particle 54 kDa

subunit [Hordeum vulgare]

Seq. No. 262182

Contig ID 3770_1.R1011

5'-most EST LIB3075-032-Q1-K1-C4

Method BLASTX NCBI GI g1871192 BLAST score 255



E value 2.0e-21 Match length 183 % identity 39

NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis

thaliana]

Seq. No. 262183

Contig ID 3770_2.R1011 5'-most EST gct701167495.h1

Seq. No. 262184

Contig ID 3774_1.R1011 5'-most EST xmt700257062.h1

Method BLASTX
NCBI GI g4519507
BLAST score 2039
E value 0.0e+00
Match length 506
% identity 76

NCBI Description (D88434) protein abundantly expressed during apple fruit

development [Malus domestica]

Seq. No. 262185

Contig ID 3774_2.R1011 5'-most EST ntr700073963.h1

Method BLASTX
NCBI GI g1084349
BLAST score 234
E value 2.0e-19
Match length 60
% identity 83

NCBI Description aldehyde dehydrogenase homolog btg-26 - rape

>gi_913941_bbs_164188 (S77096) aldehyde dehydrogenase homolog=btg-26 [Brassica napus, cv. Bridger, Peptide, 494

aa] [Brassica napus]

Seq. No. 262186 Contig ID 3774_3.R1011

5'-most EST \sim LIB3 $\overline{0}$ 66-025-Q1-K1-C4

Method BLASTX
NCBI GI g4519507
BLAST score 179
E value 5.0e-13
Match length 75
% identity 45

NCBI Description (D88434) protein abundantly expressed during apple fruit

development [Malus domestica]

Seq. No. 262187

Contig ID 3779_1.R1011 5'-most EST cyk700052093.f1

Method BLASTX
NCBI GI g2129851
BLAST score 452
E value 6.0e-45
Match length 176
% identity 55



NCBI Description tRNA adenylyltransferase (EC 2.7.7.25) - white lupine >gi_1139585 (U15930) tRNA nucleotidyltransferase [Lupinus albus]

Seq. No. 262188

Contig ID 3783_1.R1011 5'-most EST wen700334458.h1

Method BLASTX
NCBI GI g2132445
BLAST score 172
E value 1.0e-11
Match length 229
% identity 27

NCBI Description probable membrane protein YDL148c - yeast (Saccharomyces

cerevisiae) >gi_1321956_emb_CAA66343_ (X97751) D1566 [Saccharomyces cerevisiae] >gi_1431233_emb_CAA98722_ (Z74196) ORF YDL148c [Saccharomyces cerevisiae]

 Seq. No.
 262189

 Contig ID
 3792_1.R1011

 5'-most EST
 ceu700430902.h1

Method BLASTX
NCBI GI g2088652
BLAST score 939
E value 1.0e-101
Match length 265
% identity 66

NCBI Description (AF002109) 26S proteasome regulatory subunit S12 isolog

[Arabidopsis thaliana] >gi_2351376 (U54561) translation initiation factor eIF2 p47 subunit homolog [Arabidopsis

thaliana]

Seq. No. 262190

Contig ID 3792 2.R1011 5'-most EST uer700580512.h1

Method BLASTX
NCBI GI g2088652
BLAST score 149
E value 2.0e-09
Match length 68
% identity 44

NCBI Description (AF002109) 26S proteasome regulatory subunit S12 isolog [Arabidopsis thaliana] >qi 2351376 (U54561) translation

initiation factor eIF2 p47 subunit homolog [Arabidopsis

thaliana]

Seq. No. 262191 Contig ID 3792 3.R1011

5'-most EST uC-zmroteosinte019a07b1

Method BLASTX
NCBI GI g2088652
BLAST score 234
E value 2.0e-25
Match length 93
% identity 67

NCBI Description (AF002109) 26S proteasome regulatory subunit S12 isolog



initiation factor eIF2 p47 subunit homolog [Arabidopsis thaliana]

Seq. No. 262192

Contig ID 3795 1.R1011

5'-most EST uC-zmflb73006d12a1

Seq. No. 262193

Contig ID 3795 2.R1011

5'-most EST uC-zmflmo17203a05a1

Seq. No. 262194

Contig ID 3797_1.R1011

5'-most EST LIB3180-032-P2-M2-F12

Method BLASTX
NCBI GI g2499819
BLAST score 2237
E value 0.0e+00
Match length 510
% identity 83

NCBI Description ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR

>gi_2130068_pir__S66516 aspartic proteinase 1 precursor rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease
[Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic

protease [Oryza sativa]

Seq. No. 262195

Contig ID 3797_2.R1011

5'-most EST uC-zmflmo17095f09b2

Method BLASTX
NCBI GI g2499819
BLAST score 942

E value 1.0e-102 Match length 197 % identity 90

NCBI Description ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR

>gi_2130068_pir__S66516 aspartic proteinase 1 precursor rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease
[Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic

protease [Oryza sativa]

Seq. No. 262196

Contig ID 3797_3.R1011 5'-most EST rv1700455095.h1

Seq. No. 262197

Contig ID 3797 4.R1011

5'-most EST LIB3279-016-P1-K1-A4

Method BLASTX
NCBI GI g2499819
BLAST score 1222
E value 1.0e-146
Match length 327
% identity 80

NCBI Description ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR

>gi_2130068_pir__S66516 aspartic proteinase 1 precursor - rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease



[Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic protease [Oryza sativa]

Seq. No. 262198

Contig ID 3797_5.R1011 5'-most EST wty700172885.h1

Seq. No. 262199

Contig ID 3797_7.R1011 5'-most EST cjh700195724.h1

Method BLASTX
NCBI GI g2342682
BLAST score 443
E value 2.0e-43
Match length 254
% identity 41

NCBI Description (AC000106) Contains similarity to Rattus AMP-activated

protein kinase (gb_X95577). [Arabidopsis thaliana]

Seq. No. 262200

Contig ID 3797_8.R1011

5'-most EST uC-zmflb73230f09b2

Method BLASTX
NCBI GI g4506061
BLAST score 168
E value 2.0e-11
Match length 93
% identity 40

NCBI Description protein kinase, AMP-activated, gamma 1 non-catalytic

subunit >gi_1703037_sp_P54619_AAKG_HUMAN 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN) >gi_1335856 (U42412) 5'-AMP-activated protein kinase,

gamma-1 subunit [Homo sapiens]

Seq. No. 262201

Contig ID 3797 11.R1011

5'-most EST LIB143-064-Q1-E1-D11

Method BLASTX
NCBI GI g1168536
BLAST score 271
E value 1.0e-23
Match length 85
% identity 75

NCBI Description PHYTEPSIN PRECURSOR (ASPARTIC PROTEINASE)

>gi_100567_pir__S19697 aspartic proteinase (EC 3.4.23.-)

precursor - barley >gi_18904_emb_CAA39602_ (X56136)

aspartic proteinase [Hordeum vulgare]

Seq. No. 262202

Contig ID 3797_15.R1011 5'-most EST uwh700207261.h1

Seq. No. 262203

Contig ID 3797_21.R1011 5'-most EST pmx700086317.h1

Seq. No. 262204



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3797 22.R1011
Contig ID
5'-most EST
                  uC-zmflmo17426g08a1
                  262205
Seq. No.
                   3798 1.R1011
Contig ID
5'-most EST
                  afb700380950.h1
Method
                  BLASTX
                   g2982303
NCBI GI
BLAST score
                   702
                  1.0e-109
E value
Match length
                  247
% identity
                  79
NCBI Description (AF051236) hypothetical protein [Picea mariana]
Seq. No.
                  262206
Contig ID
                  3801 1.R1011
5'-most EST
                  LIB3150-077-P1-N1-C3
Method
                  BLASTX
NCBI GI
                  q4519417
BLAST score
                  800
E value
                   4.0e-85
Match length
                  290
% identity
                  52
NCBI Description (AB024327) WD-40 repeat protein [Homo sapiens]
                  262207
Seq. No.
                  3801 2.R1011
Contig ID
5'-most EST
                  uC-zmflb73120f09a1
                  262208
Seq. No.
                  3801 3.R1011
Contig ID
5'-most EST
                  LIB3061-001-Q1-K2-D5
Method
                  BLASTX
NCBI GI
                  g4519417
BLAST score
                  243
E value
                  2.0e-20
Match length
                  57
% identity
                  75
NCBI Description (AB024327) WD-40 repeat protein [Homo sapiens]
Seq. No.
                  262209
Contig ID
                  3801 5.R1011
5'-most EST
                  uC-zmflb73051f12a2
Seq. No.
                  262210
Contig ID
                  3803_1.R1011
5'-most EST
                  xsy700217580.h1
Method
                  BLASTX
NCBI GI
                  q126896
BLAST score
                  1190
                  1.0e-131
E value
```

Match length 341 % identity 71

NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR

>gi_319831_pir__DEPUMW malate dehydrogenase (EC 1.1.1.37)

precursor, mitochondrial - watermelon

>gi_18297_emb_CAA35239 (X17362) precursor protein (AA -27



to 320) [Citrullus lanatus]

Seq. No. 262211

Contig ID 3803 2.R1011

5'-most EST LIB3069-046-Q1-K1-D12

Seq. No. 262212

Contig ID 3803_3.R1011 5'-most EST tzu700204248.h1

Method BLASTX
NCBI GI g2827080
BLAST score 475
E value 1.0e-47
Match length 120
% identity 80

NCBI Description (AF020271) malate dehydrogenase precursor [Medicago sativa]

Seq. No. 262213

Contig ID 3803 4.R1011

5'-most EST LIB3078-053-Q1-K1-B8

Method BLASTX
NCBI GI g126896
BLAST score 347
E value 2.0e-32
Match length 113
% identity 65

NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR

>gi_319831_pir__DEPUMW malate dehydrogenase (EC 1.1.1.37)

precursor, mitochondrial - watermelon

>gi_18297_emb_CAA35239_ (X17362) precursor protein (AA -27

to 320) [Citrullus lanatus]

Seq. No. 262214

Contig ID 3803_7.R1011

5'-most EST uC-zmflb73088b11a1

Seq. No. 262215

Contig ID 3816 1.R1011

5'-most EST uC-zmflmo17129d07b1

Seq. No. 262216

Contig ID 3817_1.R1011 5'-most EST ntr700077206.h1

Method BLASTX
NCBI GI g4455210
BLAST score 1514
E value 1.0e-169
Match length 521
% identity 59

NCBI Description (AL035440) putative aspartate-tRNA ligase [Arabidopsis

thaliana]

Seq. No. 262217

Contig ID 3818 1.R1011

5'-most EST LIB143-041-Q1-E1-H11

Method BLASTX NCBI GI g1717957



BLAST score 1068 E value 1.0e-116 226 Match length 89 % identity UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT NCBI Description PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi 100923 pir A41607 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein precursor - maize >gi 168607 (M77224) Rieske Fe-S protein [Zea mays] Seq. No. 262218 Contig ID 3831 1.R1011 5'-most EST LIB3062-031-Q1-K1-H9 Method BLASTX q4467135 NCBI GI 927 BLAST score E value 1.0e-100 Match length 366 52 % identity NCBI Description (AL035540) putative protein [Arabidopsis thaliana] 262219 Seq. No. 3833 1.R1011 Contig ID 5'-most EST uC-zmflb73032a02a1 Method BLASTX NCBI GI g3461814 BLAST score 703 E value 3.0e-74Match length 218 % identity 62 (AC004138) hypothetical protein [Arabidopsis thaliana] NCBI Description 262220 Seq. No. Contig ID 3839 1.R1011 5'-most EST uC-zmflmo17045f10b1 Method BLASTX NCBI GI q3786007 BLAST score 193 E value 3.0e-14Match length 46 % identity 63 NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana] Seq. No. 262221 Contig ID 3840 1.R1011 5'-most EST LIB3066-029-Q1-K1-A11 Method BLASTN NCBI GI q3821780 BLAST score 36 E value 1.0e-10 Match length 36 % identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Contig ID 3841_1.R1011 5'-most EST uC-zmflb73063h03b1

262222

Seq. No.



Method BLASTX
NCBI GI g3287683
BLAST score 1422
E value 1.0e-158
Match length 603
% identity 23

NCBI Description (AC003979) Similar to apoptosis protein MA-3 gb_D50465 from

Mus musculus. [Arabidopsis thaliana]

Seq. No. 262223 Contig ID 3844 1.R1011

5'-most EST LIB3066-054-Q1-K1-C3

Method BLASTX
NCBI GI g3063469
BLAST score 294
E value 7.0e-26
Match length 281
% identity 33

NCBI Description (AC003981) F22013.31 [Arabidopsis thaliana]

Seq. No. 262224 Contig ID 3844 2.R1011

5'-most EST LIB148-049-Q1-E1-H9

Method BLASTX
NCBI GI g3063469
BLAST score 318
E value 1.0e-28

E value 1.00 Match length 321 % identity 31

NCBI Description (AC003981) F22013.31 [Arabidopsis thaliana]

Seq. No. 262225

Contig ID 3848 1.R1011

5'-most EST LIB3075-048-Q1-K1-A7

Method BLASTX
NCBI GI g1172977
BLAST score 557
E value 4.0e-57
Match length 135
% identity 79

NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic

ribosomal protein L18 [Arabidopsis thaliana]

Seq. No. 262226

Contig ID 3848_3.R1011 5'-most EST xdb700341787.h1

Method BLASTX
NCBI GI g1172977
BLAST score 403
E value 2.0e-39
Match length 104
% identity 78

NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic

ribosomal protein L18 [Arabidopsis thaliana]

Seq. No. 262227

Contig ID 3850 1.R1011



5'-most EST qmh700030220.f1 Method BLASTX NCBI GI g4455158 BLAST score 1153 E value 1.0e-126 Match length 284 % identity 74 (AL021687) kinase-like protein [Arabidopsis thaliana] NCBI Description Seq. No. 262228 Contig ID 3850 2.R1011 5'-most EST uC-zmflmo17307e07b1 Method BLASTX NCBI GI q4455158 BLAST score 259 E value 2.0e-32 Match length 84 85 % identity NCBI Description (AL021687) kinase-like protein [Arabidopsis thaliana] Seq. No. 262229 Contig ID 3850 4.R1011 5'-most EST LIB3069-051-Q1-K1-A6 Seq. No. 262230 Contig ID 3850 7.R1011 5'-most EST uC-zmflmo17018b09a1 Seq. No. 262231 Contig ID 3853 1.R1011 5'-most EST LIB3075-048-Q1-K1-B4 Method BLASTX NCBI GI g3688593 BLAST score 506 5.0e-51 E value Match length 134 % identity 77 NCBI Description (AB007506) MADS box transcription factor [Triticum aestivum] 262232 Seq. No. 3855 1.R1011 Contig ID 5'-most EST LIB3158-006-Q1-K1-D7 262233 Seq. No. 3855 2.R1011 Contig ID

5'-most EST xjt700094440.h1 Method BLASTX

NCBI GI g4512699 BLAST score 1420 E value 1.0e-158 Match length 364 74 % identity

NCBI Description (AC006569) putative NADH-ubiquinone oxireductase

[Arabidopsis thaliana]

Seq. No. 262234

```
Contig ID
                  3856 1.R1011
5'-most EST
                  uC-zmflMo17091a06b1
Method
                  BLASTX
NCBI GI
                  q3924848
BLAST score
                  320
E value
                  7.0e-29
Match length
                  292
% identity
                  31
NCBI Description
                  (Z81586) cDNA EST yk335d8.5 comes from this gene; cDNA EST
                  yk335d8.3 comes from this gene [Caenorhabditis elegans]
Seq. No.
                  262235
                  3857 1.R1011
Contig ID
5'-most EST
                  uer700577783.h1
Method
                  BLASTX
NCBI GI
                  q4406759
BLAST score
                  278
E value
                  3.0e-24
Match length
                  204
                  38
% identity
NCBI Description
                 (AC006836) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  262236
Contig ID
                  3857 2.R1011
5'-most EST
                  dyk700106267.h1
Method
                  BLASTX
NCBI GI
                  g4406759
BLAST score
                  347
E value
                  2.0e-32
Match length
                  192
% identity
                  44
NCBI Description
                 (AC006836) hypothetical protein [Arabidopsis thaliana]
                  262237
Seq. No.
Contig ID
                  3858 1.R1011
5'-most EST
                  pwr700451643.h1
Method
                  BLASTX
NCBI GI
                  q730456
BLAST score
                  719
E value
                  6.0e-76
```

E value 6.00 Match length 143 % identity 95

NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No. 262238 Contig ID 3858_2.R1011

5'-most EST LIB3067-057-Q1-K1-D5

Method BLASTX
NCBI GI g730456
BLAST score 386
E value 3.0e-37
Match length 81
% identity 91

NCBI Description 40S RIBOSOMAL PROTEIN S19

Seq. No. 262239

Contig ID 3858 3.R1011



5'-most EST pwr700451928.h1 Method BLASTX NCBI GI q730456 358 BLAST score 3.0e-34 E value Match length 70 96 % identity NCBI Description 40S RIBOSOMAL PROTEIN S19 262240 Seq. No. 3858 5.R1011 Contig ID 5'-most EST LIB3068-021-Q1-K1-H12 Method BLASTX NCBI GI g730456 BLAST score 719 E value 4.0e-76 143 Match length % identity 96 NCBI Description 40S RIBOSOMAL PROTEIN S19 262241 Seq. No. Contig ID 3861 1.R1011 5'-most EST LIB3150-007-Q1-N1-B6 Method BLASTX g2244876 NCBI GI BLAST score 1460 1.0e-162 E value Match length 423 % identity 65 NCBI Description (Z97338) hypothetical protein [Arabidopsis thaliana] 262242 Seq. No. 3863 1.R1011 Contig ID 5'-most EST LIB3075-048-Q1-K1-C4 262243 Seq. No. Contig ID 3864 1.R1011 5'-most EST LIB3075-048-Q1-K1-C5 262244 Seq. No. Contig ID 3870 1.R1011 5'-most EST uC-zmflb73134a10b1 262245 Seq. No. Contig ID 3873 1.R1011 5'-most EST hbs701185646.h1 Seq. No. 262246 Contig ID 3875 1.R1011 5'-most EST uC-zmflMo17008f05b1

Seq. No. 262247 Contig ID 3884_1.R1011 5'-most EST LIB84-030-Q1-E1-F12

Method BLASTX NCBI GI g3297819 BLAST score 590



E value 7.0e-61 Match length 138 % identity 76

NCBI Description (AL031032) protein kinase-like protein [Arabidopsis

thaliana]

Seq. No. 262248

Contig ID 3885_1.R1011

5'-most EST LIB143-006-Q1-E1-A5

Method BLASTX
NCBI GI g3212879
BLAST score 823
E value 5.0e-88
Match length 239
% identity 65

NCBI Description (AC004005) putative ribosomal protein L7 [Arabidopsis

thaliana]

Seq. No. 262249

Contig ID 3885 2.R1011

5'-most EST uC-zmflmo17127c12b1

Method BLASTX
NCBI GI g3212879
BLAST score 883
E value 4.0e-95
Match length 235
% identity 69

NCBI Description (AC004005) putative ribosomal protein L7 [Arabidopsis

thaliana]

Seq. No. 262250

Contig ID 3885 3.R1011

5'-most EST LIB3088-010-Q1-K1-F11

Method BLASTX
NCBI GI g3212879
BLAST score 459
E value 1.0e-45
Match length 116
% identity 71

NCBI Description (AC004005) putative ribosomal protein L7 [Arabidopsis

thaliana]

Seq. No. 262251

Contig ID 3885 4.R1011

5'-most EST LIB3059-013-Q1-K1-C8

Method BLASTX
NCBI GI g3212879
BLAST score 332
E value 7.0e-31
Match length 88
% identity 65

NCBI Description (AC004005) putative ribosomal protein L7 [Arabidopsis

thaliana]

Seq. No. 262252

Contig ID 3885 5.R1011

5'-most EST LIB3078-014-Q1-K1-E12



```
Method
                  BLASTX
NCBI GI
                  g3212879
                  295
BLAST score
                  2.0e-26
E value
Match length
                  125
                  57
% identity
                  (AC004005) putative ribosomal protein L7 [Arabidopsis
NCBI Description
                  thaliana]
                  262253
Seq. No.
                  3885 7.R1011
Contig ID
                  LIB3069-006-Q1-K1-E1
5'-most EST
                  BLASTX
Method
                  g4262232
NCBI GI
BLAST score
                  172
                  2.0e-12
E value
Match length
                  60
                  55
% identity
                 (AC006200) putative ribosomal protein L7 [Arabidopsis
NCBI Description
                  thaliana]
                  262254
Seq. No.
                  3886 1.R1011
Contig ID
                  LIB3075-048-Q1-K1-F4
5'-most EST
                  BLASTN
Method
                  g22429
NCBI GI
BLAST score
                 . 64
                  3.0e-27
E value
                  148
Match length
                   86
% identity
NCBI Description Maize pseudo-Gpa1 pseudogene for glyceraldehyde-3-phosphate
                  dehydrogenase subunit A
                   262255
Seq. No.
                  3890 1.R1011
Contig ID
5'-most EST
                  LIB3075-048-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                   g3023750
                   798
BLAST score
                   4.0e-85
E value
                   155
Match length
% identity
NCBI Description FERREDOXIN VI PRECURSOR (FD VI) >gi_1863997_dbj_BAA19249
                   (AB001385) Fd VI [Zea mays] >gi_1863999_dbj_BAA19250_
                   (AB001386) Fd VI [Zea mays]
Seq. No.
                   262256
Contig ID
                   3890 2.R1011
```

5'-most EST LIB3062-019-Q1-K1-E1

Method BLASTN NCBI GI q1863998 BLAST score 302 E value 1.0e-169 Match length 434 % identity 98

NCBI Description Maize DNA for Fd VI, complete cds



```
262257
Seq. No.
                   3891 1.R1011
Contig ID
                  LIB3\overline{1}36-009-Q1-K1-C3
5'-most EST
                   262258
Seq. No.
                   3891 2.R1011
Contig ID
5'-most EST
                   fdz701158956.h2
                   262259
Seq. No.
                   3891 3.R1011
Contig ID
                  LIB36-006-Q1-E1-H8
5'-most EST
                   BLASTN
Method
NCBI GI
                   g4140643
                   34
BLAST score
                   2.0e-09
E value
                   50
Match length
                   92
% identity
                   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                   complete sequence
                   262260
Seq. No.
                   3891 4.R1011
Contig ID
5'-most EST
                   ymt700220993.h1
                   262261
Seq. No.
                   3891 6.R1011
Contig ID
                   fwa700101190.hl
5'-most EST
                   262262
Seq. No.
                   3895_1.R1011
Contig ID
                   uC-zmflb73122c09b2
5'-most EST
                   BLASTX
Method
                   q3021506
NCBI GI
BLAST score
                   1570
E value
                   1.0e-175
Match length
                   339
                   87
% identity
                   (X96727) isocitrate dehydrogenase (NAD+) [Nicotiana
NCBI Description
                   tabacum]
Seq. No.
                   262263
Contig ID
                   3895 3.R1011
                   nbm700471753.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q266463
BLAST score
                   366
                   6.0e - 35
E value
Match length
                   81
                   88
% identity
```

NCBI Description 3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi_82259_pir__S25670 3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor -potato >gi_22643_emb_CAA47720_ (X67310) 3-isopropylmalate dehydrogenase [Solanum tuberosum] >gi_445064_prf__1908380A

beta isopropylmalate dehydrogenase [Solanum tuberosum]

Seq. No. 262264



Contig ID 3916_1.R1011

5'-most EST LIB3068-020-Q1-K1-E1

Seq. No. 262265

Contig ID 3918 1.R1011

5'-most EST LIB148-044-Q1-E1-H11

Method BLASTX
NCBI GI g3858935
BLAST score 233
E value 3.0e-19
Match length 92
% identity 53

NCBI Description (AL021636) synaptobrevin-like protein [Arabidopsis

thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis

thaliana]

Seq. No. 262266

Contig ID 3936_1.R1011 5'-most EST qmh700028477.f1

Method BLASTX
NCBI GI g3377797
BLAST score 619
E value 3.0e-64
Match length 185
% identity 68

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 262267

Contig ID 3936_2.R1011 5'-most EST uer700578345.h1

Method BLASTX
NCBI GI g3377797
BLAST score 608
E value 8.0e-63
Match length 185
% identity 68

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA

H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 262268

Contig ID 3936_3.R1011

5'-most EST LIB3 $\overline{2}$ 79-016-P1-K1-G9

Method BLASTX
NCBI GI g2832664
BLAST score 218
E value 2.0e-17
Match length 102
% identity 44

NCBI Description (AL021710) pollen-specific protein - like [Arabidopsis



thaliana]

 Seq. No.
 262269

 Contig ID
 3936_4.R1011

 5'-most EST
 tzu700201429.h1

 Method
 BLASTX

 NCBI GI
 g3377797

 BLAST score
 577

 E value
 3.0e-59

Match length 185 % identity 65

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by

A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 262270

Contig ID 3936_5.R1011

5'-most EST LIB3076-024-Q1-K1-C8

Method BLASTX
NCBI GI g3377797
BLAST score 333
E value 5.0e-31
Match length 89

% identity 75

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 262271

Contig ID 3936 6.R1011

5'-most EST LIB3150-036-Q1-N1-B7

Method BLASTX
NCBI GI g2832664
BLAST score 208
E value 2.0e-16
Match length 100
% identity 40

NCBI Description (AL021710) pollen-specific protein - like [Arabidopsis

thaliana]

Seq. No. 262272

Contig ID 3936_7.R1011 5'-most EST bdu700383131.h1

Method BLASTX
NCBI GI g1350677
BLAST score 193
E value 6.0e-18
Match length 55
% identity 93

NCBI Description 60S RIBOSOMAL PROTEIN L19

Seq. No. 262273

Contig ID 3938 1.R1011



5'-most EST LIB3066-009-Q1-K1-B7 Method BLASTX NCBI GI g2114016 BLAST score 156 9.0e-10 E value 233 Match length % identity 27 (Z95558) bpoC [Mycobacterium tuberculosis] NCBI Description Seq. No. 262274 Contig ID 3938 3.R1011 5'-most EST LIB3060-042-Q1-K1-G1 Seq. No. 262275 Contig ID 3942 1.R1011 5'-most EST LIB148-033-Q1-E1-G12 Method BLASTN NCBI GI g600117 BLAST score 110 9.0e-55 E value Match length 521 % identity 35 NCBI Description Z.mays (B73) gene for extensin-like protein 262276 Seq. No. Contig ID 3959 1.R1011 5'-most EST wyr700243829.h1 Seq. No. 262277 3964 1.R1011 Contig ID 5'-most EST uC-zmroteosinte107b09b2 Method BLASTX NCBI GI q4490294 BLAST score 307 1.0e-27 E value Match length 81 % identity 75 NCBI Description (AL035678) WD-repeat protein-like protein [Arabidopsis thaliana] Seq. No. 262278 3964 2.R1011 5'-most EST pmx700086323.h1 Method BLASTX NCBI GI g4490294 BLAST score 1558 E value 1.0e-174 Match length 400

Contig ID

% identity 74

NCBI Description (AL035678) WD-repeat protein-like protein [Arabidopsis thaliana]

Seq. No. 262279 Contig ID 3964 3.R1011 5'-most EST xmt700258557.h1

Method BLASTX NCBI GI g3668118



BLAST score 223 E value 7.0e-18 Match length 122 % identity 51

NCBI Description (AJ224078) hypothetical protein [Brassica napus]

262280 Seq. No. Contig ID 5'-most EST

3964 5.R1011 $kem7\overline{0}0611957.h1$

Seq. No. 262281

Contig ID 3972 1.R1011 5'-most EST fwa700099893.h1

Method BLASTX NCBI GI q2827544 BLAST score 709 E value 2.0e-74 Match length 305 % identity 64

(AL021635) HSP associated protein like [Arabidopsis NCBI Description

thaliana]

Seq. No.

262282 Contig ID 3972 2.R1011 5'-most EST rvt700550924.h1

Method BLASTX NCBI GI g2827544 BLAST score 203 3.0e-31 E value Match length 98 70 % identity

NCBI Description (AL021635) HSP associated protein like [Arabidopsis

thaliana]

Seq. No.

262283 3973 1.R1011

Contig ID 5'-most EST

LIB3069-029-Q1-K1-E9

BLASTX Method NCBI GI q3929336 BLAST score 414 E value 4.0e-40 Match length 163 % identity 49

NCBI Description BYSTIN >gi_2738509 (AF007802) bystin [Mus musculus]

Seq. No. 262284

Contig ID 3974_1.R1011

5'-most EST LIB3137-044-Q1-K1-C9

Method BLASTX NCBI GI g4204265 BLAST score 1092 E value 1.0e-119 Match length 594 % identity 43

NCBI Description (AC005223) 45643 [Arabidopsis thaliana]

Seq. No. 262285



Contig ID 3974 2.R1011 5'-most EST uC-zmflb73026c06b1 Method BLASTX q4204265 NCBI GI BLAST score 195 E value 2.0e-14 Match length 243 % identity 28 NCBI Description (AC005223) 45643 [Arabidopsis thaliana] Seq. No. 262286 Contig ID 3974 3.R1011 5'-most EST LIB3059-025-Q1-K1-G10 Seq. No. 262287 Contig ID 3974 4.R1011 5'-most EST LIB3059-008-Q1-K1-H7 Method BLASTX q4204265 250

NCBI GI BLAST score E value 5.0e-21 Match length 65 % identity 72

NCBI Description (AC005223) 45643 [Arabidopsis thaliana]

Seq. No. 262288 Contig ID 3974 5.R1011 5'-most EST gw1700616287.h1

Seq. No. 262289 Contig ID 3974 7.R1011 xdb700341918.h1 5'-most EST

262290 Seq. No. 3974 8.R1011 Contig ID 5'-most EST uC-zmflb73285b08a1

Seq. No. 262291 3982 1.R1011 Contig ID 5'-most EST uC-zmrob73077e07b1 Method BLASTX

NCBI GI g2827552 BLAST score 720 9.0e-76 E value Match length 297 50 % identity

NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]

262292 Seq. No. Contig ID 3982_3.R1011 5'-most EST LIB3059-040-Q1-K1-E10

Seq. No. 262293 3982 4.R1011 Contig ID 5'-most EST tzu700205520.h1 Method BLASTX

NCBI GI q2827552



BLAST score 207
E value 2.0e-16
Match length 57
% identity 68

NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]

Seq. No. 262294

Contig ID 3986_1.R1011 5'-most EST ntr700076532.h1

Method BLASTX
NCBI GI g3789911
BLAST score 385
E value 1.0e-36
Match length 161
% identity 46

NCBI Description (AF081802) developmental protein DG1118 [Dictyostelium

discoideum]

Seq. No. 262295 Contig ID 3986 2.R1011

5'-most EST uC-zmflb73089d02a1

Seq. No. 262296

Contig ID 3987_1.R1011

5'-most EST LIB3066-011-Q1-K1-G6

Seq. No. 262297

Contig ID 3987 2.R1011

5'-most EST LIB3076-021-Q1-K1-E1

Seq. No. 262298

Contig ID 3989 1.R1011

5'-most EST LIB3068-045-Q1-K1-A3

Method BLASTX
NCBI GI g2129473
BLAST score 253
E value 3.0e-21
Match length 142
% identity 38

NCBI Description arabinogalactan-like protein - loblolly pine >gi_607774

(U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No. 262299 Contig ID 3989 3.R1011

5'-most EST uC-zmrob73002h10b1

Seq. No. 262300 Contig ID 3990 1.R1011

5'-most EST uC-zmflb73278b09b1

Seq. No. 262301

Contig ID 3990_2.R1011

5'-most EST LIB3180-038-P2-M2-H7

Seq. No. 262302

Contig ID 3992 1.R1011

5'-most EST uC-zmflb73193b10b1



```
Method
                  BLASTX
                  g3702964
NCBI GI
BLAST score
                  883
                   5.0e-95
E value
                  182
Match length
                   91
% identity
                  (AF079485) rac GTP binding protein Aracl0 [Arabidopsis
NCBI Description
                   thaliana]
                   262303
Seq. No.
                   3992 2.R1011
Contig ID
                   yyf700351221.h1
5'-most EST
                   BLASTX
Method
                   g3702964
NCBI GI
BLAST score
                   390
                   1.0e-37
E value
                   81
Match length
% identity
                   91
                  (AF079485) rac GTP binding protein Aracl0 [Arabidopsis
NCBI Description
                   thaliana]
                   262304
Seq. No.
                   3992 3.R1011
Contig ID
                   xjt700096270.h1
5'-most EST
                   BLASTX
Method
                   g3702964
NCBI GI
                   397
BLAST score
E value
                   1.0e-38
Match length
                   76
                   97
% identity
                  (AF079485) rac GTP binding protein Arac10 [Arabidopsis
NCBI Description
                   thaliana]
                   262305
Seq. No.
                   3992_4.R1011
Contig ID
                   LIB3069-022-Q1-K1-H12
5'-most EST
Method
                   BLASTX
                   g3702964
NCBI GI
                   514
BLAST score
                   4.0e-52
E value
                   99
Match length
                   96
% identity
                  (AF079485) rac GTP binding protein Aracl0 [Arabidopsis
NCBI Description
                   thaliana]
                   262306
Seq. No.
                   3993_1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17131b10b1
Method
                   BLASTX
NCBI GI
                   g134018
BLAST score
                   688
                   5.0e-72
E value
```

Match length 136 100 % identity CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi_70915_pir__R3ZMBC NCBI Description

ribosomal protein S8 - maize chloroplast >gi_12454_emb_CAA29913_ (X06734) ribosomal protein S8 (AA



1-136) [Zea mays] >gi_902257_emb_CAA60321_ (X86563) ribosomal protein S8 [Zea mays]

Seq. No. 262307

Contig ID 4001_1.R1011

5'-most EST LIB3076-021-Q1-K1-D1

Seq. No. 262308

Contig ID 4005_1.R1011 5'-most EST xsy700212615.h1

Method BLASTX
NCBI GI g3063637
BLAST score 323
E value 1.0e-29
Match length 87
% identity 69

NCBI Description (AF056204) thioesterase homolog [Gossypium hirsutum]

Seq. No. 262309

Contig ID 4005_2.R1011 5'-most EST fdz701166437.h1

Seq. No. 262310

Contig ID 4009_1.R1011

5'-most EST uC-zmflmo17036f02b2

Method BLASTX
NCBI GI g3759184
BLAST score 337
E value 3.0e-76
Match length 281
% identity 56

NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 262311

Contig ID 4009_2.R1011 5'-most EST xsy700211643.h1

Method BLASTX
NCBI GI g3759184
BLAST score 205
E value 8.0e-21
Match length 163
% identity 42

NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 262312

Contig ID 4009 3.R1011

5'-most EST uC-zmflmo17417e09a1

Method BLASTX
NCBI GI g3759184
BLAST score 253
E value 1.0e-21
Match length 65
% identity 71

NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 262313 Contig ID 4012 1.R1011



```
5'-most EST
                  xyt700344115.h1
Seq. No.
                  262314
                  4013 1.R1011
Contig ID
5'-most EST
                  LIB3136-033-Q1-K1-H9
                  BLASTX
Method
                  q4102600
NCBI GI
BLAST score
                  838
                  1.0e-100
E value
                  549
Match length
% identity
                  45
                  (AF013467) ARF6 [Arabidopsis thaliana]
NCBI Description
                  262315
Seq. No.
                  4014 1.R1011
Contig ID
                  LIB3076-020-Q1-K1-H12
5'-most EST
Method
                  BLASTX
                  q4416305
NCBI GI
BLAST score
                   384
                   1.0e-36
E value
Match length
                   94
                   83
% identity
                  (AF105716) hypothetical protein [Zea mays]
NCBI Description
Seq. No.
                   262316
Contig ID
                   4015 1.R1011
5'-most EST
                  LIB3150-028-Q1-N1-B6
Seq. No.
                   262317
                   4015 2.R1011
Contig ID
                  LIB3076-020-Q1-K1-H4
5'-most EST
                   262318
Seq. No.
                   4017 2.R1011
Contig ID
                  uC-zmflb73158e05a1
5'-most EST
                  BLASTX
Method
                   g1707017
NCBI GI
BLAST score
                   201
                   2.0e-16
E value
                   60
Match length
                   69
% identity
NCBI Description (U78721) RNA helicase isolog [Arabidopsis thaliana]
                   262319
Seq. No.
                   4018 1.R1011
Contig ID
5'-most EST
                   uwc700150134.hl
                   BLASTX
Method
NCBI GI
                   g2459438
                   209
BLAST score
E value
                   1.0e-16
                   72
Match length
                   54
% identity
                  (AC002332) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   262320
Seq. No.
```

36352

4021 1.R1011

 $nbm7\overline{0}0465137.h1$

Contig ID

5'-most EST



```
Method
                   BLASTX
NCBI GI
                   g629783
                   922
BLAST score
                   1.0e-100
E value
Match length
                   217
                   80
% identity
NCBI Description ES43 protein - barley >gi 1345528 emb CAA54682 (X77575)
                   ES43 [Hordeum vulgare]
Seq. No.
                   262321
Contig ID
                   4021 2.R1011
5'-most EST
                   uC-zmflmo17280d01a1
Seq. No.
                   262322
Contig ID
                   4022 1.R1011
5'-most EST
                   LIB3076-021-Q1-K1-A3
Seq. No.
                   262323
Contig ID
                   4026 1.R1011
5'-most EST
                   tzu700201183.h1
Method
                   BLASTX
NCBI GI
                   g2914700
BLAST score
                   652
E value
                   3.0e-72
Match length
                   233
% identity
                   66
                  (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   262324
Contig ID
                   4027 1.R1011
5'-most EST
                   uC-zmflb73173f04b1
Method
                   BLASTX
NCBI GI
                   q1345132
BLAST score
                   864
E value
                   1.0e-175
Match length
                   468
% identity
                   65
NCBI Description
                   (U47029) ERECTA [Arabidopsis thaliana]
                   >gi_1389566_dbj_BAA11869 (D83257) receptor protein kinase
[Arabidopsis thaliana] >gi_3075386 (AC004484) receptor
                   protein kinase, ERECTA [Arabidopsis thaliana]
Seq. No.
                   262325
Contig ID
                   4032 1.R1011
5'-most EST
                   LIB3076-020-Q1-K1-G10
Seq. No.
                   262326
Contig ID
                   4034 1.R1011
5'-most EST
                   rv1700456520.h1
Method
                   BLASTX
NCBI GI
                   g3757521
```

Method BLASTX
NCBI GI g3757521
BLAST score 821
E value 1.0e-87
Match length 395
% identity 47

NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Match length

NCBI Description

% identity

201

39



```
Seq. No.
                  262327
                  4034_2.R1011
Contig ID
                  uC-zmflmo17322h11a1
5'-most EST
Seq. No.
                  262328
                  4036 1.R1011
Contig ID
5'-most EST
                  LIB3076-004-Q1-K1-A8
                  BLASTN
Method
                  g3821780
NCBI GI
                  37
BLAST score
                  3.0e-11
E value
Match length
                  37
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  262329
                  4039 1.R1011
Contig ID
5'-most EST
                  LIB3180-033-P2-M2-C5
Method
                  BLASTX
NCBI GI
                  q2196466
BLAST score
                  409
                  6.0e-40
E value
Match length
                  164
% identity
                  51
                  (Y13673) TATA binding protein-associated factor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  262330
Contig ID
                  4040 1.R1011
5'-most EST
                  LIB3076-020-Q1-K1-C8
Seq. No.
                  262331
Contiq ID
                  4042 1.R1011
5'-most EST
                  xsy700213041.hl
Method
                  BLASTX
                  g2982322
NCBI GI
BLAST score
                   466
E value
                  1.0e-46
Match length
                  101
% identity
                  87
                  (AF051246) probable proteasome subunit [Picea mariana]
NCBI Description
Seq. No.
                  262332
                  4044 1.R1011
Contig ID
5'-most EST
                  LIB3076-020-Q1-K1-B8
Seq. No.
                  262333
                  4046 1.R1011
Contig ID
5'-most EST
                  pmx700084714.h1
                  BLASTX
Method
                  g2262113
NCBI GI
BLAST score
                  300
E value
                  5.0e-27
```

36354

(AC002343) unknown protein [Arabidopsis thaliana]



```
262334
Seq. No.
                  4047 1.R1011
Contig ID
                  LIB3076-020-Q1-K1-E10
5'-most EST
Method
                  BLASTX
                  g4262186
NCBI GI
                  543
BLAST score
E value
                  1.0e-55
                  182
Match length
% identity
                  (AC005508) Highly similar to cullin 3 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  262335
Contig ID
                  4048 1.R1011
                  uC-zmflb73077d02b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1170714
BLAST score
                  1648
E value
                  0.0e + 00
                  406
Match length
                  76
% identity
                  SHAGGY RELATED PROTEIN KINASE ASK-GAMMA
NCBI Description
                  >qi 541850 pir S41597 protein kinase ASK-gamma (EC
                  2.7.1.-) - Arabidopsis thaliana >gi 456509 emb CAA53180
                   (X75431) ASK-gamma (Arabidopsis shaggy-related kinase)
                   [Arabidopsis thaliana] >gi_2059329_emb_CAA73247_ (Y12710)
                  shaggy-like kinase gamma [Arabidopsis thaliana]
Seq. No.
                  262336
Contig ID
                  4051 1.R1011
                  uC-zmflB73042f02b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1703108
BLAST score
                  1919
                  0.0e + 00
E value
Match length
                  377
                  97
% identity
NCBI Description
                  ACTIN 2/7 > gi_2129525_pir_S71210 actin 2 - Arabidopsis
                  thaliana >gi_2129528_pir S68107 actin 7 - Arabidopsis
                   thaliana >gi 1049307 (U37281) actin-2 [Arabidopsis
                   thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                  thaliana]
Seq. No.
                  262337
Contig ID
                   4051 2.R1011
                  LIB143-018-Q1-E1-G4
5'-most EST
Method
                  BLASTX
                  g3420239
NCBI GI
BLAST score
                  768
                  6.0e-82
E value
Match length
                  145
```

Seq. No. 262338 Contig ID 4051 3.R1011

99

% identity

NCBI Description

(AF059484) actin [Gossypium hirsutum]



```
5'-most EST
                   uC-zmflmo17060f10b1
Method
                   BLASTX
NCBI GI
                   g231503
BLAST score
                   801
E value
                   2.0e-85
                   161
Match length
                   96
% identity
NCBI Description
                   ACTIN 97 >gi 100417 pir S20098 actin - potato
                   >qi 21544 emb CAA39280 (X55751) actin [Solanum tuberosum]
                   262339
Seq. No.
                   4051 4.R1011
Contig ID
5'-most EST
                   LIB3076-027-Q1-K1-G12
Method
                   BLASTX
                   q1703108
NCBI GI
BLAST score
                   797
E value
                   2.0e-85
                   151
Match length
% identity
                   99
                   ACTIN 2/7 >qi 2129525 pir S71210 actin 2 - Arabidopsis
NCBI Description
                   thaliana >gi 2129528 pir S68107 actin 7 - Arabidopsis
                   thaliana >gi 1049307 (U37281) actin-2 [Arabidopsis
                   thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                   thaliana]
                   262340
Seq. No.
                   4051 5.R1011
Contig ID
5'-most EST
                   uC-zmflmo17156c06b1
Method
                   BLASTX
NCBI GI
                   g1703108
BLAST score
                   602
E value
                   2.0e-62
Match length
                   140
% identity
                   83
                   ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis
NCBI Description
                   thaliana >gi 2129528 pir S68107 actin 7 - Arabidopsis
                   thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis
                   thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                   thaliana]
                   262341
Seq. No.
                   4051 6.R1011
Contig ID
5'-most EST
                   LIB3069-006-Q1-K1-H9
Method
                   BLASTX
                   g1703108
NCBI GI
BLAST score
                   366
                   8.0e-35
E value
                   73
Match length
                   96
% identity
                   ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis
NCBI Description
```

thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis

thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis

thaliana]

262342 Seq. No.

4051_7.R1011 Contig ID

% identity

60



```
5'-most EST
                  uC-zmflb73387h04a1
Method
                  BLASTX
NCBI GI
                  q1906607
BLAST score
                   267
                   3.0e-23
E value
Match length
                  52
% identity
                  94
NCBI Description (U90325) actin [Cyanophora paradoxa]
Seq. No.
                  262343
                  4051 8.R1011
Contig ID
5'-most EST
                  hvj7\overline{0}0619927.h1
Method
                  BLASTN
NCBI GI
                  g1498385
BLAST score
                  65
E value
                   4.0e-28
Match length
                  103
% identity
                  92
NCBI Description Zea mays actin (Maz87) gene, partial cds
Seq. No.
                   262344
                  4051 14.R1011
Contig ID
5'-most EST
                  tfd700575266.h1
Method
                  BLASTN
NCBI GI
                  g1296531
BLAST score
                  37
                  3.0e-11
E value
Match length
                  73
% identity
                  88
NCBI Description H.armigera actA3a gene
Seq. No.
                  262345
Contig ID
                  4051 15.R1011
5'-most EST
                  wty700171175.h1
                  262346
Seq. No.
Contig ID
                   4053 1.R1011
5'-most EST
                  uC-zmflb73294d11b1
Method
                  BLASTX
NCBI GI
                  g1621268
BLAST score
                  1193
E value
                  1.0e-131
Match length
                  346
% identity
                   66
NCBI Description (Z81012) unknown [Ricinus communis]
Seq. No.
                  262347
Contig ID
                  4053_3.R1011
                  uC-zmflmo17022c01b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3043426
BLAST score
                  296
E value
                   1.0e-26
Match length
                  92
```

36357

NCBI Description (AJ005345) hypothetical protein [Cicer arietinum]

Seq. No.

262353



```
262348
Seq. No.
Contig ID
                   4054 1.R1011
5'-most EST
                  LIB3076-020-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g2924509
BLAST score
                   453
                   3.0e-45
E value
                  120
Match length
                   70
% identity
                  (AL022023) subtilisin proteinase - like [Arabidopsis
NCBI Description
                  thaliana]
                   262349
Seq. No.
Contig ID
                   4056 1.R1011
                   nbm700469828.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3805851
BLAST score
                   673
                   2.0e-70
E value
                  290
Match length
                   50
% identity
NCBI Description
                  (AL031986) putative protein [Arabidopsis thaliana]
                  262350
Seq. No.
Contig ID
                   4058 1.R1011
5'-most EST
                   zuv700356228.h1
Method
                  BLASTX
NCBI GI
                  g4220479
BLAST score
                   944
E value
                  1.0e-102
Match length
                   321
% identity
                   65
NCBI Description
                  (AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.
                   262351
Contig ID
                   4061_1.R1011
5'-most EST
                   pwr700452137.h1
Method
                  BLASTX
NCBI GI
                   q4469009
BLAST score
                   613
E value
                   1.0e-63
Match length
                   179
% identity
                   69
NCBI Description
                  (AL035602) putative protein [Arabidopsis thaliana]
                   262352
Seq. No.
Contig ID
                   4062 1.R1011
                  LIB3137-045-Q1-K1-E4
5'-most EST
Method
                  BLASTX
NCBI GI
                   q3080427
BLAST score
                   756
E value
                   3.0e-80
Match length
                   327
% identity
                   66
                  (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
```



Contig ID 4062 2.R1011

5'-most EST LIB3136-022-Q1-K1-C3

Method BLASTX
NCBI GI g3080427
BLAST score 697
E value 2.0e-73
Match length 208
% identity 68

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 262354

Contig ID 4062_3.R1011 5'-most EST uC-zmflmo17d09b1

Method BLASTX
NCBI GI g3080427
BLAST score 407
E value 9.0e-40
Match length 116
% identity 72

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 262355

Contig ID 4064_1.R1011 5'-most EST nwy700444185.h1

Method BLASTX
NCBI GI g2660669
BLAST score 197
E value 2.0e-14
Match length 114
% identity 40

NCBI Description (AC002342) human Mi-2 autoantigen-like protein [Arabidopsis

thaliana]

Seq. No. 262356

Contig ID 4064_2.R1011 5'-most EST fwa700100213.h1

Method BLASTX
NCBI GI g2660669
BLAST score 153
E value 7.0e-10
Match length 92
% identity 43

NCBI Description (AC002342) human Mi-2 autoantigen-like protein [Arabidopsis

thaliana]

Seq. No. 262357

Contig ID 4064_3.R1011

5'-most EST uC-zmflmo17012d10a1

Seq. No. 262358 Contig ID 4064 4.R1011

5'-most EST uC-zmflmo17066b08a1

Seq. No. 262359 Contig ID 4067 1.R1011

5'-most EST LIB3076-019-Q1-K1-H12

Method BLASTX



```
NCBI GI
                  g2924777
                  445
BLAST score
E value
                  1.0e-43
Match length
                  264
% identity
                  40
                  (AC002334) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  262360
Seq. No.
                  4067 2.R1011
Contig ID
                  xdb700339338.h1
5'-most EST
                  262361
Seq. No.
Contig ID
                  4068 1.R1011
5'-most EST
                  LIB3076-018-Q1-K1-H7
                  BLASTX
Method
                  g2500980
NCBI GI
BLAST score
                   462
                   3.0e-46
E value
Match length
                  138
                   67
% identity
                  GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE) (GLURS)
NCBI Description
                   >gi 1076718 pir S51684 glutamate--tRNA ligase (EC
                   6.1.1.17) precursor - barley >gi 603849_emb_CAA58505_
                   (X83523) glutamate--tRNA ligase [Hordeum vulgare]
Seq. No.
                   262362
Contig ID
                   4071 1.R1011
                  LIB3076-019-Q1-K1-H9
5'-most EST
Method
                   BLASTX
                   q3935184
NCBI GI
                   279
BLAST score
                   1.0e-24
E value
Match length
                   141
                   43
% identity
                  (AC004557) F17L21.27 [Arabidopsis thaliana]
NCBI Description
                   262363
Seq. No.
                   4072 1.R1011
Contig ID
                   xsy700211931.hl
5'-most EST
                   BLASTX
Method
                   g558367
NCBI GI
BLAST score
                   1669
                   0.0e + 00
E value
                   342
Match length
                   94
% identity
                  (X81830) cytochrome P450 [Zea mays]
NCBI Description
Seq. No.
                   262364
Contig ID
                   4072_3.R1011
5'-most EST
                   LIB3076-020-Q1-K1-A1
Method
                   BLASTN
                   q1870202
NCBI GI
```

BLAST score 192
E value 1.0e-104
Match length 275
% identity 93



```
NCBI Description Z.mays cyp71c3 gene
                  262365
Seq. No.
                  4073 1.R1011
Contig ID
                  LIB3059-040-Q1-K1-A4
5'-most EST
                  BLASTX
Method
                  g2129774
NCBI GI
                  576
BLAST score
                  4.0e-59
E value
                  217
Match length
% identity
                  53
                  xyloglucan endotransglycosylase-related protein XTR4 -
NCBI Description
                  Arabidopsis thaliana (fragment) >gi_1244754 (U43486)
                  xyloglucan endotransglycosylase-related protein
                   [Arabidopsis thaliana]
                  262366
Seq. No.
                  4074 1.R1011
Contig ID
                  uC-zmflb73041f11b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q480450
BLAST score
                  2252
                  0.0e + 00
E value
                  512
Match length
                  86
% identity
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
NCBI Description
                   thaliana >gi 402552 emb_CAA49506_ (X69880) ketol-acid
                   reductoisomerase [Arabidopsis thaliana]
                   262367
Seq. No.
Contig ID
                   4074 2.R1011
                   rvt700550586.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                   q480450
                   368
BLAST score
E value
                   6.0e-35
                   139
Match length
                   66
% identity
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
NCBI Description
                   thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid
                   reductoisomerase [Arabidopsis thaliana]
                   262368
Seq. No.
                   4074 4.R1011
Contig ID
                   LIB3067-044-Q1-K1-G1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q480450
                   210
BLAST score
```

2.0e-16 E value 46 Match length 91 % identity

NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid

reductoisomerase [Arabidopsis thaliana]

262369 Seq. No. Contig ID 4075 1.R1011



LIB3076-001-Q1-K1-D7 5'-most EST

Method BLASTX NCBI GI g3228517 BLAST score 149 1.0e-09 E value 34 Match length 74

% identity (AF007788) ETTIN [Arabidopsis thaliana] NCBI Description

Seq. No. 262370

4077 1.R1011 Contig ID

5'-most EST LIB3076-020-Q1-K1-A6

Seq. No. 262371

4079 1.R1011 Contig ID

LIB3059-021-Q1-K1-B9 5'-most EST

262372 Seq. No.

Contig ID 4079 2.R1011

uC-zmflb73077g07b2 5'-most EST

262373 Seq. No.

4079 3.R1011 Contig ID

LIB3062-022-Q1-K1-C3 5'-most EST

262374 Seq. No.

4080 1.R1011 Contig ID

uC-zmflb73061d06b1 5'-most EST

Method BLASTX NCBI GI q1709129 BLAST score 1913 0.0e + 00E value Match length 407 86 % identity

GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-3 NCBI Description

>gi_481018_pir__S37642 protein kinase MSK-3 (EC 2.7.1.-) alfalfa >gi_313148_emb_CAA48472_ (X68409) protein kinase

[Medicago sativa]

Seq. No. 262375

4080 2.R1011 Contig ID

 $uC-z\overline{m}f1B73008h10b1$ 5'-most EST

BLASTX Method q1709129 NCBI GI BLAST score 254 7.0e-22 E value 72 Match length 69 % identity

GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-3 NCBI Description

>gi_481018_pir__S37642 protein kinase MSK-3 (EC 2.7.1.-) alfalfa >gi_313148_emb_CAA48472_ (X68409) protein kinase

[Medicago sativa]

262376 Seq. No. 4080 3.R1011 Contig ID tzu700206359.hl 5'-most EST



```
262377
Seq. No.
                  4080 4.R1011
Contig ID
                  LIB3069-057-Q1-K1-H2
5'-most EST
                  262378
Seq. No.
                  4080 6.R1011
Contig ID
                  LIB3136-054-Q1-K1-E3
5'-most EST
                  BLASTX
Method
                  q1170714
NCBI GI
                  353
BLAST score
                  5.0e-33
E value
                  130
Match length
                  51
% identity
                  SHAGGY RELATED PROTEIN KINASE ASK-GAMMA
NCBI Description
                  >gi 541850 pir__S41597 protein kinase ASK-gamma (EC
                  2.7.1.-) - Arabidopsis thaliana >gi_456509_emb_CAA53180_
                   (X75431) ASK-gamma (Arabidopsis shaggy-related kinase)
                   [Arabidopsis thaliana] >gi 2059329_emb_CAA73247_ (Y12710)
                   shaggy-like kinase gamma [Arabidopsis thaliana]
                  262379
Seq. No.
                  4082 1.R1011
Contig ID
                  LIB148-034-Q1-E1-F1
5'-most EST
                  BLASTX
Method
                  g4585982
NCBI GI
                   699
BLAST score
                   2.0e-73
E value
                   211
Match length
                   63
% identity
NCBI Description (AC005287) Unknown protein [Arabidopsis thaliana]
                   262380
Seq. No.
                   4085 1.R1011
Contig ID
                   uwc700155696.hl
5'-most EST
                   BLASTX
Method
                   g3024432
NCBI GI
                   1125
BLAST score
                   1.0e-123
E value
                   228
Match length
% identity
                   97
NCBI Description PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
                   COMPLEX ALPHA SUBUNIT) >gi_1930070 (U92540) proteasome
                   alpha subunit [Oryza sativa]
                   262381
Seq. No.
                   4085 2.R1011
Contia ID
                   nbm700475884.h1
5'-most EST
                   BLASTX
Method
                   g3024432
NCBI GI
BLAST score
                   571
```

BLAST score 571 E value 5.0e-59 Match length 116 % identity 98

NCBI Description PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE COMPLEX ALPHA SUBUNIT) >gi_1930070 (U92540) proteasome

alpha subunit [Oryza sativa]



262382 Seq. No. Contig ID 4085 3.R1011 yne700378554.hl 5'-most EST BLASTN Method NCBI GI q1930069 51 BLAST score 1.0e-19 E value Match length 131 85 % identity NCBI Description Oryza sativa proteasome alpha subunit mRNA, complete cds 262383 Seq. No. 4086 1.R1011 Contig ID uC-zmflmo17258f09a1 5'-most EST BLASTX Method g140185 NCBI GI BLAST score 295 5.0e-26 E value Match length 189 % identity PROBABLE GYP7 PROTEIN >gi 173243 (M17741) unidentified NCBI Description peptide [Yarrowia lipolytica] 262384 Seq. No. 4087 1.R1011 Contig ID LIB143-050-Q1-E1-B4 5'-most EST BLASTX Method q3201612 NCBI GI BLAST score 521 E value 2.0e-69 354 Match length 43 % identity NCBI Description (AC004669) putative 2A6 protein [Arabidopsis thaliana] 262385 Seq. No. 4087 2.R1011 Contig ID LIB143-046-Q1-E1-E2 5'-most EST Method BLASTX NCBI GI g3201632 BLAST score 235 1.0e-19 E value 130 Match length 37 % identity NCBI Description (AC004669) putative 2A6 protein [Arabidopsis thaliana] 262386 Seq. No. 4087 3.R1011 Contig ID LIB3088-003-Q1-K1-B3 5'-most EST 262387 Seq. No. 4087 4.R1011 Contig ID 5'-most EST hvj700622923.h1 BLASTN Method

Method BLASTN
NCBI GI g168406
BLAST score 36
E value 1.0e-10
Match length 68



% identity 88

NCBI Description Z.mays alcohol dehydrogenase (ADH-1 C-m allele) gene, complete cds

Seq. No. 262388

Contig ID 4088_1.R1011

5'-most EST uC-zmflmo17246c08b1

Method BLASTX
NCBI GI g2980770
BLAST score 1298
E value 1.0e-143
Match length 430
% identity 61

NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 262389

Contig ID 4088_2.R1011

5'-most EST uC-zmflmo17292d01b1

Method BLASTX
NCBI GI g2980770
BLAST score 469
E value 2.0e-59
Match length 265
% identity 49

NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No. 262390

Contig ID 4089_1.R1011

5'-most EST LIB3076-019-Q1-K1-G3

Method BLASTX
NCBI GI g2131448
BLAST score 280
E value 1.0e-24
Match length 203
% identity 33

NCBI Description hypothetical protein YDR365c - yeast (Saccharomyces

cerevisiae) >gi_849186 (U28373) Ydr365cp [Saccharomyces

cerevisiae]

Seq. No. 262391

Contig ID 4093 1.R1011

5'-most EST uC-zmroB73028b01b1

Seq. No. 262392

Contig ID 4093 2.R1011

5'-most EST uC-zmflMo17085a11b1

Seq. No. 262393

Contig ID 4093_3.R1011 5'-most EST mwy700438312.h1

Seq. No. 262394

Contig ID 4095_1.R1011

5'-most EST LIB3115-028-P1-K1-E7

Seq. No. 262395

Contig ID 4095 2.R1011



```
zuv700352691.h1
5'-most EST
                  262396
Seq. No.
                  4096 1.R1011
Contig ID
                  LIB3076-017-Q1-K1-D12
5'-most EST
                  BLASTX
Method
                  q1296955
NCBI GI
                  1545
BLAST score
                  1.0e-172
E value
                  334
Match length
                  83
% identity
NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]
                  262397
Seq. No.
                  4096 2.R1011
Contig ID
                  LIB143-013-Q1-E1-C7
5'-most EST
                  BLASTX
Method
                  q1658313
NCBI GI
                  1518
BLAST score
                  1.0e-169
E value
                   337
Match length
                   82
% identity
NCBI Description (Y08987) osr40g2 [Oryza sativa]
                   262398
Seq. No.
                   4096 3.R1011
Contig ID
                   LIB36-010-Q1-E1-H2
5'-most EST
                   BLASTX
Method
                   q1658315
NCBI GI
BLAST score
                   961
                   1.0e-104
E value
Match length
                   183
                   91
% identity
NCBI Description (Y08988) osr40g3 [Oryza sativa]
                   262399
Seq. No.
                   4096 4.R1011
Contig ID
                   LIB3079-002-Q1-K1-D3
5'-most EST
                   BLASTX
Method
                   g1658313
NCBI GI
                   700
BLAST score
                   1.0e-73
E value
                   158
Match length
                   40
 % identity
NCBI Description (Y08987) osr40g2 [Oryza sativa]
                   262400
Seq. No.
                   4096 5.R1011
 Contig ID
                   LIB3079-025-Q1-K1-B5
 5'-most EST
                   BLASTX
Method
                   g1296955
 NCBI GI
                   661
 BLAST score
                   5.0e-69
 E value
 Match length
                   160
```

NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]

37

% identity

Match length

% identity

90



262401 Seq. No. 4096 6.R1011 Contig ID LIB3150-094-P1-N1-G11 5'-most EST BLASTX Method q1658313 NCBI GI 692 BLAST score 9.0e-73 E value 133 Match length 44 % identity (Y08987) osr40g2 [Oryza sativa] NCBI Description 262402 Seq. No. 4096 7.R1011 Contig ID LIB3079-027-Q1-K1-E2 5'-most EST BLASTX Method g1658313 NCBI GI 595 BLAST score 9.0e-62 E value 130 Match length 45 % identity (Y08987) osr40g2 [Oryza sativa] NCBI Description 262403 Seq. No. 4096 8.R1011 Contig ID LIB3\overline{1}37-017-Q1-K1-E3 5'-most EST BLASTX Method g1296955 NCBI GI 630 BLAST score 1.0e-65 E value Match length 151 39 % identity (X95402) duplicated domain structure protein [Oryza sativa] NCBI Description 262404 Seq. No. 4096 9.R1011 Contig ID tfd700574034.h1 5'-most EST 262405 Seq. No. 4096 11.R1011 Contig ID 5'-most EST dyk700104222.hl BLASTX Method q1296955 NCBI GI BLAST score 332 4.0e-31 E value Match length 73 % identity 40 (X95402) duplicated domain structure protein [Oryza sativa] NCBI Description 262406 Seq. No. 4096 12.R1011 Contig ID xsy700213184.h1 5'-most EST BLASTN Method g1658314 NCBI GI 80 BLAST score 5.0e-37 E value 221

NCBI Description



```
NCBI Description O.sativa osr40g3 gene
                  262407
Seq. No.
                  4096 15.R1011
Contig ID
5'-most EST
                  nbm700471592.hl
                  BLASTX
Method
                  q1296955
NCBI GI
BLAST score
                  307
                  3.0e-28
E value
                  71
Match length
                  41
% identity
                  (X95402) duplicated domain structure protein [Oryza sativa]
NCBI Description
                  262408
Seq. No.
                   4096 17.R1011
Contig ID
                  nbm700470909.hl
5'-most EST
                   262409
Seq. No.
Contig ID
                   4098 1.R1011
                   uC-zmflb73194b04b2
5'-most EST
                   BLASTX
Method
                   q4467097
NCBI GI
                   464
BLAST score
                   3.0e-46
E value
                   138
Match length
% identity
                  (AL035538) heat shock protein 70 like protein [Arabidopsis
NCBI Description
                   thaliana]
                   262410
Seq. No.
                   4102 1.R1011
Contig ID
                   uC-zmflmo17185e06b1
5'-most EST
                   262411
Seq. No.
                   4102 2.R1011
Contig ID
                   LIB3066-006-Q1-K1-D5
5'-most EST
Seq. No.
                   262412
Contig ID
                   4102 3.R1011
                   LIB143-005-Q1-E1-H1
5'-most EST
                   262413
Seq. No.
                   4102 5.R1011
Contig ID
                   LIB3079-023-Q1-K1-A5
5'-most EST
Seq. No.
                   262414
                   4111 1.R1011
Contig ID
                   LIB3076-020-Q1-K1-D1
 5'-most EST
                   BLASTX
Method
                   g3763927
 NCBI GI
                   353
 BLAST score
                   4.0e-33
 E value
                   103
 Match length
                   66
 % identity
                   (AC004450) putative carboxyphosphoenolpyruvate mutase
```

[Arabidopsis thaliana]



262415 Seq. No. 4112 1.R1011 Contig ID xjt700092789.hl 5'-most EST

BLASTX Method q3478700 NCBI GI 216 BLAST score 5.0e-17 E value 108 Match length 43 % identity

(AF034387) AFT protein [Arabidopsis thaliana] NCBI Description

262416 Seq. No. Contig ID 4114 1.R1011

uC-zmflb73160b02b2 5'-most EST

BLASTX Method q1710401 NCBI GI BLAST score 1403 1.0e-156 E value Match length 326 83 % identity

RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN NCBI Description

(RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)

>gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase

R2 [Nicotiana tabacum]

262417 Seq. No.

4114 3.R1011 Contig ID yyf700351979.h1 5'-most EST

Method BLASTX NCBI GI q1710401 BLAST score 405 1.0e-39 E value 95 Match length 81 % identity

RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN NCBI Description

(RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)

>gi_1044912_emb_CAA63194_ (X92443) ribónucleotide reductase

R2 [Nicotiana tabacum]

Seq. No. 262418 4114 5.R1011 Contig ID ceu700428153.h1 5'-most EST

BLASTX Method q1710401 NCBI GI 305 BLAST score 9.0e-28 E value 71 Match length 80 % identity

NCBI Description RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN

(RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)

>gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase

R2 [Nicotiana tabacum]

262419 Seq. No. 4116 1.R1011 Contig ID LIB84-010-Q1-E1-G7 5'-most EST



```
262420
Seq. No.
                  4118 1.R1011
Contig ID
                  LIB3079-037-Q1-K1-G2
5'-most EST
                  BLASTX
Method
                  g3935157
NCBI GI
                  382
BLAST score
                  7.0e-37
E value
                  101
Match length
                  72
% identity
                  (AC005106) T25N20.21 [Arabidopsis thaliana]
NCBI Description
                  262421
Seq. No.
                   4121 1.R1011
Contig ID
                  yyf700347604.h1
5'-most EST
                   BLASTX
Method
                  q4309744
NCBI GI
BLAST score
                   481
                   5.0e-48
E value
Match length
                   288
% identity
                   35
                  (AC006439) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   262422
Seq. No.
                   4121 2.R1011
Contig ID
5'-most EST
                   fdz701159578.h1
                   262423
Seq. No.
                   4124 1.R1011
Contig ID
5'-most EST
                   LIB3088-043-Q1-K1-G1
                   262424
Seq. No.
                   4124 2.R1011
Contig ID
                   LIB3067-045-Q1-K1-H6
5'-most EST
                   BLASTX
Method
NCBI GI
                   g121950
BLAST score
                   214
                   7.0e-17
E value
Match length
                   62
                   71
% identity
NCBI Description HISTONE H1 >gi 22321_emb_CAA40362_ (X57077) H1 histone [Zea
                   mays]
                   262425
Seq. No.
                   4124 4.R1011
Contig ID
                   cat7\overline{0}0016369.r1
5'-most EST
                   262426
Seq. No.
                   4124 9.R1011
Contig ID
                   wty700167226.hl
5'-most EST
                   262427
Seq. No.
                   4125 1.R1011
Contig ID
                   pmx700086829.h1
 5'-most EST
```

36370

BLASTX

377

g4469012

7.0e-36

Method

NCBI GI

E value

BLAST score



Match length 170 % identity 51

NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No. 262428

Contig ID 4127_1.R1011

5'-most EST uC-zmflmo17130g06b1

Seq. No. 262429

Contig ID 4134_1.R1011

5'-most EST uC-zmflmo17132b08b1

Method BLASTN
NCBI GI g2832242
BLAST score 270
E value 1.0e-150
Match length 507
% identity 94

% identity 94 NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 262430

Contig ID 4134_2.R1011

5'-most EST LIB3076-018-Q1-K1-C1

Method BLASTN
NCBI GI g2832242
BLAST score 57
E value 4.0e-23
Match length 135
% identity 95

% identity 95 NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 262431

Contig ID 4134_3.R1011

5'-most EST uC-zmroteosinte045b04b2

Method BLASTN
NCBI GI g2832242
BLAST score 318
E value 1.0e-179
Match length 439
% identity 93

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 262432 Contig ID 4134 4.R1011

5'-most EST LIB3061-028-Q1-K1-D5

 Seq. No.
 262433

 Contig ID
 4134_5.R1011

 5'-most EST
 fdz701165560.h1

Seq. No. 262434

Contig ID 4136_1.R1011

5'-most EST LIB3180-046-P2-M2-A11

Method BLASTX
NCBI GI g419803
BLAST score 501
E value 2.0e-50
Match length 180



```
% identity
                   58
                  zein protein - maize >gi_168705 (M72708) zein protein [Zea
NCBI Description
                   262435
Seq. No.
                   4136 2.R1011
Contig ID
                   LIB3136-018-Q1-K1-G10
5'-most EST
Method
                   BLASTX
                   q2911058
NCBI GI
                   506
BLAST score
                   7.0e-51
E value
Match length
                   172
% identity
                   58
                  (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                   262436
Seq. No.
                   4136 3.R1011
Contig ID
                   ypc700798854.hl
5'-most EST
                   BLASTN
Method
                   g168661
NCBI GI
                   78
BLAST score
                   3.0e-36
E value
Match length
                   160
                   85
% identity
                  Maize 15 kDa zein mRNA, clone cZ15A3, complete cds
NCBI Description
                   262437
Seq. No.
                   4136 4.R1011
Contig ID
                   LIB3151-012-Q1-K1-B10
5'-most EST
                   BLASTN
Method
                   q168665
NCBI GI
                   236
BLAST score
                   1.0e-130
E value
                   236
Match length
                   100
% identity
NCBI Description Maize 16-kDa zein-2 mRNA, complete cds
                   262438
Seq. No.
                   4136 6.R1011
Contig ID
                   LIB3151-038-Q1-K1-C5
5'-most EST
                   BLASTN
Method
                   g168663
NCBI GI
                   136
BLAST score
                   3.0e-70
E value
                   287
Match length
                   95
% identity
NCBI Description Maize sulfur-rich zein protein of Mr 15,000, complete cds
                   262439
Seq. No.
                   4136 9.R1011
Contig ID
                   ypc7\overline{0}0806407.h1
 5'-most EST
                   BLASTN
Method
```

Method BLASTN

NCBI GI g168704

BLAST score 166

E value 3.0e-88

Match length 278

% identity 91



NCBI Description Zea mays zein protein gene, complete cds 262440 Seq. No. 4137 1.R1011 Contig ID LIB3076-018-Q1-K1-G4 5'-most EST 262441 Seq. No. 4147 1.R1011 Contig ID $ymt7\overline{0}0219214.h1$ 5'-most EST BLASTX Method g3914996 NCBI GI 1038 BLAST score

1.0e-113 E value 285 Match length 71 % identity

PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT) NCBI Description >gi_1665831_dbj_BAA13640_ (D88541) phosphoserine

aminotransferase [Arabidopsis thaliana]

>gi 2804260_dbj_BAA24441_ (AB010408) phosphoserine

aminotransferase [Arabidopsis thaliana]

>gi 3367581_emb_CAA20033_ (AL031135) phosphoserine

aminotransferase [Arabidopsis thaliana]

262442 Seq. No.

4158 1.R1011 Contig ID cyk700051078.f15'-most EST

BLASTX Method g2506277 NCBI GI 2323 BLAST score 0.0e + 00E value 551 Match length 85 % identity

RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60 NCBI Description

KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi_806808

(U21139) chaperonin precursor [Pisum sativum]

262443 Seq. No.

4158 2.R1011 Contig ID

uC-zmflb73048f03b1 5'-most EST

BLASTX Method q1938424 NCBI GI BLAST score 1192 1.0e-131 E value Match length 632 43 % identity

NCBI Description (U97002) similar to acyl-CoA dehydrogenases and epoxide

hydrolases [Caenorhabditis elegans]

Seq. No. 262444

4158_4.R1011 Contig ID

LIB3115-022-P1-K1-F7 5'-most EST

BLASTX Method q1877279 NCBI GI BLAST score 195 6.0e-15 E value 67 Match length 58 % identity



```
(Z92770) fadE2 [Mycobacterium tuberculosis]
NCBI Description
                  262445
Seq. No.
                   4158 5.R1011
Contig ID
                  uC-z\overline{m}flB73108h09b2
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1938424
                   183
BLAST score
                   2.0e-13
E value
Match length
                   44
                   68
% identity
                  (U97002) similar to acyl-CoA dehydrogenases and epoxide
NCBI Description
                   hydrolases [Caenorhabditis elegans]
                   262446
Seq. No.
                   4158 6.R1011
Contig ID
                   uer700581907.hl
5'-most EST
                   262447
Seq. No.
                   4162 1.R1011
Contig ID
                   ymt700223514.h1
5'-most EST
                   BLASTX
Method
                   g2245394
NCBI GI
BLAST score
                   454
                   1.0e-44
E value
Match length
                   383
                   35
% identity
NCBI Description (U89771) ARF1-binding protein [Arabidopsis thaliana]
Seq. No.
                   262448
                   4162 2.R1011
Contig ID
                   LIB3115-032-P1-K1-C2
5'-most EST
                   262449
Seq. No.
Contig ID
                   4164 1.R1011
                   rvt700549105.hl
5'-most EST
                   262450
Seq. No.
Contig ID
                   4166 1.R1011
                   LIB3076-018-Q1-K1-C6
5'-most EST
                   262451
Seq. No.
                   4168 1.R1011
Contig ID
                   LIB3076-018-Q1-K1-C9
5'-most EST
Method
                   BLASTX
                   g1800217
NCBI GI
                   634
BLAST score
                   2.0e-66
E value
                   125
Match length
                   95
% identity
NCBI Description (U56730) Phytochrome B [Sorghum bicolor]
```

262452 Seq. No. 4169 1.R1011 Contig ID $uC-z\overline{m}flb73187g09b1$ 5'-most EST BLASTX Method

g4176531 NCBI GI



```
BLAST score
                  437
                  6.0e-43
E value
                  211
Match length
% identity
                  (AL035263) weak similarity to chick phosphatidylcholine-ste
NCBI Description
                  rol acetyltransferase [Schizosaccharomyces pombe]
                  262453
Seq. No.
                  4171 1.R1011
Contig ID
                  LIB3150-093-P1-N1-G6
5'-most EST
                  BLASTX
Method
                  q2829688
NCBI GI
BLAST score
                  1522
                   1.0e-170
E value
                   325
Match length
% identity
                  CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE)
NCBI Description
                   (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                   >gi_1076798_pir__S52738 cysteine synthase (EC 4.2.99.8)
                   precursor - maize >gi_758353_emb_CAA59798_ (X85803)
                   cysteine synthase [Zea mays]
                   262454
Seq. No.
                   4171 2.R1011
Contig ID
                   cat700017617.rl
5'-most EST
                   BLASTX
Method
                   q3249105
NCBI GI
                   363
BLAST score
                   2.0e-34
E value
Match length
                   142
                   53
% identity
                  (AC003114) Contains similarity to protein phosphatase 2C
NCBI Description
                   (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]
                   262455
Seq. No.
                   4171 3.R1011
Contig ID
                   LIB3179-002-P1-K2-C6
5'-most EST
                   262456
Seq. No.
                   4171 5.R1011
Contig ID
                   LIB3067-049-Q1-K1-D10
 5'-most EST
Method
                   BLASTX
                   q3249105
NCBI GI
BLAST score
                   267
                   3.0e-23
E value
Match length
                   97
                   61
 % identity
                   (AC003114) Contains similarity to protein phosphatase 2C
 NCBI Description
                   (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]
                   262457
 Seq. No.
                   4171 6.R1011
 Contig ID
```

Contig ID 4171_6.R1011 5'-most EST cyk700047458.f1

Seq. No. 262458

Contig ID 4171_7.R1011 5'-most EST nbm700474349.h1



```
262459
Seq. No.
                  4171 10.R1011
Contig ID
                  pmx700091446.hl
5'-most EST
                  BLASTN
Method
                  g758352
NCBI GI
                  78
BLAST score
                  6.0e-36
E value
                  154
Match length
% identity
                  88
NCBI Description Z.mays mRNA for cysteine synthase
                  262460
Seq. No.
                  4171 11.R1011
Contig ID
                  ntr700073507.hl
5'-most EST
                  BLASTN
Method
                  g758352
NCBI GI
                   45
BLAST score
                  3.0e-16
E value
                  53
Match length
                   96
% identity
NCBI Description Z.mays mRNA for cysteine synthase
                   262461
Seq. No.
                   4171 16.R1011
Contig ID
                   uwc700152137.hl
5'-most EST
                   BLASTX
Method
                   g2829688
NCBI GI
                   265
BLAST score
                   2.0e-23
E value
                   54
Match length
% identity
                   96
                   CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE)
NCBI Description
                   (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                   >gi_1076798_pir__S52738 cysteine synthase (EC 4.2.99.8)
                   precursor - maize >gi 758353_emb_CAA59798_ (X85803)
                   cysteine synthase [Zea mays]
                   262462
Seq. No.
                   4181 1.R1011
Contig ID
                   LIB3151-049-P1-K1-B11
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2384758
                   2136
BLAST score
                   0.0e + 00
E value
Match length
                   429
                   93
 % identity
                  (AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza
NCBI Description
                   sativa]
 Seq. No.
                   262463
                   4181 2.R1011
 Contig ID
                   uC-zmflB73008d01b1
 5'-most EST
```

262464

4181 4.R1011

uC-zmflb73197e05a1

Seq. No.

Contig ID

5'-most EST



```
262465
Seq. No.
Contig ID
                  4194 1.R1011
                  uC-zmflmo17340d11b1
5'-most EST
                  262466
Seq. No.
Contig ID
                  4194 2.R1011
                  uC-zmflmo17266g02b1
5'-most EST
                  262467
Seq. No.
                  4194 4.R1011
Contig ID
5'-most EST
                  LIB3180-017-P2-M1-D8
                  262468
Seq. No.
Contig ID
                  4194 5.R1011
5'-most EST
                  uC-zmf1b73183d07b1
                  262469
Seq. No.
                  4194 8.R1011
Contig ID
                  rvt700549428.hl
5'-most EST
                  262470
Seq. No.
Contig ID
                  4196 1.R1011
                  LIB3076-017-Q1-K1-G9
5'-most EST
                  BLASTX
Method
                  q121950
NCBI GI
BLAST score
                  344
                  6.0e-32
E value
Match length
                  119
% identity
                  64
NCBI Description HISTONE H1 >gi_22321_emb_CAA40362_ (X57077) H1 histone [Zea
                  mays]
Seq. No.
                  262471
                  4196 2.R1011
Contig ID
                  LIB3067-005-Q1-K1-D7
5'-most EST
                  BLASTX
Method
NCBI GI
                  g121950
BLAST score
                  351
                  5.0e-33
E value
                  117
Match length
% identity
                  64
NCBI Description HISTONE H1 >gi_22321_emb_CAA40362_ (X57077) H1 histone [Zea
                  mays]
                   262472
Seq. No.
                   4196_3.R1011
Contig ID
5'-most EST
                  LIB3069-028-Q1-K1-F3
                  BLASTN
Method
NCBI GI
                  g22320
                   605
```

NCBI GI g22320
BLAST score 605
E value 0.0e+00
Match length 733
% identity 97

NCBI Description Maize H1 mRNA for H1 histone

Seq. No. 262473

.36377



```
4196 5.R1011
Contig ID
                  uC-zmflmo17078f06b1
5'-most EST
                  BLASTN
Method
                  g22320
NCBI GI
                  285
BLAST score
                  1.0e-159
E value
                  454
Match length
                  98
% identity
NCBI Description Maize H1 mRNA for H1 histone
                  262474
Seq. No.
                  4196 6.R1011
Contig ID
                  LIB143-068-Q1-E1-F9
5'-most EST
                  BLASTN
Method
                  g22320
NCBI GI
                  168
BLAST score
                  2.0e-89
E value
                  235
Match length
                  98
% identity
NCBI Description Maize H1 mRNA for H1 histone
                  262475
Seq. No.
                  4200 1.R1011
Contig ID
                  uC-zmroteosinte091h01b2
5'-most EST
                  BLASTX
Method
                  g478809
NCBI GI
                   641
BLAST score
                   4.0e-67
E value
                   167
Match length
                   66
% identity
                  protein kinase 6 (EC 2.7.1.-) - soybean >gi_170047 (M67449)
NCBI Description
                   protein kinase [Glycine max] >gi 444789_prf__1908223A
                   protein kinase [Glycine max]
Seq. No.
                   262476
                   4206 1.R1011
Contig ID
                   LIB3076-017-Q1-K1-B2
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4539452
BLAST score
                   668
                   3.0e-70
E value
Match length
                   177
                   68
% identity
NCBI Description (AL049500) putative phosphoribosylanthranilate transferase
                   [Arabidopsis thaliana]
                   262477
Seq. No.
                   4207 1.R1011
Contig ID
                   LIB3137-003-Q1-K1-G2
5'-most EST
Method
                   BLASTX
                   g3915826
NCBI GI
```

Method BLASTX
NCBI GI g3915826
BLAST score 1217
E value 1.0e-134
Match length 294

% identity 80

NCBI Description 60S RIBOSOMAL PROTEIN L5



Seq. No. 262478

Contig ID 4207_2.R1011 5'-most EST vqh700053221.r1

Method BLASTX
NCBI GI g399942
BLAST score 2399
E value 0.0e+00
Match length 667
% identity 82

NCBI Description CHLOROPLAST STROMA 70 KD HEAT SHOCK-RELATED PROTEIN

PRECURSOR >gi_421881_pir__ S32818 heat shock protein, 70K, chloroplast - garden pea >gi_169023 (L03299) 70 kDa heat shock protein [Pisum sativum] >gi_871515_emb_CAA49147_ (X69213) Psst70 (stress 70 protein) [Pisum sativum]

Seq. No. 262479

Contig ID 4207_3.R1011

5'-most EST uC-zmflmo17071c07b1

Method BLASTX
NCBI GI g115771
BLAST score 1318
E value 1.0e-146
Match length 246
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll

a/b-binding protein precursor - maize

>qi 22224 emb CAA32900 (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 262480

Contig ID 4207_4.R1011 5'-most EST wty700170525.h1

Method BLASTX
NCBI GI g3915826
BLAST score 1205
E value 1.0e-133
Match length 294
% identity 78

NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 262481

Contig ID 4207_5.R1011 5'-most EST xsy700214116.h1

Method BLASTX
NCBI GI g543938
BLAST score 1285
E value 1.0e-142
Match length 264
% identity 91

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB48) (LHCP) >gi_82681_pir__S22497 chlorophyll a/b-binding protein precursor (cab-48) - maize

>gi_22228_emb_CAA44888_ (X63205) chlorophyll a /b binding

protein [Zea mays]

Seq. No. 262482



4207 6.R1011 Contig ID xjt700094086.hl 5'-most EST

BLASTX Method g3126854 NCBI GI 1284 BLAST score 1.0e-142 E value 259 Match length 95

% identity (AF061577) chlorophyll a/b binding protein [Oryza sativa] NCBI Description

262483 Seq. No.

4207 7.R1011 Contig ID

LIB84-023-Q1-E1-B7 5'-most EST

BLASTX Method g115793 NCBI GI BLAST score 1298 1.0e-143 E value 269 Match length 93 % identity

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR NCBI Description

(CAB) >gi_72749_pir__CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881_

(X63197) type III LHCII CAB precursor protein [Hordeum

vulgare]

Seq. No. 262484

4207 8.R1011 Contig ID xsy700209408.hl 5'-most EST

BLASTX Method q693920 NCBI GI 774 BLAST score 2.0e-82 E value 148 Match length 97 % identity

(U21113) chlorophyll a/b binding protein [Solanum NCBI Description

tuberosum]

262485 Seq. No.

4207 9.R1011 Contig ID pmx700087379.h1 5'-most EST

BLASTX Method q3036951 NCBI GI BLAST score 1026 1.0e-112 E value 197 Match length 97 % identity

(AB012639) light harvesting chlorophyll a/b-binding protein NCBI Description

[Nicotiana sylvestris]

262486 Seq. No.

4207 10.R1011 Contig ID xsy700217151.h1 5'-most EST

BLASTX Method NCBI GI q543938 BLAST score 611 1.0e-63 E value 129 Match length



89 % identity CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description (CAB48) (LHCP) >gi_82681_pir__S22497 chlorophyll a/b-binding protein precursor (cab-48) - maize >gi 22228 emb_CAA44888_ (X63205) chlorophyll a /b binding protein [Zea mays] 262487 Seq. No. 4207 11.R1011 Contig ID uC-zmflb73291g02b1 5'-most EST Method BLASTX NCBI GI g1488647 BLAST score 662 3.0e-69 E value Match length 181 % identity 74 NCBI Description (X99937) RNA helicase [Spinacia oleracea] 262488 Seq. No. Contig ID 4207 12.R1011 5'-most EST $LIB3\overline{6}-019-Q1-E1-D7$ Method BLASTX NCBI GI g3293555 519 BLAST score 1.0e-52 E value Match length 100 97 % identity (AF072931) chlorophyll a/b binding protein [Medicago NCBI Description sativa] 262489 Seq. No. 4207 17.R1011 Contig ID uC-zmflmo17058f10b1 5'-most EST BLASTX Method g226263 NCBI GI BLAST score 346 2.0e-32 E value 67 Match length 97 % identity NCBI Description chlorophyll a/b binding protein [Glycine max] 262490 Seq. No. 4207 19.R1011 Contig ID 5'-most EST xsy700207423.h1 BLASTX Method q542157 NCBI GI BLAST score 407 E value 8.0e-40 103 Match length % identity NCBI Description ribosomal 5S RNA-binding protein - Rice

Seq. No. 262491

Contig ID 4207_20.R1011 5'-most EST xsy700213803.h1

Method BLASTN NCBI GI q452340



BLAST score 235 1.0e-129 E value 247 Match length 99 % identity NCBI Description Z.mays mRNA for type II light-harvesting chlorophyll a/b-binding protein 262492 Seq. No. Contig ID 4207 21.R1011 5'-most EST LIB3078-012-Q1-K1-G9 Method BLASTX NCBI GI q3036951 BLAST score 653 2.0e-68 E value Match length 125 % identity 98 NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris] 262493 Seq. No. 4207 23.R1011 Contig ID 5'-most EST LIB36-021-Q1-E1-B2 BLASTX Method NCBI GI q115771 BLAST score 369 E value 3.0e-35 Match length 70 100 % identity NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll a/b-binding protein precursor - maize >qi 22224 emb CAA32900 (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays] 262494 4207_30.R1011 LIB83-002-Q1-E1-C9 BLASTX

Seq. No. Contig ID 5'-most EST Method g3036951 NCBI GI BLAST score 570

E value 1.0e-58 Match length 114 % identity 94

NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

Seq. No. 262495 4207 38.R1011 Contig ID

5'-most EST LIB3158-011-Q1-K1-G10

Method BLASTN NCBI GI q452340 BLAST score 157 4.0e-83 E value 177 Match length 97 % identity

NCBI Description Z.mays mRNA for type II light-harvesting chlorophyll

a/b-binding protein



Seq. No. 262496 4207 44.R1011 Contig ID 5'-most EST wty700171254.hl 262497 Seq. No. 4207 48.R1011 Contig ID xjt700096005.h15'-most EST BLASTN Method q22223 NCBI GI 75 BLAST score 2.0e-34 E value Match length 155 % identity 96 NCBI Description Maize cab-1 gene for chlorophyll a/b-binding protein Seq. No. 262498 Contig ID 4210 1.R1011 5'-most EST uC-zmflmo17241f12b1 Method BLASTX a1145408 NCBI GI 153 BLAST score 3.0e-09 E value 121 Match length 35 % identity (U38783) brefeldin A resistance protein NCBI Description [Schizosaccharomyces pombe] >gi_1589567_prf__2211346A brefeldin A resistance protein [Schizosaccharomyces pombe] Seq. No. 262499 4210 2.R1011 Contig ID uC-zmflMo17008a06b1 5'-most EST 262500 Seq. No. 4210 3.R1011 Contig ID uC-zmflmo17164e01b1 5'-most EST 262501 Seq. No. Contig ID 4210 4.R1011 uC-zmflmo17035b05b1 5'-most EST 262502 Seq. No. 4215 1.R1011 Contig ID xmt700261145.h1 5'-most EST BLASTX Method g3452387 NCBI GI 217 BLAST score 5.0e-17 E value 105 Match length 18 % identity (AF083253) cysteine protease inhibitor [Lycopersicon NCBI Description esculentum]

 Seq. No.
 262503

 Contig ID
 4215_2.R1011

 5'-most EST
 LIB3059-047-Q1-K1-A2

 Method
 BLASTX



g3452387 NCBI GI 195 BLAST score 2.0e-14 E value 103 Match length 17 % identity (AF083253) cysteine protease inhibitor [Lycopersicon NCBI Description esculentum] 262504 Seq. No. 4215 3.R1011 Contig ID LIB3078-015-Q1-K1-E7 5'-most EST BLASTX Method g3452387 NCBI GI 213 BLAST score 9.0e-17 E value 96 Match length 20 % identity (AF083253) cysteine protease inhibitor [Lycopersicon NCBI Description esculentum] 262505 Seq. No. 4216 1.R1011 Contig ID LIB3076-029-Q1-K1-E12 5'-most EST BLASTX Method q1345838 NCBI GI 451 BLAST score 7.0e-45 E value 89 Match length 99 % identity PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE) NCBI Description >gi 2130143 pir S65060 phytoene desaturase precursor maize >gi 1051180 (U37285) phytoene desaturase [Zea mays] 262506 Seq. No. Contig ID 4217 1.R1011 xjt700094874.h1 5'-most EST BLASTX Method NCBI GI g2583129 BLAST score 1717 E value 0.0e + 00Match length 392 % identity (AC002387) putative methionine aminopeptidase [Arabidopsis NCBI Description thaliana] Seq. No. 262507 Contig ID 4217 2.R1011 LIB3088-050-Q1-K1-C1 5'-most EST Method BLASTX

Method BLASTX
NCBI GI g2583129
BLAST score 170
E value 6.0e-12
Match length 40
% identity 85

NCBI Description (AC002387) putative methionine aminopeptidase [Arabidopsis

thaliana]



262508 Seq. No. 4217 3.R1011 Contig ID ntr700075544.h1 5'-most EST

BLASTX Method NCBI GI g2583129 234 BLAST score 2.0e-19 E value 49 Match length % identity 86

(AC002387) putative methionine aminopeptidase [Arabidopsis NCBI Description

thaliana]

262509 Seq. No.

4219 2.R1011 Contig ID

uC-zmflB73112b12b2 5'-most EST

262510 Seq. No.

4221 1.R1011 Contig ID $xjt7\overline{0}0095780.h1$ 5'-most EST

BLASTX Method NCBI GI g2829870 BLAST score 343 7.0e-32 E value 317 Match length 35 % identity

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

262511 Seq. No.

4224 1.R1011 Contig ID

5'-most EST LIB3076-017-Q1-K1-A7

262512 Seq. No. Contig ID

4227 1.R1011 kyv700142588.h1 5'-most EST

262513 Seq. No. 4227 2.R1011 Contig ID ceu700426694.hl 5'-most EST

Seq. No. 262514 4232 1.R1011 Contig ID

5'-most EST LIB3079-025-Q1-K1-C8

Method BLASTX q3056589 NCBI GI 476 BLAST score 2.0e-47 E value 248 Match length % identity

NCBI Description (AC004255) T1F9.10 [Arabidopsis thaliana]

Seq. No. 262515 4232 2.R1011 Contig ID

5'-most EST LIB3076-014-Q1-K1-F3

Method BLASTX NCBI GI q3056589 BLAST score 161 6.0e-11 E value



```
43
Match length
% identity
                  65
NCBI Description (AC004255) T1F9.10 [Arabidopsis thaliana]
                  262516
Seq. No.
                  4233 1.R1011
Contig ID
                  LIB3076-015-Q1-K1-F4
5'-most EST
                  BLASTX
Method
                  g1001312
NCBI GI
BLAST score
                  445
                  4.0e-56
E value
Match length
                  329
                   44
% identity
NCBI Description (D64006) hypothetical protein [Synechocystis sp.]
                   262517
Seq. No.
                   4238 1.R1011
Contig ID
                  rvt700552758.h1
5'-most EST
                   262518
Seq. No.
                   4238 2.R1011
Contig ID
                   LIB83-004-Q1-E1-A12
5'-most EST
                   262519
Seq. No.
                   4240 1.R1011
Contig ID
                   LIB3076-015-Q1-K1-C7
5'-most EST
Seq. No.
                   262520
                   4241 1.R1011
Contig ID
                   LIB3076-015-Q1-K1-D12
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4433618
                   209
BLAST score
                   3.0e-16
E value
                   146
Match length
                   38
% identity
                  (AF107585) putative myosin heavy chain [Dendrobium grex
NCBI Description
                   Madame Thong-IN]
                   262521
Seq. No.
                   4242 1.R1011
Contig ID
                   uC-zmflb73020f07b1
 5'-most EST
                   BLASTX
Method
                   g1666173
NCBI GI
                   510
BLAST score
                   2.0e-51
E value
                   152
Match length
 % identity
NCBI Description (Y09106) transcription factor [Nicotiana plumbaginifolia]
 Seq. No.
                   262522
                   4242 2.R1011
 Contig ID
                   uC-zmroteosinte057b04b1
 5'-most EST
                   BLASTX
 Method
                   q2982299
 NCBI GI
                   395
 BLAST score
```

36386

5.0e-38

E value



```
116
Match length
                  70
% identity
                  (AF051234) transcription factor BTF3 homolog [Picea
NCBI Description
                  mariana]
                  262523
Seq. No.
                  4242 3.R1011
Contig ID
                  xsy700217819.hl
5'-most EST
                  BLASTX
Method
                  g1666173
NCBI GI
BLAST score
                   448
                   2.0e-44
E value
                   149
Match length
                   64
% identity
NCBI Description (Y09106) transcription factor [Nicotiana plumbaginifolia]
                   262524
Seq. No.
                   4244 1.R1011
Contig ID
                   uC-zmflmo17204a01b1
5'-most EST
                   BLASTX
Method
                   g4572679
NCBI GI
BLAST score
                   270
                   4.0e-23
E value
                   100
Match length
                   54
% identity
                  (AC006954) RSZp22 splicing factor; contains RNA recognition
NCBI Description
                   motif [Arabidopsis thaliana]
                   262525
Seq. No.
                   4244 2.R1011
Contig ID
                   tzu700203527.h1
5'-most EST
Method
                   BLASTX
                   g2582643
NCBI GI
                   275
BLAST score
                   1.0e-23
E value
                   100
Match length
                   56
% identity
NCBI Description (AJ002377) RSZp21 protein [Arabidopsis thaliana]
                   262526
Seq. No.
                   4244 7.R1011
Contig ID
                   uC-zmf1b73237f08b2
5'-most EST
                   262527
 Seq. No.
                   4246 1.R1011
 Contig ID
                   afb700381508.h1
 5'-most EST
                   BLASTX
Method
                   q2624328
NCBI GI
                   454
 BLAST score
                   7.0e-45
 E value
                   121
 Match length
 % identity
```

Seq. No. 262528 Contig ID 4246_2.R1011

5'-most EST LIB3076-030-Q1-K1-D1

NCBI Description (AJ002894) OsGRP2 [Oryza sativa]

BLAST score

E value Match length 231 1.0e-24

201



```
BLASTX
Method
                   g1167955
NCBI GI
                   578
BLAST score
                   4.0e-59
E value
                   301
Match length
                   44
% identity
                   (U43497) putative 32.7 kDa jasmonate-induced protein
NCBI Description
                   [Hordeum vulgare] >gi 2465428 (AF021257) 32 kDa protein
                   [Hordeum vulgare]
                   262529
Seq. No.
                   4246 3.R1011
Contig ID
                   LIB3076-014-Q1-K1-A12
5'-most EST
                   BLASTX
Method
                   g1167955
NCBI GI
                   459
BLAST score
                   3.0e-45
E value
                   302
Match length
                   38
% identity
                   (U43497) putative 32.7 kDa jasmonate-induced protein
NCBI Description
                   [Hordeum vulgare] >gi 2465428 (AF021257) 32 kDa protein
                   [Hordeum vulgare]
                   262530
Seq. No.
                   4246 4.R1011
Contig ID
                   LIB3061-040-Q1-K1-A1
5'-most EST
                   BLASTX
Method
                   g1167955
NCBI GI
                   450
BLAST score
                   3.0e-44
E value
                   318
Match length
                   37
% identity
                   (U43497) putative 32.7 kDa jasmonate-induced protein
NCBI Description
                   [Hordeum vulgare] >gi 2465428 (AF021257) 32 kDa protein
                   [Hordeum vulgare]
Seq. No.
                   262531
                   4246 5.R1011
Contig ID
                   nbm7\overline{0}0478059.h1
5'-most EST
                   BLASTX
Method
                   g1167953
NCBI GI
BLAST score
                   489
                   8.0e-49
E value
                   297
Match length
                   41
% identity
                   (U43496) putative 32.6 kDa jasmonate-induced protein
NCBI Description
                    [Hordeum vulgare] >gi 2465426 (AF021256) 32 kDa protein
                    [Hordeum vulgare]
                   262532
Seq. No.
Contig ID
                   4246 6.R1011
                   xmt7\overline{0}0258403.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1167955
```



```
% identity
                  (U43497) putative 32.7 kDa jasmonate-induced protein
NCBI Description
                  [Hordeum vulgare] >gi_2465428 (AF021257) 32 kDa protein
                  [Hordeum vulgare]
                  262533
Seq. No.
                  4246_7.R1011
Contig ID
                  uC-zmf1b73077e06b2
5'-most EST
                  BLASTX
Method
                  q2624328
NCBI GI
                  231
BLAST score
                  6.0e-19
E value
                  68
Match length
                  65
% identity
                  (AJ002894) OsGRP2 [Oryza sativa]
NCBI Description
                  262534
Seq. No.
                  4246 8.R1011
Contig ID
                  LIB3079-017-Q1-K1-H10
5'-most EST
                  BLASTN
Method
NCBI GI
                  g3821780
                   37
BLAST score
                   4.0e-11
E value
                   37
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   262535
Seq. No.
                   4246 12.R1011
Contig ID
                   uC-zmflmo17206d06a1
5'-most EST
Seq. No.
                   262536
                   4246 14.R1011
Contig ID
                   LIB3279-059-P1-K1-E12
5'-most EST
                   262537
Seq. No.
                   4246 21.R1011
Contig ID
                   LIB3059-018-Q1-K1-E5
5'-most EST
                   262538
Seq. No.
                   4247 1.R1011
Contig ID
                   LIB3076-015-Q1-K1-E11
 5'-most EST
                   BLASTX
Method
                   g3337350
 NCBI GI
                   737
 BLAST score
                   3.0e-78
 E value
                   182
 Match length
                   77
 % identity
 NCBI Description (AC004481) putative permease [Arabidopsis thaliana]
 Seq. No.
                   262539
                   4248 1.R1011
 Contig ID
                   uC-zmflmo17301e10b1
 5'-most EST
```

Seq. No. 262540 Contig ID 4248_2.R1011

5'-most EST uC-zmflmo17339a11b1

```
262541
Seq. No.
                  4250 1.R1011
Contig ID
                  dyk700102536.h1
5'-most EST
                  BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                  36
                  3.0e-10
E value
                  36
Match length
                  100
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                  262542
Seq. No.
                  4250 2.R1011
Contig ID
                  wyr700235866.hl
5'-most EST
                  262543
Seq. No.
                   4250 3.R1011
Contig ID
                  xjt700095982.h1
5'-most EST
Seq. No.
                  262544
                   4250 6.R1011
Contig ID
                  uC-zmflb73272f10b1
5'-most EST
                   262545
Seq. No.
                   4250 9.R1011
Contig ID
                  LIB3136-006-Q1-K1-C5
5'-most EST
                   262546
Seq. No.
                   4254 1.R1011
Contig ID
5'-most EST
                   LIB3067-019-Q1-K1-D7
                   BLASTX
Method
                   q4582445
NCBI GI
                   273
BLAST score
                   7.0e-24
E value
                   64
Match length
                   70
% identity
                  (AC007071) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4589952 gb AAD26470.1 AC007169 2 (AC007169) unknown
                   protein [Arabidopsis thaliana]
                   262547
Seq. No.
                   4255 1.R1011
Contig ID
                   uC-zmflm017082c07b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q320622
BLAST score
                   738
                   2.0e-78
E value
```

Match length 163 % identity

probable protein kinase - maize (fragment) >gi_168618 NCBI Description

(M62985) protein kinase [Zea mays]

262548 Seq. No. 4260 1.R1011 Contig ID ymt700220959.hl 5'-most EST BLASTX Method



```
g1845197
NCBI GI
                   372
BLAST score
                   3.0e - 35
E value
                   102
Match length
                   75
% identity
NCBI Description (Y08298) HMGc2 [Zea mays]
                   262549
Seq. No.
                   4260 2.R1011
Contig ID
                   LIB3180-042-P2-M2-C7
5'-most EST
Seq. No.
                   262550
                   4260 3.R1011
Contig ID
                   LIB3067-038-Q1-K1-H2
5'-most EST
                   262551
Seq. No.
                   4263 1.R1011
Contig ID
                   LIB3076-015-Q1-K1-A10
5'-most EST
                   BLASTX
Method
                   q4586054
NCBI GI
                   157
BLAST score
                   2.0e-10
E value
Match length
                   78
                   44
% identity
NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]
                   262552
Seq. No.
                   4264 1.R1011
Contig ID
                   LIB3076-015-Q1-K1-A12
5'-most EST
                   262553
Seq. No.
                   4266 1.R1011
Contig ID
                   uC-z\overline{m}f1b73073f11b3
5'-most EST
                   262554
Seq. No.
                   4266 2.R1011
Contig ID
                   uC-z\overline{m}f1b73378f02a2
5'-most EST
                   262555
Seq. No.
                   4268 1.R1011
Contig ID
                   clt700045104.fl
5'-most EST
                   BLASTX
Method
                   g3122367
NCBI GI
                   200
BLAST score
                   3.0e-17
E value
                   180
Match length
                   33
 % identity
NCBI Description LIGATIN >gi_1377880 (U58337) ligatin [Mus musculus]
                    262556
 Seq. No.
                    4269 1.R1011
 Contig ID
```

 Seq. No.
 262556

 Contig ID
 4269_1.R1011

 5'-most EST
 uC-zmflb73029e07b1

 Method
 BLASTX

 NCBI GI
 g3264598

 BLAST score
 689

 E value
 2.0e-72

Match length 176



% identity 73 NCBI Description (AF057184) trypsin inhibitor [Zea mays] 262557 Seq. No. 4269 2.R1011 Contig ID 5'-most EST uC-zmflmo17163f08b1 BLASTX Method NCBI GI q3264598 BLAST score 893 E value 2.0e-96 Match length 174 % identity 87 NCBI Description (AF057184) trypsin inhibitor [Zea mays] 262558 Seq. No. Contig ID 4269 4.R1011 5'-most EST uC-zmflmo17264g11a1 BLASTN Method NCBI GI q3264597 BLAST score 248 1.0e-137 E value 289 Match length 97 % identity NCBI Description Zea mays trypsin inhibitor mRNA, complete cds 262559 Seq. No. 4273 1.R1011 Contig ID 5'-most EST $hvj7\overline{0}0621812.h1$ Method BLASTX NCBI GI q1617270 BLAST score 623 2.0e-97 E value Match length 294 % identity 60 NCBI Description (X94624) acyl-CoA synthetase [Brassica napus] Seq. No. 262560 Contig ID 4274 1.R1011 5'-most EST LIB3150-045-Q1-N1-D1 262561 Seq. No. Contig ID 4276 1.R1011 5'-most EST uC-zmflb73053c11b2Method BLASTX NCBI GI q3273200 BLAST score 490 E value 4.0e-49 Match length 215 52 % identity (AB010917) responce reactor3 [Arabidopsis thaliana] NCBI Description >gi 3894192 (AC005662) response regulator 3 [Arabidopsis thaliana]

Seq. No. 262562 Contig ID 4276_2.R1011 5'-most EST uC-zmflb73028b09b1



```
262563
Seq. No.
                  4276 3.R1011
Contig ID
                  LIB84-027-Q1-E1-G12
5'-most EST
                  BLASTX
Method
                  g3273200
NCBI GI
                  350
BLAST score
                  5.0e-33
E value
                  101
Match length
                  66
% identity
                  (AB010917) responce reactor3 [Arabidopsis thaliana]
NCBI Description
                  >gi 3894192 (AC005662) response regulator 3 [Arabidopsis
                   thaliana]
                   262564
Seq. No.
                   4276_4.R1011
Contig ID
                  ntr700077262.h1
5'-most EST
                  BLASTX
Method
                   g3273202
NCBI GI
                   188
BLAST score
                   4.0e-14
E value
                   56
Match length
                   77
% identity
                  (AB010918) responce reactor4 [Arabidopsis thaliana]
NCBI Description
                   262565
Seq. No.
                   4277 1.R1011
Contig ID
                   wty700172735.h1
5'-most EST
Method
                   BLASTX
                   g2431771
NCBI GI
                   297
BLAST score
                   1.0e-26
E value
Match length
                   113
                   61
 % identity
                  (U62753) acidic ribosomal protein P2b [Zea mays]
NCBI Description
                   262566
Seq. No.
                   4279 2.R1011
 Contig ID
                   LIB3076-014-Q1-K1-B1
5'-most EST
                   262567
 Seq. No.
                   4280 1.R1011
 Contig ID
                   uC-zmrob73078e01b1
 5'-most EST
                   262568
 Seq. No.
                   4281 1.R1011
 Contig ID
                   LIB3159-004-Q1-K1-D3
 5'-most EST
                   BLASTX
 Method
                   q4567232
 NCBI GI
                    305
 BLAST score
                   1.0e-27
 E value
                   72
 Match length
 % identity
                   (AC007119) putative 40S ribosomal protein S25 [Arabidopsis
 NCBI Description
                   thaliana]
```

36393

262569

4281 2.R1011

Seq. No.

Contig ID



5'-most EST LIB3078-040-Q1-K1-E9

Method BLASTX
NCBI GI 94567232
BLAST score 302
E value 3.0e-27
Match length 72
% identity 82

NCBI Description (AC007119) putative 40S ribosomal protein S25 [Arabidopsis

thaliana]

Seq. No. 262570

Contig ID 4281_3.R1011

5'-most EST LIB3069-010-Q1-K1-G5

Method BLASTX
NCBI GI g1173234
BLAST score 167
E value 2.0e-22
Match length 78
% identity 77

NCBI Description 40S RIBOSOMAL PROTEIN S25 >gi_481909_pir_S40089 ribosomal

protein S25 - tomato >gi_435679_emb_CAA54132_ (X76714)

ribosomal protein S25 [Lycopersicon esculentum] >gi 1584836 prf 2123431A ribosomal protein S25

[Lycopersicon esculentum]

Seq. No. 262571

Contig ID 4286_1.R1011

5'-most EST uC-zmflb73219a02b2

Seq. No. 262572

Contig ID 4288_1.R1011 5'-most EST uer700582682.h1

Seq. No. 262573

Contig ID 4288 2.R1011

5'-most EST LIB3076-013-Q1-K1-G10

Seq. No. 262574

Contig ID 4289_1.R1011

5'-most EST uC-zmflb73148h07b1

Method BLASTX
NCBI GI g3738287
BLAST score 390
E value 3.0e-37
Match length 239
% identity 39

NCBI Description (AC005309) glutathione s-transferase, GST6 [Arabidopsis

thaliana]

Seq. No. 262575 Contig ID 4290 1.R1011

5'-most EST uC-zmflb73303d03a2

Seq. No. 262576 Contig ID 4291 1.R1011

5'-most EST LIB3076-013-Q1-K1-H5



Seq. No. 262577

Contig ID 4295_1.R1011

5'-most EST uC-zmflmo17156a05a1

Method BLASTX
NCBI GI 93482933
BLAST score 151
E value 1.0e-09
Match length 76
% identity 49

NCBI Description (AC003970) Similar to cdc2 protein kinases [Arabidopsis

thaliana]

Seq. No. 262578

Contig ID 4296 1.R1011

5'-most EST uC-zmflb73154b10b2

Seq. No. 262579

Contig ID 4299_1.R1011 5'-most EST xsy700211004.h1

Method BLASTX
NCBI GI g549010
BLAST score 1974
E value 0.0e+00
Match length 413
% identity 92

NCBI Description EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1)

(OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG) >gi 322554 pir S31328 omnipotent suppressor protein SUP1

homolog (clone G18) - Arabidopsis thaliana

>gi_16514_emb_CAA49172_ (X69375) similar to yeast

omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi_1402882_emb_CAA66813_ (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis thaliana] > i 1405240 emb_CAA66118_ (X97486) epsilon

thaliana] >gi 1495249 emb CAA66118_ (X97486) eRF1-3

[Arabidopsis thaliana]

Seq. No.262580Contig ID4299_2.R10115'-most ESTxsy700213291.h1

Method BLASTX
NCBI GI g1155261
BLAST score 249
E value 2.0e-21
Match length 57
% identity 82

NCBI Description (U40217) eukaryotic release factor 1 homolog [Arabidopsis

thaliana]

Seq. No. 262581

Contig ID 4300_1.R1011 5'-most EST gwl700614446.h1

Method BLASTX

NCBI GI g2842494

BLAST score 1062

E value 1.0e-116

Match length 254

% identity 84



(AL021749) prohibitin-like protein [Arabidopsis thaliana] NCBI Description >gi 4097688 (U66591) prohibitin 1 [Arabidopsis thaliana] >gi_4097694 (U66594) prohibitin 1 [Arabidopsis thaliana] 262582 Seq. No. 4301 1.R1011 Contig ID

262583 Seq. No. 4303 1.R1011

Contig ID LIB3076-034-Q1-K1-D4 5'-most EST

262584 Seq. No.

5'-most EST

4305 1.R1011 Contig ID

5'-most EST LIB3076-013-Q1-K1-D10

262585 Seq. No.

4306 1.R1011 Contig ID

5'-most EST LIB3076-012-Q1-K1-H10

Method BLASTX q3063455 NCBI GI 239 BLAST score 4.0e-20 E value 58 Match length

69 % identity

NCBI Description (AC003981) F22013.17 [Arabidopsis thaliana]

LIB3076-034-Q1-K1-B12

262586 Seq. No.

4307 1.R1011 Contig ID

5'-most EST uC-zmflb73069g07b1

Method BLASTX q3599491 NCBI GI 1737 BLAST score 0.0e + 00E value Match length 489

% identity

(AF085149) putative aminotransferase [Capsicum chinense] NCBI Description

262587 Seq. No.

Contig ID 4307 2.R1011

uC-zmflb73285c07b1 5'-most EST

Method BLASTX q3599491 NCBI GI BLAST score 602 1.0e-112 E value Match length 278 74 % identity

NCBI Description (AF085149) putative aminotransferase [Capsicum chinense]

Seq. No. 262588

4307 4.R1011 Contig ID

uC-zmflb73069g07a1 5'-most EST

262589 Seq. No. 4307 5.R1011 Contig ID

uC-zmflb73333a10a1 5'-most EST



```
Seq. No.
                  262590
                  4308 1.R1011
Contia ID
5'-most EST
                  yne700379039.h1
                  BLASTX
Method
NCBI GI
                  g224293
BLAST score
                  410
                  1.0e-39
E value
Match length
                  82
% identity
                  100
NCBI Description histone H4 [Triticum aestivum]
                  262591
Seq. No.
                  4308 2.R1011
Contig ID
5'-most EST
                  LIB3076-012-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g70772
BLAST score
                  345
E value
                  3.0e-32
Match length
                  69
% identity
                  100
NCBI Description histone H4 - wheat >gi 70773 pir HSPM4 histone H4 - garden
                  pea
Seq. No.
                  262592
Contig ID
                  4308 4.R1011
5'-most EST
                  LIB189-020-Q1-E1-F12
Method
                  BLASTX
NCBI GI
                  g70772
BLAST score
                  410
                  4.0e-40
E value
Match length
                  82
                  100
% identity
NCBI Description histone H4 - wheat >gi_70773_pir__HSPM4 histone H4 - garden
                  pea
Seq. No.
                  262593
Contig ID
                  4308 5.R1011
5'-most EST
                  LIB3068-024-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  g70772
BLAST score
                  410
E value
                  8.0e-40
Match length
                  82
                  100
% identity
NCBI Description histone H4 - wheat >gi_70773_pir_HSPM4 histone H4 - garden
                  pea
                  262594
Seq. No.
Contig ID
                  4308 6.R1011
5'-most EST
                  LIB3070-007-Q1-N1-F12
Method
                  BLASTX
NCBI GI
                  g224293
BLAST score
                  461
E value
                  6.0e-46
Match length
                  101
                  91
% identity
```

36397

NCBI Description histone H4 [Triticum aestivum]



```
262595
Seq. No.
                   4308 7.R1011
Contig ID
                   ltv700479660.h1
5'-most EST
                   BLASTX
Method
                   g122106
NCBI GI
                   386
BLAST score
                   4.0e-37
E value
                   78
Match length
                   100
% identity
                   HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize
NCBI Description
                   >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana
                   >gi_2119028_pir__S60475 histone H4 - garden pea
                   >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum
                   aestivum] >gi 166740 (M17132) histone H4 [Arabidopsis
                   thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis
                   thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays]
                   >gi 168501 (M\overline{1}3370) histone H4 [Zea mays] >gi_168503
                   (M1\overline{3}377) histone H4 [Zea mays] >gi_498898 (U1\overline{0}042) histone
                   H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_
                   (Z79638) histone H4 homologue [Sesbania rostrata]
                   >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
                   >gi 4580385 gb AAD24364.1 AC007184_4 (AC007184) histone H4
                   [Arabidopsis thaliana] >gi_225838_prf__1314298A histone H4
                   [Arabidopsis thaliana]
                   262596
Seq. No.
                   4308 8.R1011
Contig ID
                   wyr700240304.hl
5'-most EST
                   BLASTX
Method
                   g224293
NCBI GI
                   410
BLAST score
                   7.0e-40
E value
                   82
Match length
                   100
 % identity
NCBI Description histone H4 [Triticum aestivum]
                    262597
Seq. No.
                    4308 9.R1011
 Contig ID
 5'-most EST
                    yd1700405382.h1
                    BLASTX
Method
                    q70772
 NCBI GI
 BLAST score
                    410
                    6.0e-40
 E value
                    82
 Match length
                    100
 % identity
 NCBI Description histone H4 - wheat >gi_70773_pir__HSPM4 histone H4 - garden
                    pea
                    262598
 Seq. No.
                    4308 10.R1011
 Contig ID
                    LIB3069-033-Q1-K1-H4
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    q70772
                    410
 BLAST score
```

36398

7.0e-40

82

E value

Match length



% identity 100

NCBI Description histone H4 - wheat >gi_70773_pir__HSPM4 histone H4 - garden

1

pea

Seq. No. 262599

Contig ID 4308_11.R1011 5'-most EST rvt700549263.h1

Method BLASTX
NCBI GI g70772
BLAST score 410
E value 7.0e-40
Match length 82
% identity 100

NCBI Description histone H4 - wheat >gi 70773 pir HSPM4 histone H4 - garden

pea

Seq. No. 262600

Contig ID 4308 12.R1011

5'-most EST LIB3059-017-Q1-K1-H2

Method BLASTX
NCBI GI g122106
BLAST score 398
E value 2.0e-38
Match length 80
% identity 100

NCBI Description HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize

>gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana

>gi 2119028 pir S60475 histone H4 - garden pea

>gi_21795_emb_CAA24924 (X00043) histone H4 [Triticum
aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis
thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis

thaliana] >gi_168499 (M36659) histone H4 (H4Cl3) [Zea mays]

>gi_168501 (M13370) histone H4 [Zea mays] >gi_168503
(M13377) histone H4 [Zea mays] >gi 498898 (U10042) histone

H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_

(Z79638) histone H4 homologue [Sesbania rostrata]

>gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
>gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4
[Arabidopsis thaliana] >gi_225838_prf__1314298A histone H4

[Arabidopsis thaliana]

Seq. No. 262601

Contig ID 4308_13.R1011 5'-most EST LIB36-007-Q1-E1-C1

Method BLASTX
NCBI GI g224293
BLAST score 398
E value 2.0e-38
Match length 80
% identity 100

NCBI Description histone H4 [Triticum aestivum]

Seq. No. 262602

Contig ID 4308_14.R1011 5'-most EST xyt700343892.h1

Method BLASTX NCBI GI g70772

Seq. No.

Contig ID

262608

4320 1.R1011



```
410
BLAST score
E value
                  5.0e-40
                  82
Match length
                  100
% identity
NCBI Description histone H4 - wheat >gi_70773_pir_HSPM4 histone H4 - garden
                  pea
                  262603
Seq. No.
                  4308 15.R1011
Contig ID
                  LIB3150-029-Q1-N1-H11
5'-most EST
                  BLASTX
Method
                  q1806283
NCBI GI
                  208
BLAST score
                  2.0e-26
E value
                  77
Match length
                  88
% identity
NCBI Description (Z79637) Histone H4 homologue [Sesbania rostrata]
Seq. No.
                   262604
                   4308 17.R1011
Contig ID
                  LIB3078-056-Q1-K1-E2
5'-most EST
                  BLASTN
Method
                   q51308
NCBI GI
                   45
BLAST score
                   4.0e-16
E value
                   76
Match length
                   89
% identity
NCBI Description Mouse histone H4 gene (clone 12)
Seq. No.
                   262605
Contig ID
                   4313 1.R1011
                   vmt700224220.h1
5'-most EST
                   BLASTX
Method
                   g1362009
NCBI GI
BLAST score
                   747
                   3.0e-79
E value
                   152
Match length
                   65
% identity
                  ubiquitin-like protein 7 - Arabidopsis thaliana
NCBI Description
Seq. No.
                   262606
Contig ID
                   4316 1.R1011
5'-most EST
                   LIB3076-005-Q1-K1-A7
Seq. No.
                   262607
Contig ID
                   4319 1.R1011
                   xsy700209878.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3549679
BLAST score
                   251
                   3.0e-21
E value
Match length
                   113
% identity
                   53
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
```



```
uC-zmflB73046f07b1
5'-most EST
                  262609
Seq. No.
                  4324 1.R1011
Contig ID
                  LIB3076-011-Q1-K1-F7
5'-most EST
Method
                  BLASTX
                  g3212849
NCBI GI
                  498
BLAST score
                  2.0e-61
E value
                  192
Match length
                  59
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
                  262610
Seq. No.
                  4325 1.R1011
Contig ID
                  xmt700266277.h1
5'-most EST
Method
                  BLASTX
                   g2632106
NCBI GI
                   184
BLAST score
                   1.0e-13
E value
                   61
Match length
% identity
                  (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                   262611
Seq. No.
                   4329 1.R1011
Contig ID
                   LIB3076-011-Q1-K1-H11
5'-most EST
                   262612
Seq. No.
                   4331 1.R1011
Contig ID
                   LIB3076-011-Q1-K1-H8
5'-most EST
                   262613
Seq. No.
                   4337 1.R1011
Contig ID
                   xyt700345393.h1
5'-most EST
                   BLASTX
Method
                   g4539423
NCBI GI
                   1032
BLAST score
                   1.0e-112
E value
                   261
Match length
                   76
 % identity
NCBI Description (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
                   [Arabidopsis thaliana]
                   262614
 Seq. No.
                   4338 1.R1011
 Contig ID
                   LIB3068-021-Q1-K1-C5
 5'-most EST
                   BLASTX
 Method
                   g120670
 NCBI GI
                   887
 BLAST score
                   9.0e-96
 E value
                   189
 Match length
                   91
 % identity
 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi 100879 pir_ S06879 glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) C - maize
```

>gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]



```
262615
Seq. No.
                  4338_2.R1011
Contig ID
                  uC-zmflmo17045h05b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q66009
                  555
BLAST score
                  5.0e-57
E value
                  105
Match length
% identity
                   100
                  glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C,
NCBI Description
                   cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH
                   (AA 1-337) [Zea mays]
                   262616
Seq. No.
                   4338 4.R1011
Contig ID
                   xmt7\overline{0}0263524.h1
5'-most EST
                   BLASTX
Method
                   g120670
NCBI GI
                   555
BLAST score
                   5.0e-57
E value
Match length
                   105
                   100
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_100879_pir__S06879 glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) C - maize
                   >gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]
                   262617
Seq. No.
                   4338 9.R1011
Contig ID
                   xmt700257449.h2
5'-most EST
Method
                   BLASTX
                   g3023816
NCBI GI
                   275
BLAST score
                   1.0e-24
E value
                   55
Match length
                   98
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi 968996 (U31676) glyceraldehyde-3-phosphate
                   dehydrogenase [Oryza sativa]
                   262618
Seq. No.
                   4340 1.R1011
Contig ID
                   uC-zmflb73094b01b2
5'-most EST
                   BLASTX
Method
                   q2245020
NCBI GI
BLAST score
                   368
                   1.0e-34
 E value
                   262
Match length
 % identity
NCBI Description (Z97341) growth regulator homolog [Arabidopsis thaliana]
 Seq. No.
                    262619
```

5'-most EST pmx700084875.h1
Seq. No. 262620

Contig ID

4340 2.R1011

5'-most EST



```
Contig ID
                   4342 1.R1011
5'-most EST
                  LIB3076-011-Q1-K1-B5
                   262621
Seq. No.
Contig ID
                   4343 1.R1011
5'-most EST
                   uC-zmflm017018g07b1
Method
                  BLASTX
NCBI GI
                  q4432839
BLAST score
                  176
                  2.0e-12
E value
Match length
                  160
% identity
                  36
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                  262622
                   4343 2.R1011
Contig ID
5'-most EST
                  uC-zmflMo17018g07b1
                  BLASTX
Method
NCBI GI
                  g3024950
BLAST score
                  167
                   5.0e-11
E value
                   82
Match length
                   44
% identity
NCBI Description HYPOTHETICAL PROTEIN MJ0970 >gi 2128607 pir B64421
                  hypothetical protein MJ0970 - Methanococcus jannaschii
                   >gi 1591633 (U67540) conserved hypothetical protein
                   [Methanococcus jannaschii]
Seq. No.
                   262623
                   4344 1.R1011
Contig ID
5'-most EST
                   xjt700094420.h1
                  BLASTX
Method
NCBI GI
                   g2245378
BLAST score
                   519
                   6.0e-53
E value
                  137
Match length
% identity
                   72
NCBI Description (U83245) auxin response factor 1 [Arabidopsis thaliana]
Seq. No.
                   262624
                   4345 1.R1011
Contig ID
5'-most EST
                   xsy700211462.h1
Method
                  BLASTX
NCBI GI
                   g1009234
                   577
BLAST score
E value
                   3.0e-59
Match length
                  185
% identity
                   64
NCBI Description (L38829) SUP2 gene product [Nicotiana tabacum]
Seq. No.
                   262625
                   4345 4.R1011
Contig ID
5'-most EST
                  pwr700450312.h1
Seq. No.
                   262626
Contig ID
                   4347 1.R1011
```

36403

xsy700210271.hl



```
BLASTX
Method
                  g2244813
NCBI GI
                  231
BLAST score
                  3.0e-19
E value
                  83
Match length
                  53
% identity
                  (Z97336) acylaminoacyl-peptidase homolog [Arabidopsis
NCBI Description
                  thaliana]
                  262627
Seq. No.
                  4349 1.R1011
Contig ID
                  LIB3076-010-Q1-K1-F5
5'-most EST
                  BLASTX
Method
                  g2149640
NCBI GI
                  359
BLAST score
                  4.0e-34
E value
                  96
Match length
                  73
% identity
                  (U91995) Argonaute protein [Arabidopsis thaliana]
NCBI Description
                  262628
Seq. No.
                   4350 1.R1011
Contig ID
                  uC-zmflmo17064e05a1
5'-most EST
                  BLASTX
Method
                  q1143511
NCBI GI
                   1532
BLAST score
                   1.0e-171
E value
                   303
Match length
                   92
% identity
                   (Z47076) Ser/Thr protein phosphatase homologous to PPX
NCBI Description
                   [Malus domestica] >gi_1586034_prf__2202340A Ser/Thr protein
                   phosphatase [Malus domestica]
                   262629
Seq. No.
Contig ID
                   4353 1.R1011
                   LIB3076-010-Q1-K1-G1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4467132
                   219
BLAST score
                   2.0e-17
E value
                   117
Match length
                   42
% identity
                  (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   262630
Contig ID
                   4357 1.R1011
                   LIB3076-010-Q1-K1-G3
5'-most EST
                   262631
Seq. No.
                   4359 1.R1011
Contig ID
5'-most EST
                   LIB3076-010-Q1-K1-G5
Method
                   BLASTX
NCBI GI
                   q4587533
BLAST score
                   273
```

2.0e-23

102

55

E value Match length

% identity



```
(AC007060) EST gb AA721821 comes from this gene.
NCBI Description
                  [Arabidopsis thaliana]
                  262632
Seq. No.
                  4360 1.R1011
Contig ID
                  xsy700211103.hl
5'-most EST
                  BLASTX
Method
                  g113497
NCBI GI
                  443
BLAST score
                  2.0e-48
E value
                  140
Match length
                  67
% identity
NCBI Description ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE)
                  (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE)
                  >gi 99880 pir _S07472 alpha-galactosidase (EC 3.2.1.22)
                  precursor - guar >gi_18292_emb_CAA32772_ (X14619)
                  alpha-galactosidase preproprotein [Cyamopsis tetragonoloba]
                  262633
Seq. No.
Contig ID
                  4362 1.R1011
                  LIB3076-010-Q1-K1-H12
5'-most EST
                  262634
Seq. No.
                  4363 1.R1011
Contig ID
                  LIB3076-010-Q1-K1-F3
5'-most EST
                  BLASTX
Method
                  g3402673
NCBI GI
                  345
BLAST score
                   4.0e-46
E value
Match length
                   166
                   56
% identity
NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]
                   262635
Seq. No.
Contig ID
                   4372 1.R1011
5'-most EST
                   LIB3069-015-Q1-K1-A3
                   262636
Seq. No.
                   4374 1.R1011
Contig ID
                   LIB3076-010-Q1-K1-E11
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2708532
                   970
BLAST score
                   1.0e-105
E value
Match length
                   322
% identity
                   60
NCBI Description (AF029351) putative RNA binding protein [Nicotiana tabacum]
                   262637
Seq. No.
                   4374 2.R1011
Contig ID
                   uC-zmflMo17004b06b1
5'-most EST
                   BLASTN
Method
                   g3821780
NCBI GI
                   36
BLAST score
                   1.0e-10
E value
```

36405

48

67

Match length

% identity



```
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  262638
Seq. No.
                  4374 3.R1011
Contig ID
                  uC-zmroteosinte030e12b1
5'-most EST
                  262639
Seq. No.
                   4374 4.R1011
Contig ID
                  LIB3066-001-Q1-K1-H11
5'-most EST
                  262640
Seq. No.
                   4376 1.R1011
Contig ID
                  LIB3076-010-Q1-K1-C7
5'-most EST
                   262641
Seq. No.
                   4377 1.R1011
Contig ID
                   LIB84-003-Q1-E1-F8
5'-most EST
                   BLASTX
Method
                   g4589956
NCBI GI
                   239
BLAST score
E value
                   8.0e-20
Match length
                   71
                   62
% identity
                  (AC007169) putative endonuclease III [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   262642
                   4377 2.R1011
Contig ID
                   LIB3076-010-Q1-K1-B4
5'-most EST
                   BLASTX
Method
                   g4589956
NCBI GI
                   669
BLAST score
                   4.0e-70
E value
                   235
Match length
% identity
                  (AC007169) putative endonuclease III [Arabidopsis thaliana]
NCBI Description
                   262643
Seq. No.
                   4378 1.R1011
Contig ID
                   ceu700426760.h1
5'-most EST
                   BLASTX
Method
                   g2274859
NCBI GI
BLAST score
                   394
                   6.0e-38
E value
                   73
Match length
                   96
% identity
                   (AJ000016) Cks1 protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4510420_gb_AAD21506.1_ (AC006929) putative
                   cyclin-dependent kinase regulatory subunit [Arabidopsis
                   thaliana]
                   262644
Seq. No.
Contig ID
                   4378 2.R1011
```



73 Match length % identity (AJ000016) Cksl protein [Arabidopsis thaliana] NCBI Description >qi 4510420 gb AAD21506.1 (AC006929) putative cyclin-dependent kinase regulatory subunit [Arabidopsis thaliana] Seq. No. 262645 4382 1.R1011 Contig ID pmx700089712.h1 5'-most EST BLASTX Method q2213643 NCBI GI BLAST score 2034 0.0e + 00E value 560 Match length % identity (U57338) glossyl homolog [Oryza sativa] NCBI Description Seq. No. 262646 4385 1.R1011 Contig ID LIB189-017-01-E1-D1 5'-most EST BLASTX Method q4538959 NCBI GI BLAST score 433 1.0e-42 E value 109 Match length 72 % identity (ALO49488) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 262647 4385 2.R1011 Contig ID LIB3079-032-Q1-K1-E3 5'-most EST 262648 Seq. No. 4393 1.R1011 Contig ID uC-zmroteosinte007f09b1 5'-most EST BLASTX Method q951453 NCBI GI BLAST score 673 2.0e-70 E value Match length 189 71 % identity (M95746) initiation factor (iso)4f p82 subunit [Triticum NCBI Description aestivum] 262649 Seq. No. 4393 2.R1011 Contig ID

 Seq. No.
 262649

 Contig ID
 4393_2.R1011

 5'-most EST
 uC-zmflb73122e11b2

 Method
 BLASTX

 NCBI GI
 g1170504

 BLAST score
 2589

 E value
 0.0e+00

Match length 745 % identity 70 NCBI Description FUKARYOTIC T

NCBI Description EUKARYOTIC INITIATION FACTOR (ISO)4F SUBUNIT P82 (IEIF-(ISO)4F P82) >gi 452440 (M95747) initiation factor

(iso)4f p82 subunit [Triticum aestivum]



```
262650 -
Seq. No.
Contig ID
                   4393 3.R1011
                   uC-zmrob73060c11a1
5'-most EST
                   262651
Seq. No.
                   4394 1.R1011
Contig ID
                   uC-z\overline{m}flmo17097c01b1
5'-most EST
                   BLASTX
Method
                   g1421730
NCBI GI
                   312
BLAST score
E value
                   2.0e-28
Match length
                   99
                   62
% identity
NCBI Description
                   (U43082) RF2 [Zea mays]
                   262652
Seq. No.
                   4399 1.R1011
Contig ID
                   rvt700551736.hl
5'-most EST
                   262653
Seq. No.
                   4401 1.R1011
Contig ID
                   uC\text{-}z\overline{m}f1b73079b08b2
5'-most EST
Method
                   BLASTX
                   g4091080
NCBI GI
                   748
BLAST score
                   3.0e-79
E value
Match length
                   240 -
                    59
% identity
                   (AF045571) nucleic acid binding protein [Oryza sativa]
NCBI Description
                   262654
Seq. No.
                    4401 6.R1011
Contig ID
5'-most EST
                   xdb7\overline{0}0341150.h1
                    262655
Seq. No.
                    4406_1.R1011
Contig ID
5'-most EST
                    uC-zmflb73131f10b2
                    262656
Seq. No.
                    4412 1.R1011
Contig ID
5'-most EST
                    nbm700466207.h1
Method
                    BLASTX
NCBI GI
                    g3367522
                    624
BLAST score
                    1.0e-64
E value
                    244
Match length
% identity
                    52
                   (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis
NCBI Description
                    thaliana]
Seq. No.
                    262657
Contig ID
                    4415 1.R1011
```

5'-most EST LIB3076-031-Q1-K1-C6

Seq. No. 262658 Contig ID 4417_1.R1011



LIB3076-021-Q1-K1-G2 5'-most EST BLASTX Method NCBI GI g4455171 BLAST score 1617 0.0e+00E value 469 Match length 62 % identity (AL035521) hypothetical protein [Arabidopsis thaliana] NCBI Description 262659 Seq. No. 4420 1.R1011 Contig ID uC-zmflmo17141f10a1 5'-most EST BLASTX Method g732207 NCBI GI 267 BLAST score 9.0e-23 E value 302 Match length 28 % identity HYPOTHETICAL 75.4 KD PROTEIN IN AUT1-CSE2 INTERGENIC REGION NCBI Description >qi 626466 pir S45131 probable membrane protein YNR008w yeast (Saccharomyces cerevisiae) >gi 496725_emb_CAA54576_ (X77395) N2042 [Saccharomyces cerevisiae] >qi 1302482 emb CAA96285 (Z71623) ORF YNR008w [Saccharomyces cerevisiae] 262660 Seq. No. 4423 1.R1011 Contig ID xjt700092495.h1 5'-most EST BLASTX Method NCBI GI q550438 BLAST score 1673 0.0e + 00E value 362 Match length 98 % identity (X81829) cytochrome P450 [Zea mays] NCBI Description >gi 1870201 emb CAA72208 (Y11404) cytochrome p450 [Zea mays] Seq. No. 262661 Contig ID 4425 1.R1011 fwa700098889.h1 5'-most EST Method BLASTX NCBI GI q2245394

BLAST score 539 2.0e-54 E value Match length 411 36 % identity

NCBI Description (U89771) ARF1-binding protein [Arabidopsis thaliana]

Seq. No. 262662 Contig ID 4425 2.R1011

LIB3076-009-Q1-K1-B9 5'-most EST

Method BLASTX NCBI GI g2245394 BLAST score 390 E value 2.0e-37 112 Match length

E value

Match length

% identity

6.0e-85 239

73



```
% identity
                  (U89771) ARF1-binding protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  262663
Contig ID
                  4425 4.R1011
5'-most EST
                  ypc700803417.h1
Seq. No.
                  262664
Contig ID
                  4428 1.R1011
                  LIB3076-009-Q1-K1-D2
5'-most EST
                  262665
Seq. No.
Contig ID
                  4430 1.R1011
5'-most EST
                  LIB3076-007-Q1-K1-H7
                  BLASTX
Method
NCBI GI
                  q3786007
BLAST score
                  285
E value
                   2.0e-25
Match length
                  144
                   44
% identity
                  (AC005499) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   262666
Contig ID
                   4432 1.R1011
                  xjt700093092.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4406775
BLAST score
                   202
E value
                   1.0e-15
Match length
                   111
% identity
                   44
                  (AC006836) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   262667
                   4432 2.R1011
Contig ID
                   uC-zmflb73012d07b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4406775
BLAST score
                   221
                   7.0e-18
E value
                   120
Match length
                   42
% identity
                  (AC006836) unknown protein [Arabidopsis thaliana]
NCBI Description
                   262668
Seq. No.
                   4434 1.R1011
Contig ID
                   LIB3076-008-Q1-K1-F6
5'-most EST
                   262669
Seq. No.
                   4435 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73192c03b1
                   BLASTX
Method
NCBI GI
                   q2935573
BLAST score
                   433
```

5'-most EST Method

NCBI GI



```
NCBI Description (AF050180) KNOX class homeodomain protein [Oryza sativa]
                  262670
Seq. No.
                  4436 1.R1011
Contig ID
                  vvh700281965.hl
5'-most EST
                  BLASTX
Method
                  g3461835
NCBI GI
BLAST score
                  1072
                  1.0e-117
E value
                  327
Match length
% identity
                  63
                   (AC005315) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  >qi 3927840 (AC005727) putative protein kinase [Arabidopsis
                  thaliana]
                  262671
Seq. No.
                   4438 1.R1011
Contig ID
                  fwa700099277.h1
5'-most EST
                  262672
Seq. No.
                   4439 1.R1011
Contig ID
                  LIB3136-018-Q1-K1-F6
5'-most EST
                  BLASTX
Method
                  q4191782
NCBI GI
                  1841
BLAST score
                   0.0e+00
E value
                   453
Match length
                   74
% identity
                  (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   262673
                   4439 2.R1011
Contig ID
                   yyf700351339.hl
5'-most EST
                   BLASTX
Method
                   g4191782
NCBI GI
BLAST score
                   453
                   4.0e-45
E value
                   101
Match length
                   83
% identity
NCBI Description (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
                   262674
Seq. No.
                   4439 3.R1011
Contig ID
                   LIB3078-029-Q1-K1-H6
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4191782
BLAST score
                   222
                   8.0e-18
E value
                   75
Match length
% identity
NCBI Description
                  (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
Seq. No.
                   262675
Contig ID
                   4439 4.R1011
```

36411

uC-zmromo17030g12a1

BLASTX

q4191782



```
163
BLAST score
                   4.0e-11
E value
                   55
Match length
                   55
% identity
NCBI Description (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
                   262676
Seq. No.
                   4439 6.R1011
Contig ID
                   ymt700220029.h1
5'-most EST
                   BLASTX
Method
                   q4191782
NCBI GI
                   250
BLAST score
                   1.0e-21
E value
                   104
Match length
                   46
% identity
                  (AC005917) WD-40 repeat protein [Arabidopsis thaliana]
NCBI Description
                   262677
Seq. No.
                   4440 1.R1011
Contig ID
                   fdz7\overline{0}1161490.h1
5'-most EST
                   BLASTX
Method
                   g3395440
NCBI GI
                   1033
BLAST score
                   1.0e-112
E value
                   373
Match length
                   52
% identity
                  (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   262678
Seq. No.
                   4440 2.R1011
Contig ID
5'-most EST
                   tfd700572930.h1
                   BLASTX
Method
                   q3395440
NCBI GI
                   175
BLAST score
                   9.0e-13
E value
                   55
Match length
                   51
% identity
NCBI Description (AC004683) hypothetical protein [Arabidopsis thaliana]
                   262679
Seq. No.
                   4441 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73149g09b1
                   BLASTX
Method
NCBI GI
                   q4455223
                   886
BLAST score
                   3.0e - 95
E value
                   281
Match length
 % identity
NCBI Description (AL035440) putative DNA binding protein [Arabidopsis
                   thaliana]
                   262680
 Seq. No.
                   4441 2.R1011
 Contig ID
                   uC-zmflb73294b08a1
 5'-most EST
```

Seq. No. 262681 Contig ID 4444_1.R1011



5'-most EST LIB3076-024-Q1-K1-C3 Method BLASTX q3193284 NCBI GI BLAST score 837 1.0e-89 E value 308 Match length 56 % identity (AF069298) No definition line found [Arabidopsis thaliana] NCBI Description 262682 Seq. No. 4446 1.R1011 Contig ID yyf700349403.h1 5'-most EST Method BLASTX g2760362 NCBI GI 495 BLAST score 6.0e-50 E value Match length 144 72 % identity (AF016511) 15.9 kDa subunit of RNA polymerase II NCBI Description [Arabidopsis thaliana] 262683 Seq. No. 4447 1.R1011 Contig ID 5'-most EST LIB3076-009-Q1-K1-A2 BLASTX Method q2088657 NCBI GI 167 BLAST score 4.0e-11 E value Match length 172 % identity 30 (AF002109) unknown protein [Arabidopsis thaliana] NCBI Description 262684 Seq. No. Contig ID 4451 1.R1011 zuv700353089.h1 5'-most EST BLASTX Method q4455359 NCBI GI BLAST score 1389 E value 1.0e-154 Match length 334 % identity 82 NCBI Description (AL035524) putative protein [Arabidopsis thaliana] 262685 Seq. No. 4451 2.R1011 Contig ID LIB3076-008-Q1-K1-D4 5'-most EST 262686 Seq. No. 4454 1.R1011 Contig ID LIB84-025-Q1-E1-F8 5'-most EST 262687 Seq. No. 4457 1.R1011 Contig ID

5'-most EST uC-zmrob73066h11b1 BLASTX Method g3193301 NCBI GI

BLAST score 2054



E value 0.0e+00 Match length 725 8 identity 58

NCBI Description (AF069298) Arabidopsis putative chloroplast outer envelope

86-like protein T10P11.19 (GB: AC002330) [Arabidopsis

thaliana]

Seq. No. 262688 Contig ID 4457_2.R1011

5'-most EST uC-zmflmo17076g10b1

Method BLASTX
NCBI GI g3193301
BLAST score 502
E value 2.0e-52
Match length 164

Match length 164 % identity 65

NCBI Description (AF069298) Arabidopsis putative chloroplast outer envelope

86-like protein T10P11.19 (GB: AC002330) [Arabidopsis

thaliana]

Seq. No. 262689 Contig ID 4457_4.R1011

5'-most EST uC-zmflmo17374h04a1

Seq. No. 262690

Contig ID 4463_1.R1011 5'-most EST ymt700220114.h1

Seq. No. 262691

Contig ID 4463_3.R1011

5'-most EST LIB3066-030-Q1-K1-F11

Seq. No. 262692

Contig ID 4465_1.R1011

5'-most EST uC-zmflb73135h12b2

Seq. No. 262693

Contig ID 4465_2.R1011

5'-most EST uC-zmflb73031b03b1

Seq. No. 262694 Contig ID 4465 3.R1011

5'-most EST uC-zmflm017082f08b1

Seq. No. 262695

Contig ID 4469 1.R1011

5'-most EST LIB3069-028-Q1-K1-D8

Seq. No. 262696

Contig ID 4469 2.R1011 5'-most EST uC-zmflb73127h01a1

Seq. No. 262697

Contig ID 4469 3.R1011 5'-most EST gct701172920.h2

Seq. No. 262698

5'-most EST

Method

BLASTN



```
4469 4.R1011
Contig ID
                  LIB3076-008-Q1-K1-B2
5'-most EST
                  262699
Seq. No.
                  4470 1.R1011
Contig ID
                  LIB3076-008-Q1-K1-B3
5'-most EST
                  BLASTX
Method
                  g3184285
NCBI GI
                  146
BLAST score
                  5.0e-09
E value
Match length
                  81
                   40
% identity
NCBI Description (AC004136) hypothetical protein [Arabidopsis thaliana]
                   262700
Seq. No.
                   4472 1.R1011
Contig ID
                   LIB3076-008-Q1-K1-B9
5'-most EST
                   262701
Seq. No.
                   4474 1.R1011
Contig ID
                   uC-zmflmo17150b11b1
5'-most EST
                   BLASTX
Method
                   q4512667
NCBI GI
                   1701
BLAST score
                   0.0e+00
E value
                   408
Match length
                   76
% identity
NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]
                   262702
Seq. No.
                   4475_1.R1011
Contig ID
                   uC-zmflmo17022g10b1
5'-most EST
                   BLASTX
Method
                   g3914423
NCBI GI
                   609
BLAST score
                   4.0e-63
E value
                   131
Match length
 % identity
NCBI Description PROFILIN 4 >gi_2642324 (AF032370) profilin [Zea mays]
                   262703
 Seq. No.
                   4475 2.R1011
 Contig ID
                   zuv700353108.h1
 5'-most EST
                   BLASTX
 Method
                   q1838956
 NCBI GI
 BLAST score
                   493
                   2.0e-49
 E value
                   195
Match length
                   52
 % identity
                   (Z85980) capping protein, beta3 isoform [Bos taurus]
 NCBI Description
                   >gi 2239063 emb CAA71401_ (Y10372) actin-binding protein
                   CP3 [Bos taurus]
 Seq. No.
                    262704
                    4475 3.R1011
 Contig ID
                   LIB3115-022-P1-K1-G11
```

```
g2642323
NCBI GI
                  58
BLAST score
                  1.0e-23
E value
                  110
Match length
                  89
% identity
NCBI Description Zea mays profilin (PRO4) mRNA, complete cds
                  262705
Seq. No.
                  4475 4.R1011
Contig ID
5'-most EST
                  uC-zmflmo17113d11b1
                  BLASTX
Method
                  q3914423
NCBI GI
                  354
BLAST score
                  1.0e-35
E value
                  124
Match length
                  67
% identity
NCBI Description PROFILIN 4 >gi_2642324 (AF032370) profilin [Zea mays]
                  262706
Seq. No.
                  4475_5.R1011
Contig ID
                  uC-zmflMo17064f08b1
5'-most EST
                  BLASTX
Method
                  g3914423
NCBI GI
                   375
BLAST score
                   4.0e-36
E value
                   87
Match length
                   82
% identity
NCBI Description PROFILIN 4 >gi_2642324 (AF0323 ) profilin [Zea mays]
                   262707
Seq. No.
                   4475 6.R1011
Contig ID
                   rvt700550603.h1
5'-most EST
Method
                   BLASTN
                   g2642323
NCBI GI
                   329
BLASI ...ore
                   0.0e + 00
E valu∈
                   409
Match ler.
                   99
% identity
NCBI Description Zea mays profilin (PRO4) mRNA, complete cds
                   262708
Seq. No.
                   4475 13.R1011
Contig ID
 5'-most EST
                   uC-zmflmo17077g08b1
Method
                   BLASTX
                   q3914423
NCBI GI
 BLAST score
                   219
                   2.0e-17
E value
                   43
Mat " ' rath
                   95
 8 ic
NCBI Del . lon PROFILIN 4 >gi_2642324 (AF0^
                                                     profilin [Zea mays]
                   262709
 Seq. No.
                   4475 14.R1011
 Contig ID
                   LIB3078-055-Q1-K1-A7
 5'-most EST
                   BLASTX
 Method
                   g3914423
 NCBI GI
```

36416

259

BLAST score



63

% identity

```
2.0e-22
E value
                  63
Match length
                  76
% identity
NCBI Description PROFILIN 4 >gi_2642324 (AF032370) profilin [Zea mays]
                  262710
Seq. No.
                  4480 1.R1011
Contig ID
                  qmh700028612.f1
5'-most EST
                  262711
Seq. No.
                  4482 1.R1011
Contig ID
                  LIB3076-008-Q1-K1-D12
5'-most EST
                  262712
Seq. No.
                  4487 1.R1011
Contig ID
                  uwc700155234.h1
5'-most EST
                  BLASTX
Method
                  q132935
NCBI GI
                   295
BLAST score
                   3.0e-26
E value
                   102
Match length
                   54
% identity
                   60S RIBOSOMAL PROTEIN L37A (YL37) (RP47)
NCBI Description
                   >gi 101568_pir__S18431 ribosomal protein L35a.e.c16 - yeast
                   (Saccharomyces cerevisiae) >gi_4392_emb_CAA41035_ (X57969)
                   ribosomal protein L37a [Saccharomyces cerevisiae]
                   >gi 1244773 (U43703) Lpi4p [Saccharomyces cerevisiae]
                   >gi 1370305 emb CAA97847_ (Z73499) ORF YPL143w
                   [Saccharomyces cerevisiae]
                   262713
Seq. No.
                   4487 2.R1011
Contig ID
                   LIB3150-076-P1-N1-A11
5'-most EST
                   BLASTX
Method
                   q1350742
NCBI GI
                   308
BLAST score
                   6.0e-28
E value
                   102
Match length
                   56
% identity
                   PROBABLE 60S RIBOSOMAL PROTEIN L35A >gi_1086831 (U41264)
NCBI Description
                   coded for by C. elegans cDNA yk64g10.5; coded for by C.
                   elegans cDNA yk51f3.5; coded for by C. elegans cDNA
                   yk115e7.3; coded for by C. elegans cDNA yk99d1.3; coded for
                   by C. elegans cDNA yk99d1.5; coded for by C. elegans cDNA
                   yk64g1
 Seq. No.
                   262714
                   4487 5.R1011
 Contig ID
                   LIB3070-003-Q1-N1-H12
 5'-most EST
                   BLASTX
Method
                   q1350742
 NCBI GI
 BLAST score
                   180
                   4.0e-13
 E value
 Match length
                   46
```

36417

coded for by C. elegans cDNA yk64g10.5; coded for by C.

NCBI Description PROBABLE 60S RIBOSOMAL PROTEIN L35A >gi 1086831 (U41264)



elegans cDNA yk51f3.5; coded for by C. elegans cDNA yk115e7.3; coded for by C. elegans cDNA yk99d1.3; coded for by C. elegans cDNA yk99d1.5; coded for by C. elegans cDNA yk64g1

Seq. No. 262715
Contig ID 4487_6.R1011
5'-most EST xsy700209587.h1

Seq. No. 262716

Contig ID 4487_8.R1011

5'-most EST LIB3150-090-P2-K1-G1

Seq. No. 262717

Contig ID 4487_9.R1011

5'-most EST LIB3076-042-Q1-K1-C12

Seq. No. 262718

Contig ID 4488 1.R1011

5'-most EST uC-zmflmo17035a03b1

Seq. No. 262719

Contig ID 4488_2.R1011

5'-most EST LIB3067-054-Q1-K1-B10

Seq. No. 262720

Contig ID 4497 1.R1011

5'-most EST LIB3\overline{1}36-004-Q1-K1-H5

Seq. No. 262721

Contig ID 4498_1.R1011

5'-most EST uC-zmflmo17045f04b1

Method BLASTX NCBI GI g3036816

BLAST score 662

E value 1.0e-105

Match length 775

% identity 37

NCBI Description (AL022373) myosin-like protein [Arabidopsis thaliana]

Seq. No. 262722

Contig ID 4498 2.R1011

5'-most EST uC-zmflb73146f07a2

Seq. No. 262723

Contig ID 4498_3.R1011

5'-most EST uC-zmflmo17267g07b1

Seq. No. 262724

Contig ID 4502_1.R1011

5'-most EST uC-zmflmo17289f11b1

Method BLASTX
NCBI GI g3096935
BLAST score 181
E value 4.0e-13
Match length 95

% identity 40



NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 262725
Contig ID 4505_1.R1011
5'-most EST LIB3076-007-Q1-K1-E5

Method BLASTX
NCBI GI g3395938
BLAST score 542
E value 2.0e-55
Match length 133
% identity 76

NCBI Description (AF076924) polypyrimidine tract-binding protein homolog

[Arabidopsis thaliana]

Seq. No. 262726 Contig ID 4506 1.R1011

5'-most EST LIB3076-007-Q1-K1-G10

Seq. No. 262727 Contig ID 4507 1.R1011

5'-most EST LIB3076-007-Q1-K1-F2

Method BLASTX
NCBI GI g3953477
BLAST score 199
E value 2.0e-15
Match length 90

% identity 24

NCBI Description (AC002328) F2202.22 [Arabidopsis thaliana]

Seq. No. 262728

Contig ID 4508_1.R1011

5'-most EST LIB3069-043-Q1-K1-A5

Method BLASTX
NCBI GI g3024018
BLAST score 835
E value 2.0e-89
Match length 160
% identity 100

NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

initiation factor 5A [Zea mays]

Seq. No. 262729

Contig ID 4508_2.R1011

5'-most EST LIB83-002-Q1-E1-F1

Method BLASTX
NCBI GI g3024018
BLAST score 759
E value 7.0e-81
Match length 159
% identity 98

NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

initiation factor 5A [Zea mays]



Seq. No. 262730 Contig ID 4508_3.R1011

5'-most EST uC-zmromo17096h04a1

Method BLASTX
NCBI GI g3093294
BLAST score 308
E value 1.0e-27
Match length 139
% identity 50

NCBI Description (Y12782) putative villin [Arabidopsis thaliana]

Seq. No. 262731 Contig ID 4508 4.R1011

5'-most EST LIB3078-028-Q1-K1-E6

Method BLASTX
NCBI GI g3024018
BLAST score 566
E value 2.0e-58
Match length 131
% identity 89

NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi 2668738 (AF034943) translation

initiation factor 5A [Zea mays]

Seq. No. 262732 Contig ID 4508_5.R1011

5'-most EST LIB3078-046-Q1-K1-C7

Method BLASTX
NCBI GI g3024018
BLAST score 228
E value 1.0e-18
Match length 66
% identity 76

NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

initiation factor 5A [Zea mays]

Seq. No. 262733

Contig ID 4508_6.R1011 5'-most EST xsy700211912.h1

Method BLASTX
NCBI GI g3024018
BLAST score 612
E value 2.0e-63
Match length 157
% identity 79

NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

initiation factor 5A [Zea mays]

Seq. No. 262734
Contig ID 4508_7.R1011
5'-most EST uC-zmflb73230f12b2

Method BLASTX



g3024018 NCBI GI BLAST score 521 1.0e-52 E value Match length 104 95 % identity

INITIATION FACTOR 5A (EIF-5A) (EIF-4D) NCBI Description

> >qi 1546919 emb CAA69225 (Y07920) translation initiation factor 5A [Zea mays] >gi 2668738 (AF034943) translation

initiation factor 5A [Zea mays]

262735 Seq. No. 4515 1.R1011 Contig ID

5'-most EST LIB3076-006-Q1-K1-F8

Method BLASTX q4589962 NCBI GI 1198 BLAST score E value 1.0e-132 316 Match length % identity 72

NCBI Description (AC007169) putative fructokinase [Arabidopsis thaliana]

Seq. No. 262736 Contig ID

4515 2.R1011 5'-most EST hvj700621274.h1

BLASTX Method NCBI GI q1052973 BLAST score 179 1.0e-17 E value Match length 72

% identity 55

NCBI Description (U37838) fructokinase [Beta vulgaris]

262737 Seq. No.

Contig ID 4518 1.R1011

5'-most EST LIB3067-028-Q1-K1-D4

BLASTN Method NCBI GI g22646 BLAST score 275 E value 1.0e-153 855 Match length 99 % identity

NCBI Description Z.mays MFS18 mRNA

262738 Seq. No.

Contig ID 4518 2.R1011

5'-most EST uC-zmflb73207g05b1

Method BLASTN NCBI GI g22646 549 BLAST score E value 0.0e + 00736 Match length 99 % identity

NCBI Description Z.mays MFS18 mRNA

262739 Seq. No. 4518 3.R1011 Contig ID

5'-most EST LIB3062-010-Q1-K1-A11



BLASTN Method NCBI GI q22646 BLAST score 84 4.0e-39 E value 227 Match length 95 % identity

Z.mays MFS18 mRNA NCBI Description

262740 Seq. No. 4519 1.R1011 Contig ID

LIB3076-007-Q1-K1-A7 5'-most EST

BLASTX Method NCBI GI q1076625 BLAST score 262 1.0e-22 E value 117 Match length 44 % identity

glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) precursor NCBI Description

- common tobacco >gi 473102 emb CAA82271 (Z28697)

beta-1,3-glucanase [Nicotiana tabacum]

262741 Seq. No.

4520 1.R1011 Contig ID

5'-most EST LIB143-042-Q1-E1-F10

Method BLASTX q2129944 NCBI GI BLAST score 476 1.0e-47 E value Match length 155 % identity

RNA-binding protein RZ-1 - wood tobacco NCBI Description

>qi 1395193 dbj BAA12064 (D83696) RNA-binding protein RZ-1 [Nicotiana sylvestris] >gi 1435062 dbj BAA06012 (D28861)

RNA binding protein, RZ-1 [Nicotiana sylvestris]

262742 Seq. No.

4521 1.R1011 Contig ID 5'-most EST xsy700210246.h1

Method BLASTX NCBI GI g1723239 BLAST score 669 6.0e-70 E value 274 Match length 47 % identity

HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I NCBI Description

>gi 1177358 emb CAA93234 (Z69240) putative amidohydrolase

[Schizosaccharomyces pombe]

262743 Seq. No. 4521 3.R1011 Contig ID xjt700093869.h1 5'-most EST

262744 Seq. No.

Contig ID 4524 1.R1011 xsy700211904.h1 5'-most EST

Method BLASTX NCBI GI g2689720



```
BLAST score
                  271
E value
                  8.0e-24
Match length
                  97
% identity
                  61
                  (AF037168) DnaJ homologue [Arabidopsis thaliana]
NCBI Description
                  262745
Seq. No.
                  4524 3.R1011
Contig ID
                  uC-zmflb73225g06b1
5'-most EST
                  BLASTX
Method
                  g2689720
NCBI GI
BLAST score
                  296
E value
                  1.0e-26
                  86
Match length
                  65
% identity
                  (AF037168) DnaJ homologue [Arabidopsis thaliana]
NCBI Description
                  262746
Seq. No.
Contig ID
                   4526 1.R1011
                  LIB143-037-Q1-E1-E4
5'-most EST
Method
                  BLASTX
                  g4468798
NCBI GI
BLAST score
                  336
                  8.0e-36
E value
Match length
                  115
                   67
% identity
                  (AJ010440) GST7 protein [Zea mays]
NCBI Description
Seq. No.
                   262747
Contig ID
                   4526 2.R1011
                   dyk700105019.h1
5'-most EST
                   BLASTX
Method
                   q4468798
NCBI GI
BLAST score
                   384
E value
                   4.0e-37
Match length
                   95
                   75
% identity
                  (AJ010440) GST7 protein [Zea mays]
NCBI Description
Seq. No.
                   262748
Contig ID
                   4529 1.R1011
5'-most EST
                   LIB3076-006-Q1-K1-E9
Method
                   BLASTX
NCBI GI
                   g687860
BLAST score
                   170
                   7.0e-12
E value
                   127
Match length
                   19
% identity
```

NCBI Description (U21322) similar to T09A5.9 SDS22 protein; also similar to repetitive elements in glucose repression regulatory

proteins and internalin B proteins [Caenorhabditis elegans]

 Seq. No.
 262749

 Contig ID
 4534_1.R1011

 5'-most EST
 uC-zmflb73256g03b1

Method BLASTX NCBI GI g4538911



443 BLAST score E value 3.0e-43293 Match length 34 % identity (AL049482) hypothetical protein [Arabidopsis thaliana] NCBI Description 262750 Seq. No. Contig ID 4534 2.R1011 wty700163671.hl 5'-most EST BLASTN Method q1098664 NCBI GI 54 BLAST score 3.0e-21 E value 114 Match length 87 % identity Zea mays phytoene synthase (Y1) gene, complete cds NCBI Description Seq. No. 262751 Contig ID 4534 3.R1011 5'-most EST pmx700090822.h1 262752 Seq. No. 4534 4.R1011 Contig ID 5'-most EST nwy700445789.hl 262753 Seq. No. 4534 5.R1011 Contig ID 5'-most EST hvj700619934.h1 Seq. No. 262754 4535 1.R1011 Contig ID uC-zmflb73086f02b2 5'-most EST Seq. No. 262755 4535 2.R1011 Contig ID tfd700572713.h1 5'-most EST BLASTX Method g2462744 NCBI GI BLAST score 209 2.0e-16 E value 75 Match length 56 % identity (AC002292) Hypothetical protein [Arabidopsis thaliana] NCBI Description 262756 Seq. No. 4536 1.R1011 Contig ID uC-zmflmo17058e10b1 5'-most EST 262757 Seq. No. 4536 2.R1011 Contig ID $uC-z\overline{m}flmo17310d01b1$ 5'-most EST BLASTX Method NCBI GI q4512653 BLAST score 1192

36424

1.0e-131

295

77

E value

Match length

% identity

Seq. No.

Contig ID

5'-most EST

262763

4542 1.R1011

ymt700223781.h1



```
NCBI Description (AC007048) unknown protein [Arabidopsis thaliana]
                  262758
Seq. No.
                  4536 3.R1011
Contig ID
                  uC-zmflb73017d02b1
5'-most EST
                  BLASTX
Method
                  g4512653
NCBI GI
                  485
BLAST score
                  2.0e-48
E value
                  135
Match length
                  70
% identity
                  (AC007048) unknown protein [Arabidopsis thaliana]
NCBI Description
                  262759
Seq. No.
                  4536 4.R1011
Contig ID
                  hvj700622958.h1
5'-most EST
                  BLASTX
Method
                  g4512653
NCBI GI
BLAST score
                  690
E value
                  6.0e-77
                  241
Match length
% identity
                  61
                  (AC007048) unknown protein [Arabidopsis thaliana]
NCBI Description
                  262760
Seq. No.
                  4536 5.R1011
Contig ID
                  wyr700235633.h1
5'-most EST
                  262761
Seq. No.
                  4538 1.R1011
Contig ID
                  tzu700203668.h1
5'-most EST
                  BLASTX
Method
                  a584893
NCBI GI
                   893
BLAST score
E value
                   2.0e-96
                   179
Match length
                   93
% identity
                  SERINE CARBOXYPEPTIDASE III PRECURSOR
NCBI Description
                   >gi_283002_pir__S22530 carboxypeptidase III (EC 3.4.16.-) -
                   rice >gi 218153 dbj BAA01757 (D10985) serine
                   carboxypeptidase III [Oryza sativa]
Seq. No.
                   262762
Contig ID
                   4539 1.R1011
5'-most EST
                   uC-zmflb73356b09a2
Method
                   BLASTX
NCBI GI
                   g3342802
BLAST score
                   937
                   1.0e-101
E value
Match length
                   185
                   98
% identity
                  (AF061838) putative cytosolic 6-phosphogluconate
NCBI Description
                   dehydrogenase [Zea mays]
```



Method BLASTX
NCBI GI 94646218
BLAST score 696
E value 2.0e-73
Match length 205
% identity 65
NCBI Description (AC00729
thaliana

NCBI Description (AC007290) putative GTP-binding protein [Arabidopsis thaliana]

Seq. No. 262764 Contig ID 4543 1.R1011

5'-most EST LIB3059-048-Q1-K1-A3

Method BLASTX
NCBI GI g1351666
BLAST score 771
E value 5.0e-82
Match length 249
% identity 58

NCBI Description PUTATIVE ATP-DEPENDENT RNA HELICASE C1F7.02C

>gi_2130294_pir__S62574 hypothetical protein SPAC1F7.02c -

fission yeast (Schizosaccharomyces pombe) >gi_1067204_emb_CAA91949_ (Z67998) unknown

[Schizosaccharomyces pombe]

Seq. No. 262765 Contig ID 4544_1.R1011

5'-most EST uC-zmflmo17287d06b1

Method BLASTX
NCBI GI g1698548
BLAST score 897
E value 1.0e-107

E value 1.0e-3
Match length 408
% identity 51

NCBI Description (U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No. 262766

Contig ID 4545 1.R1011

5'-most EST LIB3076-006-Q1-K1-B6

Seq. No. 262767

Contig ID 4546_1.R1011 5'-most EST cjh700197067.h1

Method BLASTX
NCBI GI g1617270
BLAST score 718
E value 8.0e-76
Match length 164
% identity 76

NCBI Description (X94624) acyl-CoA synthetase [Brassica napus]

Seq. No. 262768

Contig ID 4548_1.R1011 5'-most EST xjt700093540.h1

Method BLASTX
NCBI GI g2668750
BLAST score 473
E value 3.0e-47



Match length 112 % identity 79

NCBI Description (AF034949) ribosomal protein L30 [Zea mays]

Seq. No. 262769

Contig ID 4548 2.R1011

5'-most EST LIB3157-003-Q1-K1-A4

Seq. No. 262770

Contig ID 4552 1.R1011

5'-most EST LIB3067-007-Q1-K1-D4

Method BLASTX
NCBI GI g4582456
BLAST score 622
E value 1.0e-64
Match length 159
% identity 75

NCBI Description (AC007071) putative trithorax protein [Arabidopsis

thaliana]

Seq. No. 262771

Contig ID 4556_1.R1011

5'-most EST LIB3076-005-Q1-K1-C6

Method BLASTX
NCBI GI g2642448
BLAST score 398
E value 8.0e-39
Match length 111
% identity 41

NCBI Description (AC002391) hypothetical protein [Arabidopsis thaliana]

>qi 3169187 (AC004401) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 262772

Contig ID 4557_1.R1011 5'-most EST vux700160120.h1

Method BLASTX
NCBI GI g1363492
BLAST score 1198
E value 1.0e-132
Match length 294
% identity 72

NCBI Description outer envelope membrane protein OEP75 precursor - garden

pea >gi_576507 (L36858) outer membrane protein [Pisum
sativum] >gi_633607_emb_CAA58720_ (X83767) chloroplastic
outer envelope membrane protein (OEP75) [Pisum sativum]

Seq. No. 262773

Contig ID 4557_3.R1011 5'-most EST ymt700220652.h1

Method BLASTX
NCBI GI g1363492
BLAST score 495
E value 3.0e-50
Match length 129
% identity 67

NCBI Description outer envelope membrane protein OEP75 precursor - garden



pea >gi_576507 (L36858) outer membrane protein [Pisum sativum] >gi_633607_emb_CAA58720_ (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]

 Seq. No.
 262774

 Contig ID
 4558_1.R1011

 5'-most EST
 LIB3076-005-Q1-K1-G5

Seq. No. 262775 Contig ID 4561 1.R1011

5'-most EST LIB3076-004-Q1-K1-G7

Method BLASTX
NCBI GI g2262159
BLAST score 324
E value 1.0e-29
Match length 108
% identity 59

NCBI Description (AC002329) predicted protein similar to S.pombe protein

C5H10.03 [Arabidopsis thaliana]

Seq. No. 262776 Contig ID 4561_2.R1011

5'-most EST LIB148-022-Q1-E1-G2

Method BLASTX
NCBI GI g2262159
BLAST score 651
E value 4.0e-68
Match length 165
% identity 72

NCBI Description (AC002329) predicted protein similar to S.pombe protein

C5H10.03 [Arabidopsis thaliana]

Seq. No. 262777

Contig ID 4561_3.R1011

5'-most EST uC-zmflb73181a08b2

Method BLASTX
NCBI GI g2262159
BLAST score 839
E value 5.0e-90
Match length 279
% identity 59

NCBI Description (AC002329) predicted protein similar to S.pombe protein

C5H10.03 [Arabidopsis thaliana]

Seq. No. 262778 Contig ID 4562_1.R1011

5'-most EST uC-zmflmo17055f05b1

Seq. No. 262779 Contig ID 4563_1.R1011

5'-most EST uC-zmflb73094b04b2

Method BLASTX
NCBI GI g2465923
BLAST score 211
E value 2.0e-22
Match length 268
% identity 33



NCBI Description (AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No. 262780 Contig ID 4564 1.R1011

5'-most EST uC-zmflmo17127d03b1

Method BLASTX
NCBI GI g2440187
BLAST score 185
E value 4.0e-13
Match length 273
% identity 26

NCBI Description (Z98944) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 262781
Contig ID 4564_2.R1011
5'-most EST uer700581220.h1

Seg. No. 262782

Contig ID 4565 1.R1011

5'-most EST LIB3069-041-Q1-K1-B2

Method BLASTX
NCBI GI 94559339
BLAST score 1774
E value 0.0e+00
Match length 421
% identity 82

NCBI Description (AC007087) putative ATP-dependent RNA helicase [Arabidopsis

thaliana]

Seq. No. 262783
Contig ID 4569_1.R1011
5'-most EST tzu700206903.h1

Method BLASTX
NCBI GI g1297187
BLAST score 602
E value 5.0e-62
Match length 216
% identity 55

NCBI Description (U53501) similar to protein encoded by GenBank Accession

Number U41815, nucleoporin 98 [Arabidopsis thaliana]

Seq. No. 262784 Contig ID 4569 3.

Contig ID 4569_3.R1011 5'-most EST wty700165815.h1

Seq. No. 262785

Contig ID 4570_1.R1011 5'-most EST rv1700456634.h1

Seq. No. 262786

Contig ID 4570_2.R1011 5'-most EST LIB3088-010-Q1-K1-C6

Seq. No. 262787 Contig ID 4572 1.R1011

5'-most EST LIB3076-005-Q1-K1-E2



```
Method
                  BLASTX
NCBI GI
                  g3130051
BLAST score
                   413
                   2.0e-40
E value
Match length
                   172
                   51
% identity
                   (AL023518) conserved hypothetical protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   262788
Seq. No.
                   4577 1.R1011
Contig ID
5'-most EST
                   nwy700443627.h1
Method
                   BLASTX
NCBI GI
                   g3859548
BLAST score
                   351
                   5.0e-33
E value
Match length
                   105
                   91
% identity
                  (AF097182) protein phosphatase 2A catalytic subunit [Oryza
NCBI Description
                   sativa]
Seq. No.
                   262789
Contig ID
                   4578 1.R1011
                   uC-zmrob73066h12b1
5'-most EST
Method
                   BLASTX
                   g1362172
NCBI GI
BLAST score
                   259
E value
                   7.0e-22
Match length
                   320
                   33
% identity
NCBI Description hook-containing protein AT1 - rice >gi_871496 emb_CAA61276_
                   (X88798) putative [Oryza sativa]
                   262790
Seq. No.
                   4578 2.R1011
Contig ID
                   qmh700030517.f1
5'-most EST
                   262791
Seq. No.
                   4581 1.R1011
Contig ID
                   LIB143-033-Q1-E1-E7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1346251
BLAST score
                   303
                   2.0e-27
E value
                   104
Match length
                   66
% identity
NCBI Description HISTONE H2B.4 >gi_577819_emb_CAA49585_ (X69961) H2B histone
                   [Zea mays]
                   262792
Seq. No.
Contig ID
                   4583 1.R1011
                   qw17\overline{0}0615616.h1
5'-most EST
```

5'-most EST gwl700615616.

Method BLASTX

NCBI GI g4204284

BLAST score 522

E value 3.0e-53

Match length 155



% identity 63

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 262793

Contig ID 4584 1.R1011

5'-most EST uC-zmroteosinte040b02b1

Method BLASTX
NCBI GI g1657619
BLAST score 711
E value 5.0e-75
Match length 260
% identity 51

NCBI Description (U72504) G5p [Arabidopsis thaliana] >gi_3068710 (AF049236)

putative transmembrane protein G5p [Arabidopsis thaliana]

Seq. No. 262794

Contig ID 4588 1.R1011

5'-most EST LIB3078-033-Q1-K1-D12

Seq. No. 262795
Contig ID 4592_1.R1011
5'-most EST uer700580601.h1

Seq. No. 262796 Contig ID 4595 1.R1011

5'-most EST LIB36-021-Q1-E1-F10

Method BLASTX
NCBI GI g2130104
BLAST score 396
E value 4.0e-38
Match length 103
% identity 76

NCBI Description histone H2A type 1 (clone wcH2A-9) - wheat

>gi_536894_dbj_BAA07279_ (D38090) protein H2A [Triticum
aestivum] >gi 1095225 prf 2108279B histone H2A:ISOTYPE=9

[Triticum aestivum]

Seq. No. 262797

Contig ID 4595 2.R1011

5'-most EST uC-zmflb73305g11b2

Method BLASTX
NCBI GI g2198851
BLAST score 165
E value 4.0e-11
Match length 34
% identity 91

NCBI Description (AF007785) cystathionine gamma-synthase [Zea mays]

Seq. No. 262798 Contig ID 4595 3.R1011

5'-most EST uC-zmflB73112h08b2

Seq. No. 262799 Contig ID 4596 1.R1011

5'-most EST LIB143-052-Q1-E1-G10

Method BLASTX



NCBI GI g548774
BLAST score 1045
E value 1.0e-114
Match length 258
% identity 79

NCBI Description 60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal

protein L7a - rice >gi 303855 dbj BAA02156 (D12631)

ribosomal protein L7A [Oryza sativa]

Seq. No. 262800

Contig ID 4596_2.R1011 5'-most EST xmt700263222.h1

Method BLASTX
NCBI GI g2894534
BLAST score 1423
E value 1.0e-158
Match length 289
% identity 93

NCBI Description (AJ224327) aquaporin [Oryza sativa]

Seq. No. 262801

Contig ID 4596_3.R1011

5'-most EST uC-zmflmo17163e07b1

Method BLASTX
NCBI GI g2894534
BLAST score 1340
E value 1.0e-148
Match length 292
% identity 88

NCBI Description (AJ224327) aquaporin [Oryza sativa]

Seq. No. 262802

Contig ID 4596 4.R1011

5'-most EST LIB3059-032-Q1-K1-E5

Method BLASTX
NCBI GI g548774
BLAST score 367
E value 3.0e-57
Match length 136
% identity 87

NCBI Description 60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal

protein L7a - rice >gi_303855_dbj BAA02156 (D12631)

ribosomal protein L7A [Oryza sativa]

Seq. No. 262803

Contig ID 4596_5.R1011

5'-most EST LIB3158-010-Q1-K1-D7

Method BLASTX
NCBI GI g1848281
BLAST score 412
E value 4.0e-40
Match length 78
% identity 100

NCBI Description (U87981) Sorghum bicolor membrane intrinsic (Mip1) protein,

partial sequence

Seq. No. 262804



```
4596 6.R1011
Contig ID
5'-most EST
                  uC-zmflb73160h07b2
                  BLASTX
Method
NCBI GI
                  q548774
BLAST score
                  494
E value
                  7.0e-50
                  136
Match length
% identity
                  74
                  60S RIBOSOMAL PROTEIN L7A >qi 542158 pir S38360 ribosomal
NCBI Description
                  protein L7a - rice >gi 303855 dbj BAA02156 (D12631)
                  ribosomal protein L7A [Oryza sativa]
Seq. No.
                  262805
                  4596 8.R1011
Contig ID
                  rvt700551477.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q548774
BLAST score
                  506
E value
                  3.0e-51
                  102
Match length
% identity
                  95
                  60S RIBOSOMAL PROTEIN L7A >qi 542158 pir S38360 ribosomal
NCBI Description
                  protein L7a - rice >qi 303855 dbj BAA02156 (D12631)
                  ribosomal protein L7A [Oryza sativa]
                  262806
Seq. No.
                   4596 9.R1011
Contig ID
                  uC-zmflmo17159f09a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2696804
BLAST score
                  254
                  8.0e-22
E value
Match length
                  47
                   96
% identity
                  (AB009665) water channel protein [Oryza sativa]
NCBI Description
                   262807
Seq. No.
                  4596 10.R1011
Contig ID
5'-most EST
                  LIB3069-023-Q1-K1-C5
Method
                  BLASTX
NCBI GI
                  q548774
BLAST score
                   469
                  8.0e-47
E value
Match length
                  134
                   74
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal
                   protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
                   ribosomal protein L7A [Oryza sativa]
                   262808
Seq. No.
```

4596 12.R1011 Contig ID LIB3076-017-Q1-K1-E3 5'-most EST

Method BLASTX NCBI GI q548774 BLAST score 345 4.0e-40 E value Match length 88



% identity 98
NCBI Description 60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631) ribosomal protein L7A [Oryza sativa]

Seq. No. 262809
Contig ID 4596_14.R1011
5'-most EST LIB3088-021-Q1-K1-D4
Method BLASTN
NCBI GI q1848280

NCBI GI g1848280
BLAST score 46
E value 1.0e-16
Match length 66
% identity 92

NCBI Description Sorghum bicolor membrane intrinsic protein (Mip1) mRNA,

partial cds

Seq. No. 262810 Contig ID 4598_1.R1011

5'-most EST LIB3060-047-Q1-K1-A6

Method BLASTX
NCBI GI g397396
BLAST score 281
E value 2.0e-24
Match length 123
% identity 53

NCBI Description (X66077) DNA-binding protein [Zea mays]

Seq. No. 262811

Contig ID 4598_2.R1011

5'-most EST uC-zmflmo170114g08b1

Method BLASTX
NCBI GI g397396
BLAST score 272
E value 1.0e-27
Match length 70
% identity 88

NCBI Description (X66077) DNA-binding protein [Zea mays]

Seq. No. 262812 Contig ID 4598_4.R1011

5'-most EST uC-zmflmo17320h04b1

Method BLASTN
NCBI GI g459267
BLAST score 657
E value 0.0e+00
Match length 980
% identity 99

NCBI Description Z.mays gene for HMG protein

 Seq. No.
 262813

 Contig ID
 4598_5.R1011

 5'-most EST
 uC-zmflb73283c06b2

Method BLASTX
NCBI GI g123378
BLAST score 541
E value 4.0e-55

```
Match length
                   131
                   82
% identity
                   DNA-BINDING PROTEIN MNB1B (HMG1-LIKE PROTEIN)
NCBI Description
                   >gi_100886_pir__S16670 high mobility group protein - maize
                   >gi_539062_pir__B47150 DNA-binding protein MNB1b - maize
                   >qi 22329 emb CAA41220 (X58282) high mobility group
                   protein [Zea mays]
                   262814
Seq. No.
                   4603 1.R1011
Contig ID
                   LIB3076-005-Q1-K1-A6
5'-most EST
Method
                   BLASTX
                   q3297819
NCBI GI
                   171
BLAST score
E value
                   4.0e-12
Match length
                   69
                   59
% identity
                   (AL031032) protein kinase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   262815
Seq. No.
                   4606 1.R1011
Contig ID
                   uC-z\overline{m}flb73083a09b2
5'-most EST
                   BLASTX
Method
                   q464980
NCBI GI
                   794
BLAST score
                   1.0e-84
E value
Match length
                   152
                   96
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 166422 (L06967)
                   ubiquitin carrier protein [Medicago satīva]
                   262816
Seq. No.
                   4607_1.R1011
Contig ID
5'-most EST
                   LIB3150-068-P2-K1-G3
                   262817
Seq. No.
                   4608 1.R1011
Contig ID
                   LIB3076-005-Q1-K1-B2
5'-most EST
                   262818
Seq. No.
                   4609 1.R1011
Contig ID
```

uC-zmflb73049f02b1 5'-most EST

BLASTX Method q1168893 NCBI GI BLAST score 230 E value 9.0e-23

Match length 176 43 % identity

G2/MITOTIC-SPECIFIC CYCLIN 1 (B-LIKE CYCLIN) (CYCMS1) NCBI Description

>qi 914861 emb CAA57559 (X82039) cycMs1 [Medicago sativa

subsp. X varia]

262819 Seq. No. 4610 1.R1011 Contig ID

5'-most EST LIB3076-004-Q1-K1-H1

Seq. No.

262825

Seq. No. 262820 Contig ID 4613 1.R1011 5'-most EST xsy700217322.h1 Method BLASTX NCBI GI q2760327 BLAST score 1227 E value 1.0e-135 Match length 284 % identity NCBI Description (AC002130) F1N21.12 [Arabidopsis thaliana] Seq. No. 262821 Contig ID 4615 1.R1011 5'-most EST LIB3059-015-Q1-K1-C8 Seq. No. 262822 Contig ID 4619 1.R1011 5'-most EST uC-zmflb73296e09b2 Method BLASTX NCBI GI q129727 BLAST score 196 1.0e-14 E value Match length 211 % identity 27 PROTEIN DISULFIDE ISOMERASE (PDI) (PROLYL 4- HYDROXYLASE NCBI Description BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (RETINA COGNIN) (R-COGNIN) Seq. No. 262823 Contig ID 4629 1.R1011 5'-most EST xsy700209022.h1 Method BLASTX NCBI GI g3088575 BLAST score 168 2.0e-11 E value 132 Match length % identity 30 (AF059531) protein arginine N-methyltransferase 3 [Homo NCBI Description sapiens] 262824 Seq. No. Contig ID 4637 1.R1011 5'-most EST LIB3076-004-Q1-K1-A9 BLASTX Method NCBI GI g2497820 BLAST score 2681 E value 0.0e+00Match length 553 96 % identity NCBI Description DNA REPLICATION LICENSING FACTOR MCM3 HOMOLOG (REPLICATION ORIGIN ACTIVATOR) (ROA PROTEIN) >gi_1076823_pir__S52247 probable replication origin activator protein ROA - maize (fragment) >gi_609290_emb_CAA82556_ (Z29368) ROA protein [Zea mays]

```
Contig ID
                   4638 1.R1011
5'-most EST
                   zuv700356441.h1
Method
                   BLASTX
                   q1825645
NCBI GI
BLAST score
                   304
                   2.0e-27
E value
Match length
                   72
% identity
                   76
                  (U88173) weak similarity to Arabidopsis thaliana
NCBI Description
                   ubiquitin-like protein 8 [Caenorhabditis elegans]
Seq. No.
                   262826
Contig ID
                   4638 2.R1011
5'-most EST
                   LIB3079-034-Q1-K1-D4
Method
                   BLASTX
NCBI GI
                   g1825645
BLAST score
                   303
                   2.0e-27
E value
Match length
                   72
                   75
% identity
                  (U88173) weak similarity to Arabidopsis thaliana
NCBI Description
                   ubiquitin-like protein 8 [Caenorhabditis elegans]
Seq. No.
                   262827
Contig ID
                   4638 4.R1011
5'-most EST
                   LIB3137-024-Q1-K1-B12
Method
                   BLASTX
NCBI GI
                   q1825645
BLAST score
                   279
                   1.0e-24
E value
                   72
Match length
% identity
                   69
NCBI Description
                  (U88173) weak similarity to Arabidopsis thaliana
                   ubiquitin-like protein 8 [Caenorhabditis elegans]
                   262828
Seq. No.
                   4638 5.R1011
Contig ID
5'-most EST
                   LIB3076-039-Q1-K1-C6
Method
                   BLASTX
                   q1825645
NCBI GI
BLAST score
                   249
E value
                   3.0e-21
Match length
                   72
% identity
                   67
                  (U88173) weak similarity to Arabidopsis thaliana
NCBI Description
                   ubiquitin-like protein 8 [Caenorhabditis elegans]
Seq. No.
                   262829
Contig ID
                   4638 6.R1011
                   LIB3\overline{1}50-055-Q1-N1-F12
5'-most EST
```

262830 Seq. No.

Contig ID 4638 8.R1011

5'-most EST LIB3136-014-Q1-K2-B12

262831 Seq. No. Contig ID 4639 1.R1011



```
5'-most EST
                  xjt700094536.h1
Seq. No.
                  262832
                  4642 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73280c03b2
Method
                  BLASTX
NCBI GI
                  q2191172
BLAST score
                  150
                  1.0e-09
E value
Match length
                  33
                  73
% identity
NCBI Description
                  (AF007270) contains similarity to GATA-type zinc fingers
                   (PS:PS00344) [Arabidopsis thaliana]
Seq. No.
                   262833
Contig ID
                   4643 1.R1011
5'-most EST
                  LIB3076-004-Q1-K1-C1
Method
                  BLASTX
                  q4102600
NCBI GI
BLAST score
                  525
                   6.0e-53
E value
                  229
Match length
% identity
                  55
                  (AF013467) ARF6 [Arabidopsis thaliana]
NCBI Description
                  262834
Seq. No.
                   4643 3.R1011
Contig ID
5'-most EST
                  uC-zmflb73039d01a2
                   262835
Seq. No.
                  4646 1.R1011
Contig ID
5'-most EST
                  LIB3076-003-Q1-K1-G3
                  262836
Seq. No.
                  4647 1.R1011
Contig ID
5'-most EST
                  LIB3181-006-P1-K2-A3
Method
                  BLASTX
                   g4455787
NCBI GI
BLAST score
                   259
                   2.0e-22
E value
Match length
                   106
% identity
                   42
NCBI Description
                  (AL035536) putative DNA polymerase accessory protein
                   [Schizosaccharomyces pombe]
                   262837
Seq. No.
Contig ID
                   4647_2.R1011
5'-most EST
                   uC-zmflb73283d09b2
Method
                  BLASTX
NCBI GI
                   q4455787
                   202
BLAST score
```

8.0e-16 E value Match length 86 % identity 41

(AL035536) putative DNA polymerase accessory protein NCBI Description

[Schizosaccharomyces pombe]



 Seq. No.
 262838

 Contig ID
 4651_1.R1011

 5'-most EST
 fwa700101605.h1

Method BLASTX
NCBI GI g2760832
BLAST score 492
E value 1.0e-49
Match length 162
% identity 62

NCBI Description (AC003105) similar to barley ids-4 gene product

[Arabidopsis thaliana]

Seq. No. 262839 Contiq ID 4651 2.R1011

5'-most EST uC-zmflmo17299b09b1

Method BLASTX
NCBI GI g2760832
BLAST score 392
E value 1.0e-37
Match length 236
% identity 43

NCBI Description (AC003105) similar to barley ids-4 gene product

[Arabidopsis thaliana]

Seq. No. 262840

Contig ID 4653 1.R1011

5'-most EST LIB3076-003-Q1-K1-H2

Seq. No. 262841

Contig ID 4659_1.R1011 5'-most EST cyk700047325.f1

Method BLASTX
NCBI GI g3123161
BLAST score 547
E value 1.0e-55
Match length 430
% identity 36

NCBI Description HYPOTHETICAL 77.0 KD TRP-ASP REPEATS CONTAINING PROTEIN

F35G12.4 IN CHROMOSOME III >gi_3876723_emb_CAA86335_

(Z46242) similar to beta-transducin; cDNA EST EMBL:Z14703 comes from this gene; cDNA EST EMBL:D67532 comes from this gene; cDNA EST EMBL:D69055 comes from this gene; cDNA EST EMBL:D64515 comes from this gene; cDNA EST EMBL:D655

Seq. No. 262842

Contig ID 4659_2.R1011

5'-most EST uC-zmflmo17285b06b1

Method BLASTX
NCBI GI g3892150
BLAST score 163
E value 7.0e-11
Match length 141
% identity 30

NCBI Description (Z46242) similar to WD domain, G-beta repeat; cDNA EST yk283e3.3 comes from this gene; cDNA EST yk238e2.3 comes

from this gene; cDNA EST yk283e3.5 comes from this gene; cDNA EST yk238e2.5 comes from this gene [Caenorhabditis el



Seq. No. 262843

Contig ID 4659_4.R1011 5'-most EST tzu700203890.h1

Seq. No. 262844

Contig ID 4659 5.R1011

5'-most EST LIB3150-085-P1-N1-B2

Seq. No. 262845

Contig ID 4660 1.R1011

5'-most EST LIB3076-003-Q1-K1-E7

Seq. No. 262846

Contig ID 4663 1.R1011

5'-most EST uC-zmflmo17335g12b1

Method BLASTX
NCBI GI g3850821
BLAST score 1419
E value 1.0e-157
Match length 402
% identity 71

NCBI Description (Y18350) U2 snRNP auxiliary factor, large subunit

[Nicotiana plumbaginifolia]

Seq. No. 262847

Contig ID 4663_2.R1011

5'-most EST uC-zmflb73161d12b2

Method BLASTX
NCBI GI g4006898
BLAST score 562
E value 6.0e-58
Match length 159
% identity 75

NCBI Description (Z99708) splicing factor-like protein [Arabidopsis

thaliana]

Seq. No. 262848

Contig ID 4663_3.R1011 5'-most EST xjt700092307.h1

Method BLASTX
NCBI GI g3850821
BLAST score 482
E value 1.0e-49
Match length 150
% identity 74

NCBI Description (Y18350) U2 snRNP auxiliary factor, large subunit

[Nicotiana plumbaginifolia]

Seq. No. 262849

Contig ID 4663_5.R1011 5'-most EST xyt700342514.h1

Method BLASTX
NCBI GI g3850823
BLAST score 252
E value 3.0e-21
Match length 67

```
% identity
NCBI Description
                   (Y18351) U2 snRNP auxiliary factor, large subunit
                   [Nicotiana plumbaginifolia]
Seq. No.
                   262850
                   4663 6.R1011
Contig ID
                   uC-zmflb73144a10b1
5'-most EST
Method
                   BLASTX
                   a3850821
NCBI GI
BLAST score
                   353
                   2.0e-33
E value
                   107
Match length
% identity
                   68
                  (Y18350) U2 snRNP auxiliary factor, large subunit
NCBI Description
                   [Nicotiana plumbaginifolia]
Seq. No.
                   262851
                   4663 7.R1011
Contig ID
5'-most EST
                   xyt700342353.h1
                   BLASTX
Method
NCBI GI
                   q4006898
BLAST score
                   319
                   1.0e-29
E value
Match length
                   84
                   69
% identity
NCBI Description
                  (Z99708) splicing factor-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   262852
Contig ID
                   4663 8.R1011
5'-most EST
                   fwa700101417.hl
Method
                   BLASTX
                   q3850823
NCBI GI
BLAST score
                   253
                   3.0e-21
E value
Match length
                   140
                   61
% identity
NCBI Description
                  (Y18351) U2 snRNP auxiliary factor, large subunit
                   [Nicotiana plumbaginifolia]
                   262853
Seq. No.
                   4663 11.R1011
Contig ID
5'-most EST
                   nbm700465077.h1
                   262854
Seq. No.
                   4670_1.R1011
Contig ID
5'-most EST
                  LIB3076-003-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                   q1168749
```

Method BLASTX
NCBI GI g1168749
BLAST score 164
E value 4.0e-22
Match length 88
% identity 70

NCBI Description CALMODULIN-6 >gi_1076298_pir__ S35187 calmodulin 6 - Arabidopsis thaliana >gi_16227_emb_CAA78059_ (Z12024)

calmodulin [Arabidopsis thaliana]



```
Seq. No.
                  262855
                  4673 1.R1011
Contig ID
5'-most EST
                  uwc700154686.h1
                  BLASTX
Method
                  g1800219
NCBI GI
BLAST score
                  2435
                  0.0e+00
E value
Match length
                  515
% identity
                  92
                  (U56731) phytochrome C [Sorghum bicolor]
NCBI Description
Seq. No.
                  262856
Contig ID
                  4676 1.R1011
5'-most EST
                  LIB3076-003-Q1-K1-E1
                  262857
Seq. No.
Contig ID
                  4677 1.R1011
5'-most EST
                  LIB3076-002-Q1-K1-E4
                  262858
Seq. No.
Contig ID
                  4680 1.R1011
5'-most EST
                  LIB84-001-Q1-E1-F8
Seq. No.
                  262859
Contig ID
                  4681 1.R1011
5'-most EST
                  LIB3088-041-Q1-K1-H5
Method
                  BLASTN
NCBI GI
                  g487295
BLAST score
                  69
E value
                  2.0e-30
Match length
                  137
% identity
                  88
NCBI Description Rice mRNA EN242, partial sequence
                  262860
Seq. No.
Contig ID
                  4682_1.R1011
5'-most EST
                  LIB3156-005-Q1-K1-B10
Method
                  BLASTX
                  q3928084
NCBI GI
BLAST score
                  167
E value
                  2.0e-11
Match length
                  56
                  52
% identity
NCBI Description
                  (AC005770) retrotransposon-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  262861
Contig ID
                  4684 1.R1011
5'-most EST
                  uC-zmflb73148e07b1
Method
                  BLASTX
NCBI GI
                  g3776015
BLAST score
                  441
E value
                  1.0e-43
```

Match length 182 % identity 49

NCBI Description (AJ010471) RNA helicase [Arabidopsis thaliana] >gi_4249378_gb_AAD14475_ (AC005966) Identical to



gb_AJ010471 mRNA for DEAD box RNA helicase (RH22) from Arabidopsis thaliana. EST gb_Y11191 comes from this gene. [Arabidopsis thaliana]

Seq. No. 262862

Contig ID 4685_1.R1011 5'-most EST xmt700263306.h1

Method BLASTX
NCBI GI g1707928
BLAST score 2502
E value 0.0e+00
Match length 518
% identity 95

NCBI Description GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 2

PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE

PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE

ADENYL TRANSFERASE) >gi 1076806 pir S49439

glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) - maize >gi 558365 emb CAA86227 (Z38111) ADP-glucose

pyrophosphorylase [Zea mays]

Seq. No. 262863

Contig ID 4688 1.R1011 5'-most EST pmx700084635.h1

Method BLASTX
NCBI GI g1498053
BLAST score 1014
E value 1.0e-110
Match length 221
% identity 90

NCBI Description (U64436) ribosomal protein S8 [Zea mays]

Seq. No. 262864

Contig ID 4688_2.R1011 5'-most EST rv1700457262.h1

Method BLASTX
NCBI GI g1498053
BLAST score 985
E value 1.0e-107
Match length 221
% identity 86

NCBI Description (U64436) ribosomal protein S8 [Zea mays]

Seq. No. 262865

Contig ID 4688_3.R1011 5'-most EST pmx700090791.h1

Method BLASTX
NCBI GI g1498053
BLAST score 458
E value 1.0e-45
Match length 135
% identity 69

NCBI Description (U64436) ribosomal protein S8 [Zea mays]

Seq. No. 262866 Contig ID 4688_4.R1011

5'-most EST uC-zmflb73106b02a1



```
Method
                  BLASTX
                  g1498053
NCBI GI
BLAST score
                  253
                  7.0e-22
E value
                  49
Match length
                  100
% identity
                  (U64436) ribosomal protein S8 [Zea mays]
NCBI Description
                  262867
Seq. No.
                  4688 5.R1011
Contig ID
                  LIB3150-109-P2-K1-C8
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1498053
BLAST score
                  212
E value
                   6.0e-17
Match length
                   41
                  100
% identity
                  (U64436) ribosomal protein S8 [Zea mays]
NCBI Description
Seq. No.
                   262868
                   4688 8.R1011
Contig ID
                  xjt700093722.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g1498053
                   236
BLAST score
                  7.0e-30
E value
Match length
                  81
% identity
                   89
                  (U64436) ribosomal protein S8 [Zea mays]
NCBI Description
                   262869
Seq. No.
                   4688 9.R1011
Contig ID
5'-most EST
                   uC-zmflb73295a03a1
Method
                   BLASTN
                   g1498052
NCBI GI
                   90
BLAST score
                   8.0e-43
E value
Match length
                   193
                   92
% identity
NCBI Description Zea mays ribosomal protein S8 mRNA, complete cds
                   262870
Seq. No.
Contig ID
                   4688 13.R1011
5'-most EST
                   LIB3076-002-Q1-K1-A1
                   BLASTX
Method
NCBI GI
                   g1498053
BLAST score
                   366
E value
                   3.0e-35
Match length
                   77
% identity
                   91
NCBI Description (U64436) ribosomal protein S8 [Zea mays]
Seq. No.
                   262871
                   4689 1.R1011
Contig ID
```

Seq. No. 262872

5'-most EST

uC-zmflb73196e06b1



Contig ID

4690 1.R1011

```
5'-most EST
                     uC-zmroteosinte032e05b1
  Method
                     BLASTX
  NCBI GI
                     q122022
  BLAST score
                     452
                     9.0e-45
  E value
                     115
  Match length
  % identity
                     83
                     HISTONE H2B >gi 283025 pir S22323 histone H2B - wheat
NCBI Description
                     >qi 21801 emb CAA42530 (X59873) histone H2B [Triticum
                     aestivum]
  Seq. No.
                     262873
                     4690 2.R1011
  Contig ID
                     LIB3088-034-Q1-K1-D10
  5'-most EST
                     BLASTX
  Method
  NCBI GI
                     q399853
                     224
  BLAST score
  E value
                     4.0e-18
                     73
  Match length
                     71
   % identity
                     HISTONE H2B.1 >gi 283041 pir S28048 histone H2B - maize
  NCBI Description
                     >gi 22323 emb CAA40564 (X57312) H2B histone [Zea mays]
                     262874
  Seq. No.
                     4690 3.R1011
  Contig ID
   5'-most EST
                     pmx700082035.h1
                     BLASTX
  Method
  NCBI GI
                     g1708107
  BLAST score
                     498
                     6.0e-50
  E value
  Match length
                     116
   % identity
                     91
   NCBI Description HISTONE H2B >gi 473605 (U08226) histone H2B [Zea mays]
                     262875
   Seq. No.
                     4690 4.R1011
   Contig ID
   5'-most EST
                     LIB3088-049-Q1-K1-A5
   Method
                     BLASTX
   NCBI GI
                     g1362184
   BLAST score
                     390
                     2.0e-37
   E value
                     91
   Match length
                     88
   % identity
   NCBI Description histone H2B-8 - wheat >gi_531058_dbj_BAA07157_ (D37943)
                     protein H2B-8 [Triticum aestivum]
                     262876
   Seq. No.
                     4690 5.R1011
   Contig ID
                     uC-zmflmo17041g12b1
   5'-most EST
   Method
                     BLASTX
   NCBI GI
                     q399853
                     445
   BLAST score
   E value
                     6.0e-44
                     91
   Match length
                     100
   % identity
   NCBI Description HISTONE H2B.1 >gi_283041_pir__S28048 histone H2B - maize
```

```
>gi_22323_emb_CAA40564_ (X57312) H2B histone [Zea mays]
```

Seq. No. 262877

Contig ID 4690 6.R1011

5'-most EST LIB3076-004-Q1-K1-D12

Method BLASTX
NCBI GI g122022
BLAST score 448
E value 3.0e-44
Match length 115
% identity 82

NCBI Description HISTONE H2B >gi_283025_pir__S22323 histone H2B - wheat

>gi 21801 emb CAA42530 (X59873) histone H2B [Triticum

aestivum]

Seq. No. 262878

Contig ID 4690 7.R1011

5'-most EST LIB3068-024-Q1-K1-B6

Method BLASTX
NCBI GI g122022
BLAST score 445
E value 7.0e-44
Match length 115
% identity 81

NCBI Description HISTONE H2B >gi 283025 pir S22323 histone H2B - wheat

>gi 21801 emb CAA42530 (X59873) histone H2B [Triticum

aestivum]

Seq. No. 262879

Contig ID 4690_8.R1011

5'-most EST LIB3067-005-Q1-K1-G10

Method BLASTX
NCBI GI g3913804
BLAST score 448
E value 4.0e-44
Match length 116
% identity 82

NCBI Description HISTONE H2B.3 >gi 577825 emb CAA49584 (X69960) H2B histone

[Zea mays]

Seq. No. 262880 Contig ID 4690_9.R1011

5'-most EST uC-zmflb73163d03a1

Method BLASTX
NCBI GI g399854
BLAST score 335
E value 7.0e-31
Match length 80
% identity 88

NCBI Description HISTONE H2B.2 >gi_283042_pir__S28049 histone H2B - maize

>gi_22325_emb_CAA40565_ (X57313) H2B histone [Zea mays]

Seq. No. 262881

Contig ID 4690 10.R1011

5'-most EST LIB3068-048-Q1-K1-E11

Method BLASTX NCBI GI g122022



BLAST score 448 E value 3.0e-44 Match length 92 % identity 99

NCBI Description HISTONE H2B >gi_283025_pir__S22323 histone H2B - wheat >gi_21801_emb_CAA42530_ (X59873) histone H2B [Triticum

aestivum]

Seq. No. 262882

Contig ID 4690_11.R1011

5'-most EST uC-zmroteosinte011e09b1

Method BLASTX
NCBI GI g399854
BLAST score 391
E value 2.0e-37
Match length 91
% identity 88

NCBI Description HISTONE H2B.2 >gi_283042_pir__S28049 histone H2B - maize

>gi 22325 emb CAA $\overline{4}$ 0565 (X57 $\overline{3}\overline{1}$ 3) H2B histone [Zea mays]

Seq. No. 262883

Contig ID 4690 12.R1011

5'-most EST LIB3150-117-P2-K1-C4

Method BLASTX
NCBI GI g1708107
BLAST score 260
E value 2.0e-22
Match length 65

Match length 65 % identity 83

NCBI Description HISTONE H2B >gi_473605 (U08226) histone H2B [Zea mays]

Seq. No. 262884

Contig ID 4690_13.R1011 5'-most EST uC-zmflb73025e02a1

Method BLASTX
NCBI GI g1346251
BLAST score 370
E value 2.0e-35

Match length 87 87 identity 87

NCBI Description 'HISTONE H2B.4 >gi_577819_emb_CAA49585_ (X69961) H2B histone

[Zea mays]

Seq. No. 262885

Contig ID 4690_14.R1011

5'-most EST LIB3062-020-Q1-K1-A3

Method BLASTX
NCBI GI g1708107
BLAST score 324
E value 6.0e-30
Match length 81
% identity 83

NCBI Description HISTONE H2B >gi_473605 (U08226) histone H2B [Zea mays]

Seq. No. 262886

Contig ID 4690_15.R1011 5'-most EST uC-zmflmo17079e10a1

```
Method BLASTN
NCBI GI g531055
BLAST score 69
E value 2.0e-30
```

Match length 81 % identity 96

NCBI Description Wheat mRNA for protein H2B-6, complete cds

Seq. No. 262887

Contig ID 4690 18.R1011

5'-most EST LIB3088-046-Q1-K1-H2

Method BLASTX
NCBI GI g3021489
BLAST score 170
E value 5.0e-12
Match length 36

% identity 97

NCBI Description (AJ224934) histone H2B [Lycopersicon esculentum]

Seq. No. 262888

Contig ID 4690_27.R1011 5'-most EST xjt700094901.h1

Method BLASTN
NCBI GI g21800
BLAST score 53
E value 7.0e-21
Match length 57

% identity 98

NCBI Description T.aestivum L mRNA for histone H2B

Seq. No. 262889

Contig ID 4691_1.R1011

5'-most EST LIB3076-002-Q1-K1-A6

5'-most EST uC-zmflmo17287f10b1

Seq. No. 262891

Contig ID 4693_1.R1011

5'-most EST LIB143-015-Q1-E1-E8

Method BLASTX
NCBI GI g4646206
BLAST score 1623
E value 0.0e+00
Match length 402
% identity 75

NCBI Description (AC007230) Contains similarity to gb_D13630 KIAA0005 gene from Homo saniens ESTs gb_T45345 gb_T21086 gb_R90360

from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360, gb_T20468, gb_T45191 and gb_AI100459 come from this gene.

[Arabidopsis thaliana]

Seq. No. 262892

Contig ID - 4693 2.R1011

5'-most EST LIB3\overline{15}2-057-P1-K1-H5

Method BLASTX NCBI GI g266398



BLAST score 734 E value 1.0e-77 Match length 155 % identity 85

NCBI Description TRYPSIN/FACTOR XIIA INHIBITOR PRECURSOR (HAGEMAN FACTOR INHIBITOR) (CHFI) >gi 68849 pir TIZM1 trypsin/factor XIIa

inhibitor precursor - maize >gi 22327 emb CAA37998 (X54064) corn Hageman factor inhibitor [Zea mays]

Seq. No. 262893

Contig ID 4693 3.R1011

5'-most EST uC-zmflmo17317b07a1

Method BLASTX
NCBI GI 94646206
BLAST score 1613
E value 1.0e-180
Match length 403
% identity 74

NCBI Description (AC007230) Contains similarity to gb_D13630 KIAA0005 gene

from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360, gb T20468, gb T45191 and gb AI100459 come from this gene.

[Arabidopsis thaliana]

Seq. No. 262894

Contig ID 4693 5.R1011

5'-most EST LIB3150-110-P2-K1-E1

Seq. No. 262895

Contig ID 4693_7.R1011

5'-most EST LIB3059-033-Q1-K1-E6

Method BLASTN
NCBI GI g22326
BLAST score 226
E value 1.0e-124
Match length 264
% identity 97

NCBI Description Z.mays gene for Hageman factor inhibitor

Seq. No. 262896

Contig ID 4694_1.R1011 5'-most EST ntr700075370.h1

Seq. No. 262897

Contig ID 4698 1.R1011

5'-most EST LIB $3\overline{0}88$ -045-Q1-K1-D2

Seq. No. 262898

Contig ID 4698 2.R1011

5'-most EST LIB3067-038-Q1-K1-E8

Seq. No. 262899

Contig ID 4699_1.R1011 5'-most EST pwr700453341.h1

Method BLASTX
NCBI GI g1869901
BLAST score 240
E value 7.0e-20



```
120
Match length
                   33
% identity
                  (X99699) XIAP associated factor-1 (ZAP-1) [Homo sapiens]
NCBI Description
                  262900
Seq. No.
                   4700 1.R1011
Contig ID
                  uC\text{-}zmflb73013g04b1\\
5'-most EST
Method
                  BLASTX
                   g4204281
NCBI GI
BLAST score
                   261
                   4.0e-22
E value
Match length
                   264
                   28
% identity
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   262901
                   4700 2.R1011
Contig ID
5'-most EST
                  LIB3076-001-Q1-K1-H8
                   BLASTN
Method
                   q949979
NCBI GI
                   50
BLAST score
                   8.0e-19
E value
Match length
                   69
                   93
% identity
NCBI Description Z.mays Glossy2 locus DNA
                   262902
Seq. No.
Contig ID
                   4700 4.R1011
                   LIB3158-003-Q1-K1-F7
5'-most EST
                   262903
Seq. No.
Contig ID
                   4701 1.R1011
5'-most EST
                   uC-zmflb73235a12b2
                   262904
Seq. No.
                   4701 2.R1011
Contig ID
5'-most EST
                   yyf700351715.h1
                   262905
Seq. No.
                   4705 1.R1011
Contig ID
5'-most EST
                   uC-zmrob73077h05b1
Method
                   BLASTX
NCBI GI
                   g4056500
                   773
BLAST score
E value
                   4.0e-82
Match length
                   213
                   70
% identity
NCBI Description
                  (AC005896) putative acetyltransferase [Arabidopsis
                   thaliana]
                   262906
Seq. No.
```

Contig ID 4705_2.R1011
5'-most EST zuv700356235.h1
Method BLASTX
NCBI GI g4056500
BLAST score 690

8.0e-73

E value



Match length 185 % identity 71

(AC005896) putative acetyltransferase [Arabidopsis NCBI Description

thaliana]

262907 Seq. No.

4709 1.R1011 Contig ID ntr700072506.h1 5'-most EST

BLASTX Method g3044214 NCBI GI BLAST score 2728 E value 0.0e+00Match length 647 79 % identity

(AF057044) acyl-CoA oxidase [Arabidopsis thaliana] NCBI Description

262908 Seq. No.

Contig ID 4710 1.R1011

LIB3076-001-Q1-K1-H5 5'-most EST

262909 Seq. No.

Contig ID 4712 1.R1011

5'-most EST uC-zmflb73091b05b2

Method BLASTX g3341688 NCBI GI BLAST score 986

1.0e-107 E value Match length 259 % identity 68

(AC003672) putative casein kinase II beta subunit NCBI Description

[Arabidopsis thaliana]

262910 Seq. No. 4712 3.R1011 Contig ID 5'-most EST ypc700804642.h1

Seq. No. 262911 Contig ID 4712 4.R1011 5'-most EST dyk700103435.hl

262912 Seq. No.

Contig ID 4713 1.R1011

5'-most EST uC-zmflb73158g11b2

Method BLASTX NCBI GI g3152605 BLAST score 380 E value 7.0e-36 Match length 87 % identity

NCBI Description (AC004482) hypothetical protein [Arabidopsis thaliana]

262913 Seq. No. Contig ID 4713 2.R1011

5'-most EST LIB3088-006-Q1-K1-C3

Method BLASTX NCBI GI g3152605 BLAST score 398

5'-most EST

```
E value
                     1.0e-38
  Match length
                     91
% identity
                     77
                    (AC004482) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
  Seq. No.
                     262914
  Contig ID
                     4714 1.R1011
                     LIB3069-003-Q1-K1-G12
  5'-most EST
  Method
                     BLASTX
  NCBI GI
                     g4335763
  BLAST score
                     438
                     3.0e-43
  E value
  Match length
                     124
                     72
  % identity
  NCBI Description
                    (AC006284) unknown protein [Arabidopsis thaliana]
  Seq. No.
                     262915
  Contig ID
                     4717 1.R1011
  5'-most EST
                     uwc700150831.h1
  Method
                     BLASTX
  NCBI GI
                     q2444174
  BLAST score
                     2142
  E value
                     0.0e + 00
  Match length
                     549
  % identity
                     74
  NCBI Description (U94781) unconventional myosin [Helianthus annuus]
  Seq. No.
                     262916
  Contig ID
                     4717 2.R1011
  5'-most EST
                     LIB3069-054-Q1-K1-B8
                     BLASTX
  Method
  NCBI GI
                     q479413
  BLAST score
                     536
                     1.0e-54
  E value
                     233
  Match length
  % identity
                     52
  NCBI Description myosin-like protein - Arabidopsis thaliana
                     262917
  Seq. No.
  Contig ID
                     4718 1.R1011
  5'-most EST
                     wty700165417.h1
  Method
                     BLASTX
                     g1172977
  NCBI GI
  BLAST score
                     807
  E value
                     3.0e-86
  Match length
                     187
                     82
  % identity
  NCBI Description
                     60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
                     ribosomal protein L18 [Arabidopsis thaliana]
                     262918
  Seq. No.
  Contig ID
                     4718 2.R1011
  5'-most EST
                     afb700380931.h1
                     262919
  Seq. No.
                     4718 3.R1011
  Contig ID
```

36452

LIB3088-025-Q1-K1-F4

Method BLASTX NCBI GI g3334112 392 BLAST score 9.0e-38 E value 89 Match length 84 % identity ACYL-COA-BINDING PROTEIN (ACBP) >qi 1938236 emb CAA70200 NCBI Description (Y08996) acyl-CoA-binding protein [Ricinus communis] 262920 Seq. No. 4718 4.R1011 Contig ID LIB3151-038-Q1-K1-C3 5'-most EST BLASTX Method NCBI GI q1172977 BLAST score 451 1.0e-44 E value Match length 121 % identity 74 60S RIBOSOMAL PROTEIN L18 >qi 606970 (U15741) cytoplasmic NCBI Description ribosomal protein L18 [Arabidopsis thaliana] 262921 Seq. No. Contig ID 4718 5.R1011 LIB3059-040-Q1-K1-H4 5'-most EST BLASTX Method NCBI GI g1172977 BLAST score 610 E value 3.0e-63146 Match length

79 % identity NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic

ribosomal protein L18 [Arabidopsis thaliana]

4718 6.R1011 Contig ID 5'-most EST LIB3115-008-Q1-K1-A3 Method BLASTX NCBI GI g3334112 392 BLAST score 9.0e-38 E value 89

262922

Match length 84 % identity

Seq. No.

NCBI Description ACYL-COA-BINDING PROTEIN (ACBP) >gi 1938236 emb CAA70200_

(Y08996) acyl-CoA-binding protein [Ricinus communis]

262923 Seq. No.

4718_7.R1011 Contig ID 5'-most EST xsy700209004.h1

Method BLASTX NCBI GI q1172977 BLAST score 499 E value 3.0e-50 Match length 118 81 % identity

60S RIBOSOMAL PROTEIN L18 >qi 606970 (U15741) cytoplasmic NCBI Description

ribosomal protein L18 [Arabidopsis thaliana]



Seq. No. 262924

Contig ID 4719_1.R1011

5'-most EST uC-zmflb73114c05a2

Method BLASTX
NCBI GI g3980417
BLAST score 224
E value 4.0e-18
Match length 59
% identity 69

NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No. 262925

Contig ID 4719_2.R1011 5'-most EST xmt700258345.h1

Method BLASTX
NCBI GI g4512675
BLAST score 2052
E value 0.0e+00
Match length 503
% identity 78

NCBI Description (AC006931) putative citrate synthase [Arabidopsis thaliana]

Seq. No. 262926

Contig ID 4719_3.R1011

5'-most EST uC-zmflb73086c07b2

Method BLASTX
NCBI GI g3421102
BLAST score 1175
E value 1.0e-129
Match length 270

% identity 81

NCBI Description (AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis

thaliana]

Seq. No. 262927

Contig ID 4719_4.R1011

5'-most EST uC-zmflb73180c03b1

Seq. No. 262928

Contig ID 4719 5.R1011

5'-most EST LIB3059-002-Q1-K2-G5

Method BLASTX
NCBI GI g3421102
BLAST score 536
E value 2.0e-54
Match length 131
% identity 78

NCBI Description (AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis

thaliana]

Seq. No. 262929

Contig ID 4719_6.R1011 5'-most EST dyk700104985.h1

Method BLASTX
NCBI GI g3421104
BLAST score 613
E value 8.0e-64



Match length 135 % identity 85

NCBI Description (AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis

thaliana]

Seq. No. 262930

Contig ID 4719_7.R1011 5'-most EST tfd700574359.h2

Seq. No. 262931

Contig ID 4727_1.R1011 5'-most EST nbm700475015.h1

Method BLASTN
NCBI GI g2342495
BLAST score 62

E value 6.0e-26 Match length 162 % identity 85

NCBI Description Ananas comosus mRNA for bromelain, complete cds

Seq. No. 262932

Contig ID 4733_1.R1011 5'-most EST mwy700441262.h1

Method BLASTX
NCBI GI g3367537
BLAST score 330
E value 2.0e-30
Match length 141
% identity 53

NCBI Description (AC004392) Contains similarity to ANK repeat region of

Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi_485107 from Caenorhabditis elegans cosmid gb_U00049. This gene is continued from unannotated gene on BAC F19K23 gb_AC000375.

[Arabid

Seq. No. 262933

Contig ID 4736_1.R1011 5'-most EST ceu700429238.h1

Method BLASTX
NCBI GI g1076715
BLAST score 272
E value 1.0e-23
Match length 85
% identity 52

NCBI Description abscisic acid-induced protein HVA22 - barley >gi_404589

(L19119) A22 [Hordeum vulgare]

Seq. No. 262934

Contig ID 4739_1.R1011

5'-most EST uC-zmflb73245b10b2

Seq. No. 262935

Contig ID 4741 1.R1011

5'-most EST uC-zmflmo17269a08b1

Method BLASTX
NCBI GI g1169528
BLAST score 2272



E value 0.0e + 00446 Match length 100 % identity ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2) NCBI Description (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi 602253 (U17973) enolase [Zea mays] 262936 Sea. No. 4741 2.R1011 Contig ID uC-zmflmo17270g02a1 5'-most EST BLASTX Method NCBI GI g1076715 BLAST score 280 2.0e-24 E value Match length 92 53 % identity abscisic acid-induced protein HVA22 - barley >gi 404589 NCBI Description (L19119) A22 [Hordeum vulgare] 262937 Seq. No. 4741 3.R1011 Contig ID uC-zmroteosinte102d07b2 5'-most EST BLASTX Method g1076715 NCBI GI BLAST score 280 9.0e-25 E value Match length 85 55 % identity abscisic acid-induced protein HVA22 - barley >gi_404589 NCBI Description (L19119) A22 [Hordeum vulgare] 262938 Seq. No. 4741 4.R1011 Contig ID uC-zmflb73379d08a1 5'-most EST BLASTX Method g1076660 NCBI GI 735 BLAST score E value 7.0e-79 295 Match length 60 % identity D13F(MYBST1) protein - potato >gi 786426_bbs_159122 NCBI Description (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum] 262939 Seq. No.

Seq. No. 262939 Contig ID 4741_5.R1011 5'-most EST uC-zmflMo17018g08b1

Method BLASTX
NCBI GI g1076660
BLAST score 426
E value 7.0e-42
Match length 138
% identity 67

NCBI Description D13F(MYBST1) protein - potato >gi_786426_bbs_159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes,



262940

4741 8.R1011

leaf, Peptide, 342 aa] [Solanum tuberosum]

uC-zmflb73169c02a1 5'-most EST Method BLASTN NCBI GI q602252 219 BLAST score 1.0e-120 E value Match length 239 99 % identity

Seq. No.

Contig ID

Zea mays enolase (eno2) mRNA, complete cds NCBI Description

Seq. No. 262941 Contig ID 4741 9.R1011

5'-most EST LIB3118-003-Q1-K1-C12

Method BLASTX NCBI GI g1169528 BLAST score 549 3.0e-56 E value Match length 136 % identity 84

ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2) NCBI Description

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi 602253 (U17973)

enolase [Zea mays]

262942 Seq. No. Contig ID 4743 1.R1011

uC-zmroB73070c01b1 5'-most EST

BLASTX Method q3201627 NCBI GI BLAST score 1543 1.0e-172 E value Match length 342

80 % identity

(AC004669) putative SWH1 protein [Arabidopsis thaliana] NCBI Description

Seq. No. 262943

4744_1.R1011 Contig ID

LIB3076-055-Q1-K1-F7 5'-most EST

Method BLASTX NCBI GI q3121829 BLAST score 204 5.0e-16E value Match length 75 51 % identity

NCBI Description CHROMATIN ASSEMBLY FACTOR I P60 SUBUNIT (CAF-I 60 KD

SUBUNIT) >gi_2134915_pir__B56731 chromatin assembly factor I p60 chain - human >gi 882260 (U20980) chromatin assembly

factor-I p60 subunit [Homo sapiens]

262944 Seq. No.

Contig ID 4747 1.R1011 rv1700454956.h1 5'-most EST

Method BLASTX g2500195 NCBI GI BLAST score 872



E value 1.0e-93 Match length 197 % identity 84

NCBI Description RAC-LIKE GTP BINDING PROTEIN RHO1 >gi_974780_emb_CAA89050_

(Z49191) small G protein [Beta vulgaris]

Seq. No. 262945

Contig ID 4750_1.R1011 5'-most EST uwc700154395.h1

Method BLASTX
NCBI GI g1170507
BLAST score 1085
E value 1.0e-119
Match length 221
% identity 94

NCBI Description EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3)

>gi_100276_pir__S22579 translation initiation factor eIF-4A
- curled-leaved tobacco >gi_19699_emb_CAA43514_ (X61206)
nicotiana eukaryotic translation initiation factor 4A

[Nicotiana plumbaginifolia]

Seq. No. 262946

Contig ID 4750 2.R1011

5'-most EST LIB3\overline{1}58-017-Q1-K1-A8

Method BLASTX
NCBI GI g2773184
BLAST score 246
E value 7.0e-21
Match length 49
% identity 94

NCBI Description (AF039720) similar to the "DEAD" box family of helicases;

most similar to eukaryotic initiation factor 4A

[Caenorhabditis elegans]

Seq. No. 262947

Contig ID 4752 1.R1011

5'-most EST LIB3076-030-Q1-K1-C2

Method BLASTX
NCBI GI g2995380
BLAST score 451
E value 2.0e-44
Match length 110
% identity 78

NCBI Description (AJ001903) thioredoxin H [Triticum durum]

Seq. No. 262948

Contig ID 4752_2.R1011

5'-most EST uC-zmflmo17265f12b1

Method BLASTX
NCBI GI g2995380
BLAST score 253
E value 7.0e-22
Match length 60
% identity 77

NCBI Description (AJ001903) thioredoxin H [Triticum durum]

Seq. No. 262949

Seq. No.

262954

```
Contig ID
                  4757 1.R1011
5'-most EST
                  LIB3076-055-Q1-K1-E2
                  BLASTX
Method
NCBI GI
                  q516118
BLAST score
                  1322
E value
                  1.0e-151
                  341
Match length
                  79
% identity
NCBI Description
                  (L08469) envelope Ca2+-ATPase [Arabidopsis thaliana]
Seq. No.
                  262950
                  4759 1.R1011
Contig ID
5'-most EST
                  ymt700219148.h1
Method
                  BLASTX
NCBI GI
                  g1362162
BLAST score
                  1668
E value
                  0.0e+00
                  469
Match length
                  63
% identity
                  beta-glucosidase BGQ60 precursor - barley >gi 804656
NCBI Description
                  (L41869) beta-glucosidase [Hordeum vulgare]
                  262951
Seq. No.
                  4759 2.R1011
Contig ID
5'-most EST
                  uC-zmflmo17176c05b1
Method
                  BLASTX
                  g1143864
NCBI GI
BLAST score
                  361
E value
                  3.0e - 34
Match length
                  91
                  73
% identity
NCBI Description
                  (U28047) beta glucosidase [Oryza sativa]
                  262952
Seq. No.
Contig ID
                  4759_3.R1011
5'-most EST
                  uC-zmflmo17071e02b1
Method
                  BLASTX
NCBI GI
                  g1362162
BLAST score
                  565
                   7.0e-58
E value
Match length
                  176
% identity
                  73
                  beta-glucosidase BGQ60 precursor - barley >gi_804656
NCBI Description
                   (L41869) beta-glucosidase [Hordeum vulgare]
Seq. No.
                  262953
Contig ID
                  4759 4.R1011
5'-most EST
                  uC-zmroteosinte074g02b1
Method
                  BLASTX
NCBI GI
                  g3236248
BLAST score
                  521
E value
                  8.0e-53
Match length
                  164
% identity
                  83
NCBI Description
                  (AC004684) unknown protein [Arabidopsis thaliana]
```



```
4759 5.R1011
Contig ID
5'-most EST
                  uC-zmflb73177b06b1
Method
                  BLASTX
NCBI GI
                  q1143864
                  356
BLAST score
                  5.0e-68
E value
Match length
                  237
% identity
                  56
NCBI Description (U28047) beta glucosidase [Oryza sativa]
                  262955
Seq. No.
Contig ID
                  4759 8.R1011
5'-most EST
                  uC-zmflb73106c01a1
Method
                  BLASTX
NCBI GI
                  g1143864
BLAST score
                  277
                  1.0e-24
E value
                  52
Match length
                  94
% identity
NCBI Description
                 (U28047) beta glucosidase [Oryza sativa]
                  262956
Seq. No.
                  4759 10.R1011
Contig ID
5'-most EST
                  pwr700451810.h1
                  262957
Seq. No.
Contig ID
                  4759 12.R1011
5'-most EST
                  uC-zmflmo17241c07a1
                  262958
Seq. No.
                  4764 1.R1011
Contig ID
5'-most EST
                  LIB3069-015-Q1-K1-A8
                  262959
Seq. No.
Contig ID
                  4773 1.R1011
5'-most EST
                  uC-zmflb73260b10b2
Method
                  BLASTX
NCBI GI
                  g3861189
BLAST score
                  270
E value
                  2.0e-23
Match length
                  119
% identity
                  50
                  (AJ235272) 50S RIBOSOMAL PROTEIN L14 (rplN) [Rickettsia
NCBI Description
                  prowazekii]
Seq. No.
                  262960
Contig ID
                  4774_1.R1011
5'-most EST
                  LIB3076-053-Q1-E1-H6
Method
                  BLASTX
NCBI GI
                  a112785
BLAST score
                  280
```

E value 2.0e-30

Match length 181 % identity 41

NCBI Description DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I) >gi_67508_pir__DGECM1

3-methyladenine DNA glycosylase (EC 3.2.2.-) I-



Escherichia coli >gi_43030_emb_CAA27472_ (X03845) TAGI (aa 1-187) [Escherichia coli] >gi_147920 (J02606) 3-methyladenine-DNA glycosylase I (tag) [Escherichia coli] >gi_466687 (U00039) 3-methyladenine DNA glycosylase I, constitutive [Escherichia coli] >gi_1789971 (AE000432) 3-methyl-adenine DNA glycosylase I, constitutive [Escherichia coli]

Seq. No. 262961

Contig ID 4774 2.R1011

5'-most EST LIB3066-034-Q1-K1-A6

Method BLASTX
NCBI GI g112785
BLAST score 365
E value 2.0e-34
Match length 178
% identity 41

NCBI Description DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA

GLYCOSYLASE I, CONSTITUTIVE) (TAG I) >gi_67508_pir__DGECM1

3-methyladenine DNA glycosylase (EC 3.2. $\overline{2}$.-) $\overline{1}$ -

Escherichia coli >gi 43030 emb CAA27472 (X03845) TAGI (aa

1-187) [Escherichia coli] >gi_147920 (J02606)

3-methyladenine-DNA glycosylase I (tag) [Escherichia coli] >gi_466687 (U00039) 3-methyladenine DNA glycosylase I, constitutive [Escherichia coli] >gi_1789971 (AE000432)

3-methyl-adenine DNA glycosylase I, constitutive

[Escherichia coli]

 Seq. No.
 262962

 Contig ID
 4774_3.R1011

5'-most EST LIB3068-038-Q1-K1-F10

Seq. No. 262963

Contig ID 4776_1.R1011 5'-most EST wyr700243514.h1

Method BLASTX
NCBI GI g2813966
BLAST score 357
E value 3.0e-33
Match length 335
% identity 32

NCBI Description (Z97053) placental protein Diff33 [Homo sapiens]

>gi_4545219 gb AAD22448.1 (AF112227) TDE homolog [Homo

sapiens]

 Seq. No.
 262964

 Contig ID
 4776_2.R1011

 5'-most EST
 pmx700086507.h1

Seq. No. 262965 Contig ID 4779_1.R1011

5'-most EST LIB3076-055-Q1-K1-A5

Seq. No. 262966 Contig ID 4780_1.R1011

5'-most EST LIB $3\overline{0}$ 76-055-Q1-K1-A7

```
262967
Seq. No.
Contig ID
                  4786 1.R1011
                  uC-zmflmo17181d11b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2335099
BLAST score
                  1041
                  1.0e-113
E value
Match length
                  343
                  60
% identity
                  (AC002339) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  262968
                  4792 1.R1011
Contig ID
                  pmx700087417.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1346530
BLAST score
                  341
E value
                  1.0e-31
Match length
                  66
                  97
% identity
NCBI Description MAGO NASHI PROTEIN HOMOLOG
Seq. No.
                  262969
                   4792 2.R1011
Contig ID
                  uC-zmroteosinte005h09b1
5'-most EST
Method
                  BLASTX
                  q3123515
NCBI GI
BLAST score
                   690
                  1.0e-72
E value
Match length
                  142
                   90
% identity
                  (Y08761) Mago Nashi-like protein [Euphorbia lagascae]
NCBI Description
                   262970
Seq. No.
                   4792 4.R1011
Contig ID
5'-most EST
                  LIB3180-045-P2-M2-F1
Method
                  BLASTX
NCBI GI
                   g3123515
BLAST score
                   594
                   2.0e-61
E value
Match length
                   122
% identity
                  (Y08761) Mago Nashi-like protein [Euphorbia lagascae]
NCBI Description
                   262971
Seq. No.
                   4792_5.R1011
Contig ID
5'-most EST
                   uC-zmflb73135b03b2
Method
                   BLASTX
NCBI GI
                   g3123515
BLAST score
                   380
                   2.0e-36
E value
Match length
                   81
% identity
                   89
NCBI Description
                  (Y08761) Mago Nashi-like protein [Euphorbia lagascae]
```

36462

262972

4792_6.R1011

Seq. No. Contig ID



```
5'-most EST
                  pmx700085733.h1
Method
                  BLASTX
NCBI GI
                  g1346530
BLAST score
                  401
                  3.0e-39
E value
Match length
                  80
% identity
                  93
NCBI Description MAGO NASHI PROTEIN HOMOLOG
Seq. No.
                  262973
Contig ID
                  4803 1.R1011
5'-most EST
                  LIB3078-023-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g2392771
BLAST score
                  467
E value
                  2.0e-63
Match length
                  176
                  73
% identity
                  (AC002534) putative kinesin-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  262974
Seq. No.
Contig ID
                   4804 1.R1011
5'-most EST
                  cyk700048913.f1
Method
                  BLASTX
NCBI GI
                  g115840
BLAST score
                  758
E value
                  1.0e-80
Match length
                  150
                  97
% identity
                 CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y
NCBI Description
                   PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN
                  SUBUNIT B)
                  262975
Seq. No.
Contig ID
                   4804 2.R1011
5'-most EST
                  xmt700268080.h1
Method
                  BLASTX
NCBI GI
                   q22380
BLAST score
                   657
E value
                   1.0e-68
Match length
                   171
% identity
                   73
NCBI Description (X59714) CAAT-box DNA binding protein subunit B (NF-YB)
                   [Zea mays]
Seq. No.
                   262976
Contig ID
                   4804 3.R1011
5'-most EST
                  LIB3150-073-P1-N1-D5
Method
                  BLASTX
```

Method BLASTX
NCBI GI g22380
BLAST score 489
E value 3.0e-49

E value 3.0e-Match length 100 % identity 91

NCBI Description (X59714) CAAT-box DNA binding protein subunit B (NF-YB)

[Zea mays]



```
262977
Seq. No.
                  4804 4.R1011
Contig ID
                  LIB3061-023-Q1-K1-H1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q22380
                  233
BLAST score
                  2.0e-19
E value
                  84
Match length
% identity
                  65
                  (X59714) CAAT-box DNA binding protein subunit B (NF-YB)
NCBI Description
                  [Zea mays]
                  262978
Seq. No.
Contig ID
                  4806 1.R1011
5'-most EST
                  LIB3137-009-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  q2501182
BLAST score
                  302
                  3.0e-27
E value
                  177
Match length
% identity
                   45
                  OSMOTIN-LIKE PROTEIN PRECURSOR >gi 2129934 pir JC5237
NCBI Description
                  osmotin-like protein - tomato >gi 1220537 (L76632)
                  osmotin-like protein [Lycopersicon esculentum]
Seq. No.
                  262979
Contig ID
                   4809 1.R1011
                  LIB3060-016-Q1-K1-H9
5'-most EST
                  262980
Seq. No.
                  4809 2.R1011
Contig ID
                  LIB3076-052-Q1-E1-G1
5'-most EST
                  BLASTX
Method
NCBI GI
                   g3025189
BLAST score
                   405
E value
                   5.0e-39
Match length
                   287
                   34
% identity
NCBI Description HYPOTHETICAL 67.1 KD PROTEIN SLL1770
                   >gi 1652753 dbj BAA17672 (D90908) ABC1-like [Synechocystis
                   sp.]
                   262981
Seq. No.
                   4809 3.R1011
Contig ID
5'-most EST
                   rvt700553278.h1
Seq. No.
                   262982
Contig ID
                   4809 4.R1011
5'-most EST
                   LIB3062-034-Q1-K1-C8
Method
                   BLASTX
NCBI GI
                   q3025189
BLAST score
                   418
E value
                   6.0e-41
Match length
                  170
% identity
                   44
```

NCBI Description HYPOTHETICAL 67.1 KD PROTEIN SLL1770



>gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis sp.]

Seq. No. 262983

Contig ID 4809_5.R1011 5'-most EST wyr700238447.h1

Seq. No. 262984

Contig ID 4809 6.R1011

5'-most EST uC-zmflb73012a04b1

Seq. No. 262985

Contig ID 4815_1.R1011 5'-most EST rv1700454288.h1

Method BLASTX
NCBI GI g1737492
BLAST score 1942
E value 0.0e+00
Match length 621
% identity 63

NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No. 262986 Contig ID 4815 2.R1011

5'-most EST uC-zmflmo17078a03b1

Method BLASTX
NCBI GI g2213871
BLAST score 224
E value 4.0e-18
Match length 73
% identity 73

NCBI Description (AF003126) poly(A)-binding protein [Mesembryanthemum

crystallinum]

Seq. No. 262987 Contig ID 4815 4.R1011

5'-most EST uC-zmflb73200b10b1

Seq. No. 262988

Contig ID 4821 1.R1011

5'-most EST uC-zmflmo17071b04b1

Method BLASTX
NCBI GI g131528
BLAST score 714
E value 5.0e-75
Match length 437
% identity 38

NCBI Description POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I) (57 KD RNA-BINDING

PROTEIN PPTB-1) >gi_35768_emb_CAA43973_ (X62006) polypirimidine tract binding protein [Homo sapiens]

>gi_35774_emb_CAA43056_ (X60648) polypyrimidine tract-binding protein (pPTB) [Homo sapiens] >gi_4096061 (AC006273) PTB_HUMAN; PTB; HETEROGENEOUS NUCLEA; HNRNP I;

57 KD RNA-BINDING PROTEIN PPTB-1 [Homo sapiens]

Seq. No. 262989



Contig ID 4821 2.R1011 nbm700470940.h1 5'-most EST 262990 Seq. No. 4822 1.R1011 Contig ID uC-zmflb73242a01b2 5'-most EST 262991 Seq. No. 4823 1.R1011 Contig ID $ceu7\overline{0}0428194.h1$ 5'-most EST BLASTX Method NCBI GI g1931638 542 BLAST score 1.0e-105 E value Match length 367 % identity 60 (U95973) transcription factor RUSH-lalpha isolog NCBI Description [Arabidopsis thaliana] 262992 Seq. No. 4826 1.R1011 Contig ID LIB3076-052-Q1-E1-D2 5'-most EST Method BLASTX g3292824 NCBI GI BLAST score 473 1.0e-47 E value Match length 114 % identity 78 (AL031018) putative protein [Arabidopsis thaliana] NCBI Description 262993 Seq. No. 4827 1.R1011 Contig ID LIB3059-005-Q1-K1-F5 5'-most EST 262994 Seq. No. 4836 1.R1011 Contig ID 5'-most EST LIB3059-028-Q1-K1-D1 Method BLASTX g1565223 NCBI GI BLAST score 548 7.0e-56 E value 220 Match length % identity 53 NCBI Description (Y08301) MCM2-related protein [Arabidopsis thaliana] 262995 Seq. No. Contig ID 4838 1.R1011 5'-most EST LIB3076-052-Q1-E1-B10 262996 Seq. No. 4839 1.R1011 Contig ID 5'-most EST LIB3150-021-Q1-N1-G6

Method BLASTX NCBI GI g464705 BLAST score 745 E value 5.0e-79Match length 151

% identity 97 40S RIBOSOMAL PROTEIN S13 >gi 419802 pir_S30146 ribosomal NCBI Description protein S13.e - maize >gi 288059 emb CAA44311 (X62455) cytoplasmatic ribosomal protein S13 [Zea mays] 262997 Seq. No. 4839 2.R1011 Contig ID LIB3156-010-Q1-K1-G7 5'-most EST BLASTX Method NCBI GI g464705 BLAST score 709 7.0e-75 E value 142 Match length 98 % identity 40S RIBOSOMAL PROTEIN S13 >gi 419802 pir S30146 ribosomal NCBI Description protein S13.e - maize >gi 288059 emb CAA44311 (X62455) cytoplasmatic ribosomal protein S13 [Zea mays] 262998 Seq. No. 4839 3.R1011 Contiq ID 5'-most EST pmx700089787.h1 Method BLASTX NCBI GI q464705 BLAST score 636 2.0e-66 E value Match length 156 % identity 84 NCBI Description 40S RIBOSOMAL PROTEIN S13 >gi 419802 pir S30146 ribosomal protein S13.e - maize >gi 288059 emb CAA44311 (X62455) cytoplasmatic ribosomal protein S13 [Zea mays] 262999 Seq. No. Contig ID 4839 4.R1011 LIB3076-024-Q1-K1-H7 5'-most EST BLASTX Method NCBI GI q464705 BLAST score 420 E value 6.0e - 4194 Match length 91 % identity 40S RIBOSOMAL PROTEIN S13 >gi 419802 pir S30146 ribosomal NCBI Description protein S13.e - maize >gi_288059_emb_CAA44311_ (X62455) cytoplasmatic ribosomal protein S13 [Zea mays] 263000 Seq. No. 4844_1.R1011 Contig ID 5'-most EST $wyr7\overline{0}0242559.h1$ BLASTX q2924772 644 E value 4.0e-67 143

Method NCBI GI BLAST score

Match length % identity 81

(AC002334) unknown protein [Arabidopsis thaliana] NCBI Description

263001 Seq. No. Contig ID 4844_2.R1011

```
5'-most EST
                  LIB3150-047-Q1-N1-A8
Method
                  BLASTX
NCBI GI
                  q2924772
BLAST score
                  442
E value
                  1.0e-43
Match length
                  144
                   60
% identity
NCBI Description
                  (AC002334) unknown protein [Arabidopsis thaliana]
Seq. No.
                  263002
Contig ID
                  4844 3.R1011
                  wen700333257.hl
5'-most EST
                  263003
Seq. No.
Contig ID
                  4844 4.R1011
5'-most EST
                  LIB3066-013-Q1-K1-D9
Method
                  BLASTX
                  g2924772
NCBI GI
BLAST score
                  252
                  2.0e-30
E value
Match length
                   99
                  79
% identity
                  (AC002334) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  263004
                   4847 1.R1011
Contig ID
5'-most EST
                  uC-zmflMo17014h11b1
Method
                  BLASTX
NCBI GI
                  q4508021
BLAST score
                   712
E value
                   6.0e-85
Match length
                   457
% identity
                   22
                  UNKNOWN >gi 3510462 (AF019767) zinc finger protein [Homo
NCBI Description
                   sapiens]
Seq. No.
                   263005
Contig ID
                   4848 1.R1011
5'-most EST
                  LIB3076-047-Q1-K1-B1
Method
                  BLASTX
NCBI GI
                   g2961293
BLAST score
                   163
E value
                   3.0e-11
Match length
                   75
% identity
                   43
NCBI Description
                  (AJ225023) RagC [Bradyrhizobium japonicum]
Seq. No.
                   263006
Contig ID
                   4850 1.R1011
5'-most EST
                   cyk700051430.f1
Method
                  BLASTX
NCBI GI
                   g4335752
BLAST score
                   385
E value
                   1.0e-36
                  297
Match length
                   35
% identity
                 (AC006284) putative myb transcription factor-like protein
NCBI Description
```

Seq. No.

Contig ID

263013

4872_2.R1011

```
[Arabidopsis thaliana]
```

Seq. No. 263007 4850 2.R1011 Contig ID 5'-most EST LIB148-033-Q1-E1-E2 Seq. No. 263008 Contig ID 4855 1.R1011 5'-most EST wyr700238949.h1 Method BLASTX NCBI GI g4490297 BLAST score 1419 E value 1.0e-157 Match length 545 % identity 55 NCBI Description (AL035678) putative protein [Arabidopsis thaliana] Seq. No. 263009 Contig ID 4856 1.R1011 5'-most EST LIB3076-048-Q1-E1-E12 Method BLASTX NCBI GI g2911046 BLAST score 150 5.0e-10 E value 75 Match length % identity 44 NCBI Description (AL021961) cyclin delta-3 [Arabidopsis thaliana] 263010 Seq. No. 4857 1.R1011 Contig ID 5'-most EST LIB3180-039-P2-M2-H12 Method BLASTX NCBI GI g2342724 BLAST score 230 E value 6.0e-19 Match length 107 % identity 47 NCBI Description (AC002341) unknown protein [Arabidopsis thaliana] Seq. No. 263011 Contig ID 4867 1.R1011 5'-most EST uC-zmflb73099f04b1 Seq. No. 263012 Contig ID 4872 1.R1011 5'-most EST uC-zmflmo17306g12b1 Method BLASTX NCBI GI q1083160 BLAST score 839 E value 1.0e-89 Match length 395 % identity mannosyl-oligosaccharide 1,2-alpha-mannosidase (EC NCBI Description 3.2.1.113) - rabbit (fragment)



5'-most EST uC-zmflmo17399g06a1

Seq. No. 263014

Contig ID 4874 1.R1011

5'-most EST LIB3076-048-Q1-E1-C9

Method BLASTX
NCBI GI g1255829
BLAST score 155
E value 7.0e-10
Match length 162
% identity 23

NCBI Description (U53336) coded for by C. elegans cDNA yk29e8.5; coded for

by C. elegans cDNA yk17b5.5; coded for by C. elegans cDNA yk34d5.5; coded for by C. elegans cDNA yk38d6.5; coded for by C. elegans cDNA yk38d6.3; coded for by C. elegans cDNA

yk34d5.3

Seq. No. 263015

Contig ID 4875 1.R1011

5'-most EST uC-zmflb73169d05b2

Method BLASTX
NCBI GI g1888357
BLAST score 1538
E value 1.0e-171
Match length 495
% identity 59

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]

>gi 1890154 emb CAA72432 (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

Seq. No. 263016

Contig ID 4875 2.R1011

5'-most EST uC-zmroteosinte075c01b1

Method BLASTX
NCBI GI g1888357
BLAST score 515
E value 3.0e-52
Match length 149
% identity 59

NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]

>gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase

precursor [Arabidopsis thaliana]

Seq. No. 263017

Contig ID 4876 1.R1011

5'-most EST LIB3180-021-P2-M1-A1

Method BLASTX
NCBI GI g4093169
BLAST score 544
E value 1.0e-55
Match length 142
% identity 73

NCBI Description (AF095933) p20-Arc [Dictyostelium discoideum]

Seq. No. 263018 Contig ID 4877_1.R1011 5'-most EST xyt700345443.h1

```
Method
                   BLASTX
NCBI GI
                   q1806140
BLAST score
                   1736
                   0.0e + 00
E value
Match length
                   405
                   80
% identity
NCBI Description
                  (X97314) cdc2MsC [Medicago sativa]
Seq. No.
                   263019
Contig ID
                   4877 3.R1011
5'-most EST
                   LIB3076-048-Q1-E1-D6
                   BLASTX
Method
NCBI GI
                   q1806140
BLAST score
                   497
```

4.0e-50 E value Match length 121 % identity 82

(X97314) cdc2MsC [Medicago sativa] NCBI Description

263020 Seq. No.

Contig ID 4878 1.R1011

LIB3076-048-Q1-E1-B9 5'-most EST

Method BLASTX NCBI GI g2564680 BLAST score 177 9.0e-13E value Match length 128 32 % identity

NCBI Description (AF023484) putative KP78 protein kinase [Drosophila

melanogaster]

Seq. No. 263021

Contig ID 4882 1.R1011 5'-most EST xyt700345890.h1

BLASTN Method g4589415 NCBI GI BLAST score 37 E value 3.0e-11 53 Match length 92 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K14A3, complete sequence

Seq. No. 263022 4883 1.R1011 Contig ID

5'-most EST LIB3076-047-Q1-K1-G4

Method BLASTX NCBI GI g3121981 BLAST score 483 E value 1.0e-48 Match length 174 52 % identity

NCBI Description PROBABLE ATP-DEPENDENT RNA HELICASE DDX10 (DEAH BOX PROTEIN

10) >gi 1142710 (U28042) similar to DEAD box RNA helicases [Homo sapiens] >gi 1589113 prf 2210303A RNA helicase [Homo

sapiens]



Seq. No. 263023

Contig ID 4889 1.R1011

5'-most EST uC-zmflmo17046c08a1

Seq. No. 263024

Contig ID 4890_1.R1011 5'-most EST afb700381188.h1

Method BLASTX
NCBI GI g3212877
BLAST score 1078
E value 1.0e-118
Match length 276
% identity 71

NCBI Description (AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No. 263025

Contig ID 4892 1.R1011

5'-most EST LIB3182-004-P2-M1-A8

Seq. No. 263026

Contig ID 4902 1.R1011

5'-most EST uC-zmflb73137d06b1

Method BLASTX
NCBI GI g3176690
BLAST score 2310
E value 0.0e+00
Match length 893
% identity 55

NCBI Description (AC003671) Similar to ubiquitin ligase qb D63905 from S.

cerevisiae. EST gb R65295 comes from this gene.

[Arabidopsis thaliana]

 Seq. No.
 263027

 Contig ID
 4902_3.R1011

 5'-most EST
 nbm700473104.h1

Method BLASTX
NCBI GI g3176690
BLAST score 294
E value 3.0e-26
Match length 65
% identity 86

NCBI Description (AC003671) Similar to ubiquitin ligase gb D63905 from S.

cerevisiae. EST gb R65295 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 263028

Contig ID 4902 4.R1011

5'-most EST uC-zmflmo17335h11b1

Method BLASTX
NCBI GI g3176690
BLAST score 646
E value 5.0e-70
Match length 167
% identity 80

NCBI Description (AC003671) Similar to ubiquitin ligase gb_D63905 from S.

cerevisiae. EST gb R65295 comes from this gene.

[Arabidopsis thaliana]

5'-most EST

Method

```
263029
Seq. No.
Contig ID
                   4903 1.R1011
5'-most EST
                   uC-zmflmo17126c11b1
                   263030
Seq. No.
                   4903 2.R1011
Contig ID
                   uC-zmflmo17099b01b1
5'-most EST
                   263031
Seq. No.
                   4905 1.R1011
Contig ID
5'-most EST
                   LIB3076-047-Q1-K1-E1
Method
                   BLASTN
NCBI GI
                   g342661
BLAST score
                   344
E value
                   0.0e+00
Match length
                   367
% identity
                   99
NCBI Description Maize mitochondrial 26S rRNA gene and flanks
                   263032
Seq. No.
                   4908 1.R1011
Contig ID
5'-most EST
                   LIB3\overline{1}36-016-Q1-K1-D3
Method
                   BLASTX
                   q2618699
NCBI GI
                   520
BLAST score
                   3.0e-52
E value
Match length
                   357
% identity
                   32
                  (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   263033
Contig ID
                   4916 1.R1011
5'-most EST
                   LIB3060-008-Q1-K1-G6
Method
                   BLASTX
NCBI GI
                   g4115377
BLAST score
                   1341
E value
                   1.0e-148
Match length
                   643
% identity
                   44
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
                   263034
Seq. No.
Contig ID
                   4920 1.R1011
                   LIB3068-025-Q1-K1-C1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4587577
BLAST score
                   310
E value
                   3.0e-28
Match length
                   161
% identity
                   39
NCBI Description (AC006550) F1003.17 [Arabidopsis thaliana]
                   263035
Seq. No.
Contig ID
                   4923 1.R1011
```

36473

uC-zmflmo17117f12b1

BLASTX



NCBI GI g4512667

BLAST score 426

E value 1.0e-41

Match length 130
% identity 63

NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No. 263036 Contig ID 4927 1.R1011

5'-most EST LIB3076-046-Q1-K1-G6

Method BLASTX
NCBI GI g4104060
BLAST score 502
E value 6.0e-51
Match length 135
% identity 71

NCBI Description (AF031231) S222 [Triticum aestivum]

Seq. No. 263037 Contig ID 4929 1.R1011

5'-most EST LIB3088-046-Q1-K1-D7

Seq. No. 263038
Contig ID 4929_2.R1011

5'-most EST LIB3180-062-P2-M1-G2

Method BLASTX
NCBI GI g629669
BLAST score 145
E value 3.0e-09
Match length 82
% identity 34

NCBI Description hypothetical protein - tomato

Seq. No. 263039

Contig ID 4929_3.R1011

5'-most EST uC-zmflmo17057a02b1

Seq. No. 263040

Contig ID 4929 4.R1011

5'-most EST LIB3069-015-Q1-K1-C3

Seq. No. 263041 Contig ID 4929 5.R1011

5'-most EST LIB3115-002-Q1-K1-A9

Seq. No. 263042 Contig ID 4929_9.R1011

5'-most EST LIB3069-008-Q1-K1-E2

Seq. No. 263043

Contig ID 4932_1.R1011 5'-most EST wyr700241033.h1

Method BLASTX
NCBI GI g2880043
BLAST score 1026
E value 1.0e-112
Match length 327

Contig ID

% identity 60 (AC002340) putative 3-hydroxyisobutyryl-coenzyme A NCBI Description hydrolase [Arabidopsis thaliana] 263044 Seq. No. 4933 1.R1011 Contig ID nbm700471436.h15'-most EST Method BLASTX g3549665 NCBI GI BLAST score 472 1.0e-46 E value Match length 311 % identity 41 (AL031394) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 263045 4933 2.R1011 Contig ID 5'-most EST LIB3117-012-Q1-K1-A8 Method BLASTX NCBI GI g3549665 BLAST score 160 2.0e-10 E value Match length 35 80 % identity (AL031394) hypothetical protein [Arabidopsis thaliana] NCBI Description 263046 Seq. No. Contig ID 4938 1.R1011 5'-most EST LIB3076-046-Q1-K1-C6 263047 Seq. No. 4939 1.R1011 Contig ID LIB3076-046-Q1-K1-C7 5'-most EST BLASTX Method NCBI GI g4567203 BLAST score 672 E value 2.0e-70 Match length 142 90 % identity NCBI Description (AC007168) putative beta-hydroxyacyl-ACP dehydratase [Arabidopsis thaliana] 263048 Seq. No. 4940 1.R1011 Contig ID 5'-most EST LIB143-047-Q1-E1-B8 Method BLASTX NCBI GI g1352613 BLAST score 640 E value 2.0e-66 Match length 145 90 % identity NCBI Description OCS-ELEMENT BINDING FACTOR 1 (OCSBF-1) >gi_444047_emb_CAA44607 (X62745) ocs-binding factor 1 [Zea mays] 263049 Seq. No.

36475

4940 2.R1011



5'-most EST gct701173396.h2 Method BLASTX NCBI GI g3608138 BLAST score 271 E value 4.0e-48 Match length 206 50 % identity (AC005314) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 263050 Contig ID 4940 4.R1011 5'-most EST LIB3156-010-Q1-K1-D4 Method BLASTN NCBI GI q444046 BLAST score 176 E value 3.0e-94 Match length 261 % identity 92 NCBI Description Z.mays OBF1 mRNA for ocs-element binding factor Seq. No. 263051 Contig ID 4941 1.R1011 5'-most EST nbm700477167.h1 Method BLASTN NCBI GI q2832242 BLAST score 196 E value 1.0e-106 Match length 497 % identity 95 NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence Seq. No. 263052 Contig ID 4941 2.R1011 5'-most EST uwh700207238.h1BLASTN Method NCBI GI g2832242 BLAST score 83 3.0e-38 E value 107 Match length 94 % identity

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 263053 Contig ID 4941 3.R1011 5'-most EST uC-zmflb73263d10b1

Seq. No. 263054 Contig ID 4941 4.R1011

5'-most EST LIB3066-001-Q1-K1-A3

263055 Seq. No. 4941_5.R1011 Contig ID

5'-most EST uC-zmflMo17087c01b1

BLASTN Method NCBI GI q2832242 BLAST score 63 E value 2.0e-26

107 Match length 90 % identity

Zea mays 22-kDa alpha zein gene cluster, complete sequence NCBI Description

263056 Seq. No.

4941 6.R1011 Contig ID xyt700343822.h1 5'-most EST

BLASTN Method g2832242 NCBI GI 143 BLAST score 3.0e-74E value 234 Match length 94 % identity

Zea mays 22-kDa alpha zein gene cluster, complete sequence NCBI Description

263057 Seq. No.

4941 8.R1011 Contig ID $dyk7\overline{0}0103624.h1$ 5'-most EST

BLASTX Method g2408068 NCBI GI 193 BLAST score 7.0e-15 E value 108

Match length 34 % identity

(Z99165) hypothetical protein [Schizosaccharomyces pombe] NCBI Description

263058 Seq. No.

4943 1.R1011 Contig ID

LIB3069-036-Q1-K1-D1 5'-most EST

BLASTX Method q730510 NCBI GI 935 BLAST score

1.0e-101 E value 235 Match length 96 % identity

NCBI Description RAS-RELATED PROTEIN RIC1 >gi_542150_pir__ S38740 GTP-binding protein - rice >gi_432607_gb_AAB28535_ (S66160) ras-related GTP binding protein possessing GTPase activity=ric1 [Oryza sativa=rice, var. Yamahoushi, callus, Peptide, 202 aa]

[Oryza sativa]

263059 Seq. No.

Contig ID 4945 1.R1011 $yne7\overline{0}0379131.h1$ 5'-most EST

BLASTX Method q1711036 NCBI GI BLAST score 550 E value 3.0e-56 Match length 146 % identity

(U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum NCBI Description

sativum]

263060 Seq. No.

4945 2.R1011 Contig ID

LIB3150-108-P2-K1-G7 5'-most EST

Method BLASTX

```
NCBI GI g1711036
BLAST score 356
E value 2.0e-33
Match length 96
% identity 74
NCBI Description (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum sativum]
```

Seq. No. 263061 Contig ID 4945 3.R1011

Contig ID 4945_3.R1011 5'-most EST LIB3076-046-Q1-K1-B3

Method BLASTX
NCBI GI g4586027
BLAST score 243
E value 1.0e-20
Match length 61
% identity 77

% identity 77 NCBI Description (AC007109) putative ribosomal protein L14 [Arabidopsis

thaliana]

Seq. No. 263062 Contig ID 4945_4.R1011

5'-most EST LIB3118-010-Q1-K1-G4

Method BLASTX
NCBI GI g4490705
BLAST score 242
E value 3.0e-20
Match length 62
% identity 74

% identity 74
NCBI Description (AL035680) ribosomal protein L14-like protein [Arabidopsis

thaliana]

Seq. No. 263063 Contig ID 4945_5.R1011

5'-most EST uC-zmflmo17153h01b1

Method BLASTX
NCBI GI g1711036
BLAST score 326
E value 3.0e-30
Match length 79
% identity 81

NCBI Description (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum

sativum]

Seq. No. 263064

Contig ID 4945_6.R1011 5'-most EST xsy700208042.h1

Method BLASTX
NCBI GI g4586027
BLAST score 146
E value 3.0e-09
Match length 61
% identity 54

NCBI Description (AC007109) putative ribosomal protein L14 [Arabidopsis

thaliana]

Seq. No. 263065

```
4946 1.R1011
 Contig ID
 5'-most EST
                    LIB3076-045-Q1-K1-E9
                    BLASTX
 Method
 NCBI GI
                    q3688191
 BLAST score
                    181
                    3.0e-13
 E value
                    102
 Match length
                    46
 % identity
                    (AJ010090) MAP3K alpha protein kinase [Arabidopsis
 NCBI Description
                    thaliana]
                    263066
 Seq. No.
 Contig ID
                    4949 1.R1011
                    wyr700237259.h1
 5'-most EST
                    BLASTX
 Method
                    g2196672
 NCBI GI
 BLAST score
                    590
                    8.0e-61
 E value
 Match length
                    115
 % identity
 NCBI Description (Y08807) HMGd1 [Zea mays]
 Seq. No.
                    263067
 Contig ID
                    4949 2.R1011
                    uC-zmflb73140f12b1
 5'-most EST
 Method
                    BLASTX
 NCBI GI
                    q3157945
 BLAST score
                    569
 E value
                    1.0e-58
 Match length
                    184
                    61
  % identity
                   (AC002131) Contains similarity to axi 1 gene gb X80301 from
 NCBI Description
                    Nicotiana tabacum. [Arabidopsis thaliana]
                    263068
 Seq. No.
                    4949 3.R1011
 Contig ID
                    LIB3088-021-Q1-K1-A2
  5'-most EST
 Method
                    BLASTN
 NCBI GI
                    g2196671
 BLAST score
                    276
 E value
                    1.0e-154
 Match length
                    327
                    97
  % identity
 NCBI Description Z.mays mRNA for HMG protein
                    263069
  Seq. No.
                    4950 1.R1011
 Contig ID
  5'-most EST
                    fdz701164609.h1
                    BLASTX
 Method
 NCBI GI
                    q3152587
                    951
 BLAST score
                    1.0e-103
 E value
 Match length
                    198
                    84
% identity
                   (AC002986) Similar to CREB-binding protein homolog
  NCBI Description
```

gb U88570 from D. melanogaster and contains similarity to callus-associated protein gb U01961 from Nicotiana tabacum.



EST gb W43427 comes from this gene. [Arabidopsis thaliana]

263070 Seq. No. 4952 1.R1011 Contig ID fdz701163059.hl 5'-most EST BLASTX Method g1617036 NCBI GI 1226 BLAST score 1.0e-135 E value 322 Match length 74 % identity (Y08624) Ted2 [Vigna unguiculata] NCBI Description 263071 Seq. No. 4952 2.R1011 Contig ID 5'-most EST zuv700355711.hl BLASTX Method g1617036 NCBI GI 276 BLAST score 3.0e-24E value 89 Match length 64 % identity (Y08624) Ted2 [Vigna unguiculata] NCBI Description 263072 Seq. No. 4953 1.R1011 Contig ID $uC-z\overline{m}flmo17030b02b1$ 5'-most EST Method BLASTX g2623310 NCBI GI 198 BLAST score 9.0e-15 E value 145 Match length % identity 41 (AC002409) unknown protein [Arabidopsis thaliana] NCBI Description >gi 3402721 (AC004261) unknown protein [Arabidopsis thaliana] 263073 Seq. No. 4953 2.R1011 Contig ID uwc700153483.h1 5'-most EST BLASTX Method NCBI GI q2623310 411 BLAST score 8.0e-40 E value Match length 155 % identity NCBI Description (AC002409) unknown protein [Arabidopsis thaliana] >gi 3402721 (AC004261) unknown protein [Arabidopsis thaliana]

Seq. No. 263074 Contig ID 4953 3.R1011

5'-most EST uC-zmflMo17009c07b1

 Seq. No.
 263075

 Contig ID
 4953_6.R1011

 5'-most EST
 uC-zmflb73227f08a1



```
Seq. No.
                  263076
                  4953 7.R1011
Contig ID
5'-most EST
                  uC-zmflmo17202h02a1
                  263077
Seq. No.
                  4953 8.R1011
Contig ID
5'-most EST
                  rvt700551421.h1
                  BLASTX
Method
NCBI GI
                  g2623310
BLAST score
                  230
                  2.0e-19
E value
Match length
                  76
                  59
% identity
                  (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3402721 (AC004261) unknown protein [Arabidopsis
                  thaliana]
Seq. No.
                  263078
Contig ID
                  4955 1.R1011
5'-most EST
                  LIB143-035-Q1-E1-B4
Method
                  BLASTX
NCBI GI
                  q3128168
BLAST score
                  1419
                  1.0e-157
E value
Match length
                  376
                  66
% identity
NCBI Description
                  (AC004521) putative carboxyl-terminal peptidase
                   [Arabidopsis thaliana]
                  263079
Seq. No.
                  4955 2.R1011
Contig ID
                  LIB3062-050-Q1-K1-E11
5'-most EST
Method
                  BLASTX
                  g3128168
NCBI GI
BLAST score
                  216
                  3.0e-17
E value
Match length
                  54
                  65
% identity
                  (AC004521) putative carboxyl-terminal peptidase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  263080
                  4958 1.R1011
Contig ID
5'-most EST
                  LIB3076-045-Q1-K1-E6
                  BLASTX
Method
NCBI GI
                  g2244771
BLAST score
                  160
E value
                  1.0e-10
                  87
Match length
                  39
% identity
NCBI Description (Z97335) kinesin homolog [Arabidopsis thaliana]
```

 Seq. No.
 263081

 Contig ID
 4963_1.R1011

 5'-most EST
 uC-zmflb73237e02b2

Method BLASTX



NCBI GI g3372230 BLAST score 495 E value 9.0e-50 Match length 142 % identity 65

NCBI Description (AF017074) RNA polymerase I, II and III 16.5 kDa subunit [Arabidopsis thaliana] >gi_4585968_gb_AAD25604.1_AC005287_6

(AC005287) RNA polymerase I, II and III 16.5 kDa subunit

[Arabidopsis thaliana]

Method BLASTX
NCBI GI g3372230
BLAST score 179
E value 3.0e-13
Match length 51
% identity 65

NCBI Description (AF017074) RNA polymerase I, II and III 16.5 kDa subunit

[Arabidopsis thaliana] >gi_4585968_gb_AAD25604.1_AC005287_6 (AC005287) RNA polymerase I, II and III 16.5 kDa subunit

[Arabidopsis thaliana]

Seq. No. 263083

Contig ID 4964_1.R1011

5'-most EST uC-zmroteosinte070e06b1

Seq. No. 263084

Contig ID 4968_1.R1011

5'-most EST uC-zmflb73180h01b1

Method BLASTX
NCBI GI g1877480
BLAST score 628
E value 5.0e-65
Match length 262
% identity 55

NCBI Description (U89270) short-chain alcohol dehydrogenase [Tripsacum

dactyloides]

Seq. No. 263085

Contig ID 4969_1.R1011

5'-most EST LIB3078-012-Q1-K1-H6

Method BLASTX
NCBI GI g2253278
BLAST score 283
E value 2.0e-25
Match length 105
% identity 68

NCBI Description (AF005492) RF2a [Oryza sativa]

Seq. No. 263086 Contig ID 4971 1.R1011

5'-most EST LIB3076-041-Q1-K1-C9

Seq. No. 263087 Contig ID 4972_1.R1011



fdz701164902.h1 5'-most EST

BLASTX Method g4406772 NCBI GI 189 BLAST score 8.0e-14 E value Match length 75 63 % identity

(AC006836) putative nitrilase-associated protein NCBI Description

[Arabidopsis thaliana]

263088 Seq. No.

4974 1.R1011 Contig ID

LIB3152-053-P1-K1-F8 5'-most EST

263089 Seq. No.

4975 1.R1011 Contig ID

LIB3060-034-Q1-K1-H1 5'-most EST

Method BLASTX q2462837 NCBI GI 1940 BLAST score 0.0e + 00E value Match length 645 % identity 62

(AF000657) hypothetical protein [Arabidopsis thaliana] NCBI Description

263090 Seq. No.

4985 1.R1011 Contig ID

5'-most EST uC-zmflmo17342d11b1

Method BLASTX g1707642 NCBI GI BLAST score 836 6.0e-90 E value 179 Match length 91 % identity

NCBI Description (Y07748) TMK [Oryza sativa]

Seq. No. 263091 4991 1.R1011 Contig ID hbs701182722.h1 5'-most EST

263092 Seq. No.

Contig ID 4998 1.R1011

uC-zmflb73041b05b1 5'-most EST

BLASTX Method NCBI GI q347855 BLAST score 297 E value 1.0e-26 Match length 134 % identity 46

(L21753) glucose transporter [Saccharum hybrid cultivar NCBI Description

H65-7052]

263093 Seq. No.

4998 2.R1011 Contig ID

uC-zmflb73049e01b15'-most EST

Method BLASTX NCBI GI g100347



BLAST score 275 E value 3.0e-24 Match length 113 % identity 50

NCBI Description monosaccharide transport protein MST1 - common tobacco >gi 19885 emb CAA47324 (X66856) monosaccharid transporter

[Nicotiana tabacum]

Seq. No. 263094

Contig ID 5017 1.R1011

5'-most EST LIB3076-027-Q1-K1-D3

Method BLASTX
NCBI GI g266410
BLAST score 889
E value 8.0e-96
Match length 194
% identity 86

NCBI Description CDC2+/CDC28-RELATED PROTEIN KINASE R2 >gi_82507_pir__S13934

protein kinase (EC 2.7.1.37) chain cdc2/cdc28 homolog -

rice >gi_20194_emb_CAA41172_ (X58194) cdc2+/CDC28-related

protein kinase [Oryza sativa]

 Seq. No.
 263095

 Contig ID
 5018_1.R1011

 5'-most EST
 rvt700550170.h1

Method BLASTX
NCBI GI g3928871
BLAST score 1296
E value 1.0e-143
Match length 254
% identity 100

NCBI Description (AF093627) poly(ADP)-ribose polymerase [Zea mays]

Seq. No. 263096

Contig ID 5023_1.R1011

5'-most EST uC-zmflb73012c07b1

Method BLASTX
NCBI GI g4432860
BLAST score 971
E value 1.0e-138
Match length 489
% identity 29

NCBI Description (AC006300) putative glucose-induced repressor protein

[Arabidopsis thaliana]

Seq. No. 263097

Contig ID 5023_2.R1011

5'-most EST uC-zmflmo17257c09b1

Seq. No. 263098

Contig ID 5024_1.R1011

5'-most EST LIB3150-002-Q1-N1-B8

Method BLASTX
NCBI GI g118719
BLAST score 657
E value 2.0e-68
Match length 350



```
% identity
                  DNAJ PROTEIN >gi_72228_pir__HHECDJ heat shock protein dnaJ
NCBI Description
                  - Escherichia coli >gi_145769 (M12565) heat shock protein
                  dnaJ [Escherichia coli] >gi_216441_dbj_BAA01292_ (D10483)
                  DnaJ [Escherichia coli] >gi_1786197 (AE000112) Chaperone
                  with DnaK; heat shock protein [Escherichia coli]
Seq. No.
                  263099
                  5033 1.R1011
Contig ID
                  LIB3079-030-Q1-K1-F5
5'-most EST
                  BLASTX
Method
                  g1923256
NCBI GI
BLAST score
                  819
                  1.0e-87
E value
Match length
                  218
                  72
% identity
                  (U86782) 26S proteasome-associated padl homolog [Homo
NCBI Description
                  sapiens]
                  263100
Seq. No.
                  5033 2.R1011
Contig ID
                  xjt700096525.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2505940
BLAST score
                  615
                  1.0e-70
E value
                  167
Match length
% identity
                  (Y13071) 26S proteasome, non-ATPase subunit [Mus musculus]
NCBI Description
Seq. No.
                   263101
                   5033 3.R1011
Contig ID
                  LIB3076-043-Q1-K1-A1
5'-most EST
                  BLASTX
Method
                   q1923256
NCBI GI
BLAST score
                   382
                   7.0e-37
E value
Match length
                   126
% identity
                   61
                  (U86782) 26S proteasome-associated pad1 homolog [Homo
NCBI Description
                   sapiens]
                   263102
Seq. No.
                   5042 1.R1011
Contig ID
                   LIB3076-042-Q1-K1-C6
5'-most EST
                   263103
Seq. No.
                   5046_1.R1011
Contig ID
                   LIB3067-030-Q1-K1-B11
5'-most EST
                   BLASTX
Method
                   g626040
NCBI GI
BLAST score
                   166
                   1.0e-14
E value
Match length
                   71
                   62
% identity
```

NCBI Description protein kinase SNF1 homolog wpk4-p58 - wheat



```
263104
Seq. No.
                  5048 1.R1011
Contig ID
                  LIB3151-035-Q1-K1-A3
5'-most EST
Method
                  BLASTX
                  g3980378
NCBI GI
BLAST score
                  1361
                  1.0e-151
E value
Match length
                  305
% identity
                  79
                  (AC004561) putative RNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  263105
                  5052 1.R1011
Contig ID
                  uC-zmroteosinte066a02b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3228517
                  595
BLAST score
E value
                   4.0e-61
                   318
Match length
                   45
% identity
                  (AF007788) ETTIN [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   263106
                   5053 1.R1011
Contig ID
                   LIB3076-042-Q1-K1-F5
5'-most EST
                   263107
Seq. No.
Contig ID
                   5054 1.R1011
                   uC-zmflmo170114b08b1
5'-most EST
Method
                   BLASTX
                   g730450
NCBI GI
                   773
BLAST score
                   3.0e-82
E value
                   194
Match length
                   77
% identity
                   60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B)
NCBI Description
                   >gi_480649_pir__S37134 cold-induced protein BnC24B - rape
                   >gi 398922 emb CAA80343 (Z22620) cold induced protein
                   (BnC24B) [Brassica napus]
                   263108
Seq. No.
                   5054 2.R1011
Contig ID
                   LIB3059-021-Q1-K1-A5
5'-most EST
                   BLASTX
Method
                   g730526
NCBI GI
                   491
BLAST score
                   2.0e-49
E value
```

121 Match length 80 % identity

60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) NCBI Description

>gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis thaliana $>gi_404166_{emb_CAA53005_{emb_CX}}$ (X75162) BBC1 protein

[Arabidopsis thaliana]

263109 Seq. No. 5054 6.R1011 Contig ID



```
5'-most EST
                   uC-zmflmo17133f02b1
                   BLASTX
Method
                   g730450
NCBI GI
                   203
BLAST score
                   3.0e-16
E value
                   54
Match length
                   67
% identity
                   60S RIBOSOMAL PROTEIN L13-2 (COLD INDUCED PROTEIN C24B)
NCBI Description
                   >gi 480649 pir S37134 cold-induced protein BnC24B - rape
                   >gi 398922 emb CAA80343 (Z22620) cold induced protein
                    (BnC24B) [Brassica napus]
                   263110
Seq. No.
                   5059 1.R1011
Contig ID
                   uC-zmflb73128f04b1
5'-most EST
                   BLASTX
Method
                   q2129825
NCBI GI
                   320
BLAST score
E value
                   2.0e-29
                   114
Match length
                    60
% identity
                   dynamin-like protein phragmoplastin 12 - soybean
NCBI Description
                    >gi 1217994 (U25547) SDL [Glycine max]
                    263111
Seq. No.
                    5060 1.R1011
Contig ID
                    LIB3076-041-Q1-K1-H6
5'-most EST
                    263112
Seq. No.
Contig ID
                    5067 1.R1011
                    uC-zmflmo17001g11b1
5'-most EST
                    BLASTX
Method
                    q417497
NCBI GI
                    354
BLAST score
                    5.0e-33
E value
                    198
Match length
                    36
% identity
                   MITOCHONDRIAL INTERMEDIATE PEPTIDASE PRECURSOR (MIP)
NCBI Description
                    >gi_423909_pir__A46273 mitochondrial intermediate peptidase (EC 3.4.24.-) - rat >gi_206272 (M96633) intermediate
                    peptidase precursor [Rattus norvegicus]
                    263113
Seq. No.
                    5068 1.R1011
Contig ID
                    LIB3062-039-Q1-K1-D11
 5'-most EST
                    263114
 Seq. No.
                    5068 2.R1011
 Contig ID
                    uC-z\overline{m}flmo17217a12b1
 5'-most EST
                    263115
 Seq. No.
```

5070 1.R1011 Contig ID

LIB189-002-Q1-E1-H12 5'-most EST

BLASTX Method g3834302 NCBI GI 1412 BLAST score 1.0e-159 E value



```
465
Match length
                  75
% identity
                  (AC005679) Similar to gb_D45384 vacuolar H+-pyrophosphatase
NCBI Description
                  from Oryza sativa. ESTs gb_F14272 and gb_F14273 come from
                  this gene. [Arabidopsis thaliana]
                  263116
Seq. No.
                  5074 1.R1011
Contig ID
                  LIB3076-041-Q1-K1-F9
5'-most EST
                  BLASTX
Method
                  q4584345
NCBI GI
                  588
BLAST score
                  2.0e-65
E value
                  160
Match length
                  81
% identity
                  (AC007127) putative serine/threonine protein kinase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  263117
                  5076 1.R1011
Contig ID
5'-most EST
                  LIB3076-041-Q1-K1-G12
                  263118
Seq. No.
                  5077 1.R1011
Contig ID
                  LIB3067-053-Q1-K1-C7
5'-most EST
                  BLASTN
Method
                  g7431
NCBI GI
                   36
BLAST score
                  1.0e-10
E value
Match length
                  64
                  89
% identity
NCBI Description D. HYDEI HISTONE GENES
                   263119
Seq. No.
Contig ID
                   5078 1.R1011
                   uC-zmflb73066g12b1
5'-most EST
                   BLASTX
Method
                   g2737882
NCBI GI
BLAST score
                   2332
E value
                   0.0e + 00
Match length
                   613
% identity
                   73
NCBI Description (U46014) polyphenol oxidase [Saccharum sp.]
Seq. No.
                   263120
                   5078 2.R1011
Contig ID
                   uC-zmflb73273b08a1
5'-most EST
Method
                   BLASTN
                   g2737881
NCBI GI
```

Method BLASTN
NCBI GI g2737881
BLAST score 129
E value 4.0e-66
Match length 261
% identity 88

NCBI Description Saccharum sp. polyphenol oxidase mRNA, complete cds

Seq. No. 263121

Contig ID 5078_3.R1011



5'-most EST uC-zmflb73114a03a2 Method BLASTN g2737881 NCBI GI BLAST score 95 7.0e-46E value 263 Match length 84 % identity Saccharum sp. polyphenol oxidase mRNA, complete cds NCBI Description 263122 Seq. No. 5079 1.R1011 Contig ID LIB36-019-Q1-E1-A6 5'-most EST Method BLASTN g4185305 NCBI GI BLAST score 245 1.0e-135 E value 492 Match length 47 % identity Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 NCBI Description (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes 263123 Seq. No. 5079 2.R1011 Contig ID LIB3150-089-P1-N1-G4 5'-most EST BLASTN Method q4185305 NCBI GI BLAST score 388 0.0e + 00E value 890 Match length 42 % identity Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 NCBI Description (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes 263124 Seq. No. 5079 3.R1011 Contig ID LIB148-034-Q1-E1-C11 5'-most EST BLASTN Method g3452305 NCBI GI 250 BLAST score 1.0e-138 E value 1028 Match length 91 % identity NCBI Description Zea mays retrotransposon Opie-3 3' LTR, partial sequence

 Seq. No.
 263125

 Contig ID
 5079_4.R1011

 5'-most EST
 uC-zmflmo17220f03b1

 Method
 BLASTN

 NCBI GI
 g1657766

 BLAST score
 490

 E. value
 0.0e+00

E value 0.0e+
Match length 1074
% identity 65



NCBI Description Zea mays retrotransposon Opie-2 5' LTR, primer binding site, gag gene, pol gene, complete cds, polypurine tract

and 3' LTR

Seq. No. 263126

Contig ID 5079_5.R1011 5'-most EST wty700163223.h1

Method BLASTX
NCBI GI g3953458
BLAST score 302
E value 7.0e-27
Match length 67
% identity 81

NCBI Description (AC002328) F20N2.3 [Arabidopsis thaliana]

Seq. No. 263127

Contig ID 5079 8.R1011

5'-most EST uC-zmflmo17028d10a1

Method BLASTN NCBI GI g3452306

BLAST score 88 E value 1.0e-41 Match length 124 % identity 93

NCBI Description Zea mays retrotransposon Opie-3 5' LTR, partial sequence

Seq. No. 263128

Contig ID 5079_9.R1011

5'-most EST uC-zmflB73045b06b1

Method BLASTN
NCBI GI g3452304
BLAST score 160
E value 2.0e-84
Match length 669
% identity 89

NCBI Description Zea mays retrotransposon Opie-1 5' LTR, partial sequence

Seq. No. 263129

Contig ID 5079 13.R1011

5'-most EST LIB3062-047-Q1-K1-F2

Method BLASTN
NCBI GI g22447
BLAST score 128
E value 2.0e-65
Match length 458
% identity 85

NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein

Seq. No. 263130

Contig ID 5079_14.R1011

5'-most EST LIB3279-008-P1-K1-E10

88

Method BLASTN
NCBI GI g3452305
BLAST score 229
E value 1.0e-125
Match length 671

% identity



```
263131
Seq. No.
                  5079 15.R1011
Contig ID
                  hvj700622635.hl
5'-most EST
                  BLASTX
Method
                  q3953458
NCBI GI
                  940
BLAST score
                  1.0e-102
E value
                  242
Match length
                  75
% identity
                  (AC002328) F20N2.3 [Arabidopsis thaliana]
NCBI Description
                  263132
Seq. No.
                  5079 17.R1011
Contig ID
                  LIB3279-054-P1-K1-C10
5'-most EST
                  BLASTN
Method
                  q4185305
NCBI GI
BLAST score
                   64
                   2.0e-27
E value
                   93
Match length
                   93
% identity
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                   protein, polyprotein, and copia protein genes, complete
                   cds; and unknown genes
                   263133
Seq. No.
Contig ID
                   5080 1.R1011
5'-most EST
                   LIB3076-041-Q1-K1-G8
                   263134
Seq. No.
                   5080 2.R1011
Contig ID
5'-most EST
                   tzu700203612.h1
                   263135
Seq. No.
                   5084 1.R1011
Contig ID
                   uC-zmflmo17025d11a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3212854
BLAST score
                   585
                   7.0e-60
E value
                   353
Match length
                   42
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
                   263136
Seq. No.
                   5084 2.R1011
Contig ID
                   LIB148-032-Q1-E1-E5
5'-most EST
Method
                   BLASTX
                   g3415115
NCBI GI
                   1205
BLAST score
                   1.0e-135
E value
Match length
                   550
                   31
% identity
NCBI Description (AF081202) villin 2 [Arabidopsis thaliana]
```

NCBI Description Zea mays retrotransposon Opie-3 3' LTR, partial sequence



```
263137
Seq. No.
                   5084 3.R1011
Contig ID
                   xyt700343457.h1
5'-most EST
                   BLASTX
Method
                   g3451071
NCBI GI
                   1765
BLAST score
                   0.0e+00
E value
Match length
                   450
                   81
% identity
                   (AL031326) beta adaptin - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   263138
Seq. No.
                   5084 6.R1011
Contig ID
                   yyf700348741.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3415115
                   797
BLAST score
E value
                   3.0e-85
                   232
Match length
                   43
% identity
                  (AF081202) villin 2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   263139
                   5084 8.R1011
Contig ID
                   uC-zmflmo17310e06a1
5'-most EST
                   263140
Seq. No.
                   5084 9.R1011
Contig ID
                   uC-zmflMo17004g01b1
5'-most EST
                   BLASTX
Method
                   q3415117
NCBI GI
                   211
BLAST score
                   1.0e-16
E value
                   76
Match length
                   53
% identity
                  (AF081203) villin 3 [Arabidopsis thaliana]
NCBI Description
                   263141
Seq. No.
                   5084 12.R1011
Contig ID
                   uC-zmflb73184h06a1
5'-most EST
                   263142
Seq. No.
                   5084 14.R1011
Contig ID
                   uC-zmflmo17050b12b2
5'-most EST
                   BLASTX
Method
                   q3451071
NCBI GI
BLAST score
                   390
                   9.0e - 38
E value
                   95
Match length
                   84
% identity
```

NCBI Description (AL031326) beta adaptin - like protein [Arabidopsis thaliana]

Seq. No. 263143

Contig ID 5084_21.R1011 5'-most EST uC-zmflb73115a06a1



```
Seq. No.
                  263144
                  5086 1.R1011
Contig ID
                  LIB3076-041-Q1-K1-E11
5'-most EST
                  263145
Seq. No.
Contig ID
                  5089 1.R1011
                  LIB3076-015-Q1-K1-G8
5'-most EST
                  263146
Seq. No.
                  5090 1.R1011
Contig ID
5'-most EST
                  xmt700262285.h1
Method
                  BLASTX
                   q2435519
NCBI GI
                   446
BLAST score
                   3.0e-44
E value
Match length
                   103
                   81
% identity
                  (AF024504) similar to mouse MEM3 (GB:U47024 and S.
NCBI Description
                   cerevisiae vacuolar sorting protein 35 (SW; P34110)
                   [Arabidopsis thaliana]
                   263147
Seq. No.
Contig ID
                   5092 1.R1011
5'-most EST
                   LIB3076-040-Q1-K1-G8
                   263148
Seq. No.
                   5094 1.R1011
Contig ID
5'-most EST
                   LIB3076-040-Q1-K1-H4
Method
                   BLASTX
                   q498040
NCBI GI
BLAST score
                   211
                   3.0e-16
E value
Match length
                   55
                   75
% identity
NCBI Description (L33793) ORF [Senecio odorus]
                   263149
Seq. No.
                   5094 2.R1011
Contig ID
                   uC-zmroteosinte012c11b1
5'-most EST
                   BLASTX
Method
                   g498040
NCBI GI
                   455
BLAST score
                   9.0e-51
E value
                   177
Match length
% identity
NCBI Description (L33793) ORF [Senecio odorus]
                   263150
Seq. No.
                   5094 3.R1011
Contig ID
                   LIB3150-047-Q1-N1-A7
```

Contig ID 5094_3.R1011
5'-most EST LIB3150-047-Q1-1
Method BLASTX
NCBI GI g498040
BLAST score 321
E value 1.0e-29
Match length 94
% identity 63



```
NCBI Description (L33793) ORF [Senecio odorus]
                  263151
Seq. No.
                  5099 1.R1011
Contig ID
                  ceu700430121.h1
5'-most EST
                  263152
Seq. No.
                  5102 2.R1011
Contig ID
                  ymt700221459.h1
5'-most EST
                  BLASTX
Method
                  g1906830
NCBI GI
                  1616
BLAST score
                  0.0e+00
E value
                  466
Match length
                  66
% identity
                  (Y11829) heat shock protein [Arabidopsis thaliana]
NCBI Description
                  263153
Seq. No.
                  5106 1.R1011
Contig ID
                  LIB3066-001-Q1-K1-D6
5'-most EST
                  BLASTX
Method
                  q1370601
NCBI GI
                  1380
BLAST score
                  1.0e-153
E value
                  289
Match length
                  94
% identity
                 (X98244) annexin p33 [Zea mays]
NCBI Description
                  263154
Seq. No.
                  5106 2.R1011
Contig ID
                  LIB3069-025-Q1-K1-C4
5'-most EST
                  BLASTX
Method
                  q1370601
NCBI GI
                   605
BLAST score
                   5.0e-63
E value
                   136
Match length
% identity
                   88
NCBI Description (X98244) annexin p33 [Zea mays]
Seq. No.
                   263155
Contig ID
                   5109 1.R1011
                   xsy700212431.h1
5'-most EST
                   BLASTX
Method
                   q3785989
NCBI GI
BLAST score
                   511
                   4.0e-51
E value
                   224
Match length
                   52
% identity
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]
                   263156
Seq. No.
                   5109 2.R1011
Contig ID
                   uC-zmflm017214d02b1
5'-most EST
                   BLASTX
Method
```

36494

g4220488

4.0e-32

346

NCBI GI

E value

BLAST score



```
186
Match length
                  48
% identity
                  (AC006069) unknown protein, 5' partial [Arabidopsis
NCBI Description
                  thaliana]
                  263157
Seq. No.
                  5109 3.R1011
Contig ID
                  LIB3156-001-Q1-K1-F3
5'-most EST
                  BLASTX
Method
                  g4539459
NCBI GI
                  693
BLAST score
                  7.0e-73
E value
                  250
Match length
                   55
% identity
                  (AL049500) putative protein [Arabidopsis thaliana]
NCBI Description
                   263158
Seq. No.
                   5109 7.R1011
Contig ID
                  uC-zmf1b73062b04b1
5'-most EST
                  BLASTN
Method
                   g3819531
NCBI GI
                   143
BLAST score
                   3.0e-74
E value
                   190
Match length
                   94
% identity
NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG2067.uni
                   263159
Seq. No.
                   5109 8.R1011
Contig ID
                   uC-zmflmo17295g04b1
5'-most EST
                   BLASTX
Method
                   q3785989
NCBI GI
                   1077
BLAST score
                   1.0e-120
E value
                   279
Match length
                   74
% identity
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]
Seq. No.
                   263160
Contig ID
                   5109 11.R1011
                   ymt700223425.h1
5'-most EST
                   263161
Seq. No.
                   5109 12.R1011
Contig ID
5'-most EST
                   uC-zmflb73137g02b1
                   263162
Seq. No.
                   5109 13.R1011
Contig ID
                   LIB3150-051-Q1-N1-G4
5'-most EST
```

Method BLASTX
NCBI GI g3785989
BLAST score 505
E value 3.0e-51
Match length 118
% identity 78

NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]



```
263163
Seq. No.
                  5109 14.R1011
Contig ID
                  LIB3079-022-Q1-K1-B6
5'-most EST
                  263164
Seq. No.
                  5109 15.R1011
Contig ID
                  uC-zmflmo17306h01b1
5'-most EST
                  BLASTN
Method
NCBI GI
                  a3819531
                  135
BLAST score
                  1.0e-69
E value
                  166
Match length
                  95
% identity
NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG2067.uni
                  263165
Seq. No.
                  5109 16.R1011
Contig ID
                  uC-zmflmo17210a02a1
5'-most EST
Method
                  BLASTN
                  a3819531
NCBI GI
                  163
BLAST score
                  2.0e-86
E value
                  190
Match length
                   96
% identity
NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG2067.uni
                   263166
Seq. No.
                   5109 17.R1011
Contig ID
5'-most EST
                   gct701176543.h1
                   263167
Seq. No.
                   5109 18.R1011
Contig ID
5'-most EST
                   fwa700101509.hl
Seq. No.
                   263168
                   5109 19.R1011
Contig ID
                   nbm700477758.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3785989
BLAST score
                   257
E value
                   3.0e-22
                   67
Match length
                   69
% identity
NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]
                   263169
Seq. No.
                   5110 1.R1011
Contig ID
                   LIB3059-021-Q1-K1-H6
5'-most EST
                   BLASTX
Method
                   g2500380
NCBI GI
```

Method BLASTX
NCBI GI g2500380
BLAST score 411
E value 6.0e-40
Match length 105
% identity 74

NCBI Description 60S RIBOSOMAL PROTEIN L44 >gi_2119128_pir__ JC4923 ribosomal protein RL44 - upland cotton >gi_1553129 (U64677) ribosomal

protein L44 isoform a [Gossypium hirsutum] >gi_1553131



```
(U64678) ribosomal protein L44 isoform b [Gossypium
                  hirsutum]
                  263170
Seq. No.
                  5110 3.R1011
Contig ID
                  uC-zmflmo17309h09b1
5'-most EST
                  BLASTX
Method
                  q170920
NCBI GI
                  297
BLAST score
                  5.0e-35
E value
                  104
Match length
                  75
% identity
                  (M62396) ribosomal protein L41 [Candida maltosa]
NCBI Description
                  263171
Seq. No.
                   5110 4.R1011
Contig ID
                  LIB3076-039-Q1-K1-D6
5'-most EST
                  BLASTX
Method
                  q3122753
NCBI GI
BLAST score
                   312
                   1.0e-28
E value
                   93
Match length
                   68
% identity
                   60S RIBOSOMAL PROTEIN L44 >gi_2244789 emb CAB10211.1
NCBI Description
                   (Z97336) ribosomal protein [Arabidopsis thaliana]
                   263172
Seq. No.
                   5110 6.R1011
Contig ID
                   uwc700156345.h1
5'-most EST
                   BLASTX
Method
                   q3122753
NCBI GI
                   244
BLAST score
                   8.0e-21
E value
                   94
Match length
                   60
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L44 >gi_2244789_emb_CAB10211.1_
                   (Z97336) ribosomal protein [Arabidopsis thaliana]
                   263173
Seq. No.
                   5112 1.R1011
Contig ID
5'-most EST
                   LIB3076-039-Q1-K1-E4
                   263174
Seq. No.
                   5119 1.R1011
Contig ID
                   uC-z\overline{m}flb73099g06b1
5'-most EST
Method
                   BLASTX
                   g3757521
NCBI GI
                   741
BLAST score
                   2.0e-78
E value
Match length
                   262
                   53
% identity
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]
                   263175
Seq. No.
```

Contig ID 5121_1.R1011
5'-most EST uC-zmflb73201b01b1
Method BLASTX



NCBI GI g3510259 BLAST score 888 E value 1.0e-95 Match length 198 % identity 83

NCBI Description (AC005310) putative inorganic pyrophosphatase [Arabidopsis

thaliana] >gi 3522960 (AC004411) putative inorganic

pyrophosphatase [Arabidopsis thaliana]

Seq. No. 263176

Contig ID 5121_2.R1011 5'-most EST uer700583268.h1

Method BLASTX
NCBI GI g3510259
BLAST score 731
E value 4.0e-77
Match length 199
% identity 83

NCBI Description (AC005310) putative inorganic pyrophosphatase [Arabidopsis

thaliana] >gi_3522960 (AC004411) putative inorganic

pyrophosphatase [Arabidopsis thaliana]

Seq. No. 263177

" Contig ID 5121 5.R1011

5'-most EST LIB3076-039-Q1-K1-A9

Method BLASTX
NCBI GI g3695383
BLAST score 397
E value 3.0e-38
Match length 111
% identity 73

NCBI Description (AF096370) similar to inorganic pyrophosphatase (Pfam:

PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis

thaliana]

Seq. No. 263178
Contig ID 5128_1.R1011

5'-most EST LIB3076-039-Q1-K1-B7

Seq. No. 263179 Contig ID 5130_1.R1011

5'-most EST LIB3076-039-Q1-K1-B9

 Seq. No.
 263180

 Contig ID
 5132_1.R1011

 5'-most EST
 nbm700477709.h1

Seq. No. 263181 Contig ID 5134 1.R1011

5'-most EST uC-zmflMo17004e11b1

Method BLASTN
NCBI GI g3821780
BLAST score 37
E value 3.0e-11
Match length 49
% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1



Seq. No. 263182

Contig ID 5138_1.R1011

5'-most EST uC-zmflb73305h11b2

Method BLASTX
NCBI GI g3063444
BLAST score 557
E value 1.0e-62
Match length 154
% identity 75

NCBI Description (AC003981) F22013.5 [Arabidopsis thaliana]

Seq. No. 263183

Contig ID 5138_2.R1011 5'-most EST dyk700102443.h1

Seq. No. 263184

Contig ID 5142 2.R1011

5'-most EST LIB3076-038-Q1-K1-G6

Seq. No. 263185

Contig ID 5144_1.R1011

5'-most EST uC-zmflmo17241d08b1

Method BLASTX
NCBI GI g3929376
BLAST score 146
E value 1.0e-08
Match length 101
% identity 37

NCBI Description SPLICING FACTOR, ARGININE/SERINE-RICH 8 (SUPPRESSOR OF

WHITE APRICOT PROTEIN HOMOLOG) >gi 508231 (U08377) similar

to the Drosophila splicing regulator,

suppressor-of-white-apricot: Swiss-Prot Accession Number

P12297 [Homo sapiens]

Seq. No. 263186

Contig ID 5145_1.R1011

5'-most EST LIB3076-038-Q1-K1-E7

Seq. No. 263187

Contig ID 5147_1.R1011

5'-most EST LIB3067-005-Q1-K1-G9

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 2.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 263188

Contig ID 5147_2.R1011 5'-most EST xsy700211438.h1

Seq. No. 263189 Contig ID 5148_1.R1011 5'-most EST tfd700572004.h1



```
BLASTX
Method
                  g3128220
NCBI GI
                  910
BLAST score
                  2.0e-98
E value
                  186
Match length
                  92
% identity
                   (AC004077) putative urease accessory protein [Arabidopsis
NCBI Description
                  thaliana] >gi 3337375 (AC004481) putative urease accessory
                  protein [Arabidopsis thaliana]
                  263190
Seq. No.
                  5148 3.R1011
Contig ID
5'-most EST
                  pmx700085546.h1
                  BLASTX
Method
                   q4324678
NCBI GI
                   550
BLAST score
                   2.0e-56
E value
Match length
                   120
                   88
% identity
                   (AF109374) urease accessory protein UREG [Arabidopsis
NCBI Description
                   thaliana]
                   263191
Seq. No.
                   5150 1.R1011
Contig ID
                   vux700161546.hl
5'-most EST
                   BLASTX
Method
                   q4507131
NCBI GI
                   340
BLAST score
                   8.0e-32
E value
Match length
                   74
% identity
                   small nuclear ribonucleoprotein polypeptide F
NCBI Description
                   >gi 1085384 pir S55053 Sm protein F - human
                   >gi 806564 emb CAA59688 (X85372) Sm protein F [Homo
                   sapiens]
                   263192
Seq. No.
                   5150 2.R1011
Contig ID
                   cat7\overline{0}0016893.r1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4507131
BLAST score
                   340
                   1.0e-31
E value
Match length
                   74
                   81
% identity
                   small nuclear ribonucleoprotein polypeptide F
NCBI Description
                   >gi 1085384 pir_ S55053 Sm protein F - human
                   >gi_806564_emb_CAA59688_ (X85372) Sm protein F [Homo
                   sapiens]
                   263193
Seq. No.
                   5151 1.R1011
Contig ID
                   ntr700076636.hl
5'-most EST
                   BLASTX
Method
```

36500

q2959358

4.0e-69

660

NCBI GI

E value

BLAST score



Match length % identity

NCBI Description (X96758) clathrin coat assembly protein AP17 [Zea mays]

Seq. No. Contig ID 263194

5156 1.R1011 5'-most EST nbm700465135.h1

Seq. No.

263195

Contig ID 5156 2.R1011

5'-most EST uC-zmflmo17337a07a1

Seq. No.

263196

5157 1.R1011 Contig ID

uC-zmflmo17109e10b1 5'-most EST

BLASTX Method NCBI GI q4538961 BLAST score 468 E value 3.0e-46Match length 254 49 % identity

(AL049488) isoleucine-tRNA ligase-like protein [Arabidopsis NCBI Description

thaliana]

Seq. No.

263197 5157 3.R1011

Contig ID 5'-most EST

uC-zmflb73319c12b1

Method BLASTX g4538961 NCBI GI 512 BLAST score 5.0e-52 E value Match length 158 63

% identity

(AL049488) isoleucine-tRNA ligase-like protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 263198

5158 1.R1011 Contig ID 5'-most EST gct701174940.h1

Seq. No. 263199

5158 2.R1011 Contig ID

5'-most EST LIB3117-001-Q1-K1-D11

Seq. No. 263200

Contig ID 5160 1.R1011

LIB3067-043-Q1-K1-B2 5'-most EST

Method BLASTX NCBI GI g339878 BLAST score 194 E value 2.0e-14 196 Match length % identity

NCBI Description (M55169) tripeptidyl peptidase II [Homo sapiens]

Seq. No. 263201

Contig ID 5160 2.R1011



```
5'-most EST
                  uC-zmflmo17306g03a1
                  263202
Seq. No.
                  5161 1.R1011
Contig ID
                  xmt7\overline{0}0267874.h1
5'-most EST
                  BLASTX
Method
                  g541824
NCBI GI
BLAST score
                  1989
E value
                  0.0e + 00
                  501
Match length
                  76
% identity
NCBI Description protein kinase - spinach > gi 457709 emb CAA82991 (Z30330)
                  protein kinase [Spinacia oleracea]
Seq. No.
                  263203
Contig ID
                  5163 1.R1011
5'-most EST
                  uC-zmflb73123h01a1
Method
                  BLASTX
NCBI GI
                  q629669
BLAST score
                  318
                  5.0e-29
E value
Match length
                  155
% identity
                  46
NCBI Description hypothetical protein - tomato
                  263204
Seq. No.
Contig ID
                  5164 1.R1011
5'-most EST
                  nwy700443706.h1
                  263205
Seq. No.
                  5168_1.R1011
Contig ID
5'-most EST
                  LIB3076-038-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  g2194126
BLAST score
                  331
E value
                  3.0e-59
Match length
                  222
                  59
% identity
NCBI Description (AC002062) EST gb T43335 comes from this gene. [Arabidopsis
                  thaliana]
                  263206
Seq. No.
                  5174 1.R1011
Contig ID
5'-most EST
                  LIB3076-038-Q1-K1-E12
Method
                  BLASTX
                  q3924605
NCBI GI
BLAST score
                  260
E value
                  2.0e-22
Match length
                  90
% identity
                  57
NCBI Description (AF069442) putative inhibitor of apoptosis [Arabidopsis
                  thaliana]
```

36502

263207

5175 1.R1011

uC-zmroteosinte041f10b1

Seq. No.

Contig ID 5'-most EST



```
263208
Seq. No.
                  5176 1.R1011
Contig ID
                  uC-zmflmo17100d05b1
5'-most EST
Seq. No.
                  263209
                  5176 2.R1011
Contig ID
                  LIB3279-055-P1-K1-C3
5'-most EST
                  263210
Seq. No.
                  5176 3.R1011
Contig ID
5'-most EST
                  uC-zmflb73285b01a1
                  263211
Seq. No.
                  5179 1.R1011
Contig ID
                  uC-z\overline{m}flmo17309h10b1
5'-most EST
                  BLASTX
Method
                   q4490316
NCBI GI
                   788
BLAST score
                   1.0e-83
E value
Match length
                   381
                   45
% identity
                  (AL035678) nucellin-like protein [Arabidopsis thaliana]
NCBI Description
                   263212
Seq. No.
                   5180 1.R1011
Contig ID
                   uC-zmflmo17042d10b1
5'-most EST
                   BLASTX
Method
                   g128191
NCBI GI
BLAST score
                   160
E value
                   2.0e-10
                   73
Match length
% identity
                  NITRATE REDUCTASE (NAD(P)H) >gi 66210 pir RDBHNP nitrate
NCBI Description
                   reductase (NAD(P)H) (EC 1.6.6.2) - barley
                   >gi 19065_emb_CAA42739_ (X60173) nitrate reductase
                   (NAD(P)H) [Hordeum vulgare]
                   263213
Seq. No.
Contig ID
                   5183 1.R1011
                   LIB3059-048-Q1-K1-E5
5'-most EST
Method
                   BLASTX
                   q1350707
NCBI GI
                   178
BLAST score
                   7.0e-13
E value
Match length
                   47
```

68 % identity

60S RIBOSOMAL PROTEIN L29 >gi_539923_pir__JC2012 ribosomal NCBI Description protein 17K - mouse >gi_404766 (L08651) ribosomal protein

[Mus musculus]

263214 Seq. No. 5183 2.R1011 Contig ID 5'-most EST LIB3078-034-Q1-K1-E9

BLASTX Method g132964 NCBI GI

178 BLAST score 8.0e-13 E value



Match length % identity 68

60S RIBOSOMAL PROTEIN L29 (P23) >gi_71376_pir__R6RT43 NCBI Description ribosomal protein RL43 - rat >gi 57145 emb CAA43146

(X60744) ribosomal protein [Rattus norvegicus]

>gi 312208 emb CAA48344 (X68283) rat ribosomal protein L29

[Rattus norvegicus]

263215 Seq. No.

5183 4.R1011 Contig ID

LIB143-039-Q1-E1-D1 5'-most EST

BLASTX Method NCBI GI g1350707 BLAST score 187 E value 6.0e-14

Match length 50 68 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L29 >gi 539923 pir JC2012 ribosomal

protein 17K - mouse >gi 404766 (L08651) ribosomal protein

[Mus musculus]

Seq. No. 263216

Contig ID 5183 5.R1011

5'-most EST LIB3078-001-Q1-K1-F12

Method BLASTX g1350707 NCBI GI BLAST score 197 4.0e-15 E value 52 Match length

69 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L29 >gi_539923_pir__JC2012 ribosomal

protein 17K - mouse >gi_404766 (L08651) ribosomal protein

[Mus musculus]

Seq. No. 263217

Contig ID 5183 8.R1011

5'-most EST uC-zmroteosinte006h09b1

263218 Seq. No.

5186 1.R1011 Contig ID tfd700572106.hl 5'-most EST

BLASTX Method NCBI GI q2414584 BLAST score 228 E value 4.0e-18 Match length 156 % identity

NCBI Description (299292) dna repair protein [Schizosaccharomyces pombe]

Seq. No. 263219

Contig ID 5187 1.R1011

5'-most EST uC-zmflb73346d05a2

Method BLASTX NCBI GI q4539452 BLAST score 437 4.0e-85 E value Match length 219



72

% identity

NCBI Description

% identity (AL049500) putative phosphoribosylanthranilate transferase NCBI Description [Arabidopsis thaliana] 263220 Seq. No. 5190 1.R1011 Contig ID ymt700223490.h1 5'-most EST BLASTX Method NCBI GI q4512707 1012 BLAST score 1.0e-110 E value 365 Match length 59 % identity (AC006569) hypothetical protein [Arabidopsis thaliana] NCBI Description 263221 Seq. No. 5191 1.R1011 Contig ID ymt700221266.h1 5'-most EST 263222 Seq. No. 5195 1.R1011 Contig ID uC-zmflmo17293b07b1 5'-most EST BLASTX Method NCBI GI g3378104 219 BLAST score 1.0e-17 E value 96 Match length % identity (AF047473) testis mitotic checkpoint BUB3 [Homo sapiens] NCBI Description 263223 Seq. No. 5195 2.R1011 Contig ID uC-zmflmo17150e08b1 5'-most EST BLASTX Method g2921873 NCBI GI 928 BLAST score 1.0e-100 E value 317 Match length 55 % identity (AF047472) spleen mitotic checkpoint BUB3 [Homo sapiens] NCBI Description >gi 2981231_gb_AAC06258_ (AF053304) mitotic checkpoint component Bub3 [Homo sapiens] >gi_3639060 (AF081496) kinetochore protein BUB3 [Homo sapiens] 263224 Seq. No. 5196 1.R1011 Contig ID $uC-z\overline{m}flb73143b08b1$ 5'-most EST BLASTX Method g2129471 NCBI GI 1075 BLAST score 1.0e-117 E value 293 Match length

36505

precursor - Scotch pine >gi_1100223 (L32560)

glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)

glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]



```
263225
Seq. No.
                  5196 2.R1011
Contig ID
                  LIB3279-051-P1-K1-C3
5'-most EST
                  BLASTX
Method
                  g2129471
NCBI GI
BLAST score
                  862
                  1.0e-92
E value
                  209
Match length
                  78
% identity
                  glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
NCBI Description
                  precursor - Scotch pine >gi 1100223 (L32560)
                  glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
                  263226
Seq. No.
                  5196 3.R1011
Contig ID
                  LIB3076-037-Q1-K1-G11
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2129471
BLAST score
                   205
E value
                   5.0e-16
                   45
Match length
                   84
% identity
                  glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
NCBI Description
                  precursor - Scotch pine >gi 1100223 (L32560)
                   glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
                   263227
Seq. No.
                   5198 1.R1011
Contig ID
5'-most EST
                   uC-zmroteosinte100a10b2
Method
                   BLASTX
                   q4090257
NCBI GI
                   465
BLAST score
                   2.0e-46
E value
                   91
Match length
% identity
                   97
                  (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
NCBI Description
Seq. No.
                   263228
                   5198 2.R1011
Contig ID
                   LIB3076-013-Q1-K1-D4
5'-most EST
                   BLASTX
Method
                   q4090257
NCBI GI
BLAST score
                   465
                   2.0e-46
E value
Match length
                   91
                   97
% identity
                  (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
NCBI Description
                   263229
Seq. No.
                   5198 3.R1011
Contig ID
                   LIB3088-027-Q1-K1-D8
5'-most EST
                   BLASTX
Method
                   q4090257
NCBI GI
                   465
BLAST score
                   3.0e-46
E value
                   91
Match length
```

97

% identity



```
(AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
NCBI Description
                   263230
Seq. No.
Contig ID
                   5198 4.R1011
5'-most EST
                  LIB3069-012-Q1-K1-B10
Method
                  BLASTX
                   q4090257
NCBI GI
BLAST score
                   424
                   1.0e-41
E value
                   84
Match length
                   95
% identity
                  (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
NCBI Description
Seq. No.
                   263231
                   5198 5.R1011
Contig ID
5'-most EST
                   LIB3078-011-Q1-K1-G8
Method
                   BLASTX
                   q4090257
NCBI GI
BLAST score
                   465
                   2.0e-46
E value
                   91
Match length
                   97
% identity
                  (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
NCBI Description
                   263232
Seq. No.
                   5198 6.R1011
Contig ID
                   LIB143-006-Q1-E1-F1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4090257
BLAST score
                   384
                   7.0e-37
E value
                   88
Match length
                   82
% identity
                   (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
NCBI Description
Seq. No.
                   263233
                   5198 9.R1011
Contig ID
                   vux700159177.h1
5'-most EST
Method
                   BLASTX
                   g4090257
NCBI GI
BLAST score
                   163
                   2.0e-15
E value
                   48
Match length
                   96
% identity
                   (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
NCBI Description
                   263234
Seq. No.
                   5198 10.R1011
Contig ID
5'-most EST
                   vux700156640.hl
Method
                   BLASTX
NCBI GI
                   g4090257
BLAST score
                   371
                   1.0e-35
E value
                   87
Match length
                   83
% identity
NCBI Description (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
```



```
263235
Seq. No.
Contig ID
                  5199 1.R1011
                  pmx700086687.hl
5'-most EST
                  263236
Seq. No.
                  5201 1.R1011
Contig ID
                  wyr700237308.hl
5'-most EST
                  BLASTX
Method
                  a2492519
NCBI GI
                   2146
BLAST score
                  0.0e + 00
E value
                   426
Match length
                   97
% identity
                  26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
NCBI Description
                   7) >gi 1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase
                   subunit [Spinacia oleracea]
                   263237
Seq. No.
                   5201 3.R1011
Contig ID
5'-most EST
                  LIB3151-046-Q1-K1-E5
                  BLASTX
Method
                   q3914449
NCBI GI
BLAST score
                   513
                   3.0e-52
E value
Match length
                   111
                   88
% identity
                   26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
NCBI Description
                   7) >gi 3172331 (AF041258) 26S proteasome subunit 7 [Prunus
                   persica]
                   263238
Seq. No.
Contig ID
                   5201 4.R1011
                   LIB3150-110-P2-K1-A1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2492519
BLAST score
                   240
                   4.0e-20
E value
Match length
                   49
                   94
% identity
                   26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
NCBI Description
                   7) >qi 1395191 dbj BAA13021 (D86121) 26S proteasome ATPase
                   subunit [Spinacia oleracea]
Seq. No.
                   263239
Contig ID
                   5201 7.R1011
                   ntr700072994.h1
5'-most EST
Method
                   BLASTX
                   g3914449
NCBI GI
                   348
BLAST score
                   4.0e-33
E value
                   77
```

Match length 86 % identity

26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT NCBI Description 7) >gi 3172331 (AF041258) 26S proteasome subunit 7 [Prunus

persica]

263240 Seq. No.



5201 10.R1011 Contig ID xsy700208318.hl 5'-most EST BLASTX Method g3914449 NCBI GI 411 BLAST score 4.0e-40 E value 129 Match length 66 % identity 26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT NCBI Description 7) >gi 3172331 (AF041258) 26S proteasome subunit 7 [Prunus persica] 263241 Seq. No. 5203 1.R1011 Contig ID uC-zmflb73220g08b2 5'-most EST 263242 Seq. No. 5203 2.R1011 Contig ID $\texttt{tzu7}\overline{\texttt{0}}\texttt{0206189.h1}$ 5'-most EST 263243 Seq. No. 5205 1.R1011 Contig ID LIB3061-050-Q1-K1-A11 5'-most EST BLASTX Method q4105782 NCBI GI 925 BLAST score 1.0e-100 E value 215 Match length 79 % identity NCBI Description (AF049922) PGP169-12 [Petunia x hybrida] 263244 Seq. No. 5205 2.R1011 Contig ID dyk700106826.h15'-most EST BLASTN Method g3821780 NCBI GI 34 BLAST score 2.0e-09 E value 34 Match length 100 % identity NCBI Description Xenopus laevis cDNA clone 27A6-1 263245 Seq. No. 5206 1.R1011 Contig ID uC-zmroteosinte098g12b2 5'-most EST BLASTX Method q4567283 NCBI GI BLAST score 844 2.0e-90 E value 234 Match length

72 % identity NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

263246 Seq. No. 5206 2.R1011 Contig ID

LIB3067-006-Q1-K1-F1 5'-most EST

Method BLASTX



g4567283 NCBI GI 811 BLAST score 1.0e-86 E value 344 Match length 55 % identity (AC006841) unknown protein [Arabidopsis thaliana] NCBI Description 263247 Seq. No. 5206 3.R1011 Contig ID $yyf7\overline{0}0348566.h1$ 5'-most EST BLASTX Method q4567235 NCBI GI 726 BLAST score 8.0e-77 E value 203 Match length 67 % identity (AC007119) putative phosphatidylinositol/phophatidylcholine NCBI Description transfer protein [Arabidopsis thaliana] 263248 Seq. No. 5208 1.R1011 Contig ID rvt700548345.h1 5'-most EST 263249 Seq. No. 5210 1.R1011 Contig ID uC-zmflb73097e01b1 5'-most EST BLASTX Method g4263779 NCBI GI 195 BLAST score 2.0e-22 E value 194 Match length 36 % identity (AC006068) hypothetical protein [Arabidopsis thaliana] NCBI Description 263250 Seq. No. 5211 1.R1011 Contig ID 5'-most EST uC-zmflmo17103e01b1 263251 Seq. No. 5213 1.R1011 Contig ID hvj700619610.h1 5'-most EST BLASTX Method g2737973 NCBI GI 1833 BLAST score 0.0e + 00E value Match length 355 100 % identity NCBI Description (U83625) protein kinase ZmMEK1 [Zea mays] 263252 Seq. No. 5214 1.R1011 Contig ID rv1700456358.h1 5'-most EST BLASTX Method

g464806 NCBI GI BLAST score 166 1.0e-16 E value Match length 191



% identity 32
NCBI Description
NCBI Description
SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72)
>gi_423182_pir__A40692 signal recognition particle 72K
chain - dog >gi_297768_emb_CAA48014_ (X67813) signal

recognition particle, 72 kDa subunit [Canis familiaris]

Seq. No. 263253

Contig ID 5218 1.R1011 5'-most EST xsy700217842.h1

Method BLASTX
NCBI GI g4587570
BLAST score 148
E value 3.0e-09
Match length 192
% identity 26

NCBI Description (AC006550) Strong similarity to gi_2244833 centromere

protein homolog from Arabidopsis thaliana chromosome 4 contig gb Z97337. ESTs gb T20765 and gb AA586277 come from

this gene

Seq. No. 263254

Contig ID 5219_1.R1011 5'-most EST pmx700091847.h1

Method BLASTX
NCBI GI g2252863
BLAST score 839
E value 9.0e-90
Match length 392
% identity 47

NCBI Description (AF013294) similar to nucleolin protein [Arabidopsis

thaliana]

Seq. No. 263255

Contig ID 5219_3.R1011 5'-most EST cat700020393.r1

Seq. No. 263256

Contig ID 5220 1.R1011

5'-most EST LIB3076-037-Q1-K1-E2

Method BLASTX
NCBI GI g401621
BLAST score 204
E value 8.0e-16
Match length 138
% identity 40

NCBI Description HYPOTHETICAL 20.4 KD PROTEIN IN TNAB-BGLB INTERGENIC REGION

>gi 290561 (L10328) o188 [Escherichia coli] >gi_1790149
(AE000448) orf, hypothetical protein [Escherichia coli]

Seq. No. 263257
Contig ID 5221_1.R1011

5'-most EST LIB3076-037-Q1-K1-B6

Seq. No. 263258

Contig ID 5227_1.R1011

5'-most EST uC-zmroB73013a01b1

Method BLASTX

```
g3269293
                    NCBI GI
                                                                                472
                    BLAST score
                                                                                9.0e-47
                    E value
                                                                                184
                    Match length
                                                                                54
                     % identity
                    NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
                                                                                263259
                     Seq. No.
                     Contig ID
                                                                                5227 2.R1011
                                                                                uC-z\overline{m}flmo17175d02a1
                     5'-most EST
                                                                                263260
                     Seq. No.
                                                                                5227 3.R1011
                     Contig ID
                                                                                uC-zmflmo17175d02b1
                     5'-most EST
                                                                                BLASTX
                     Method
                                                                                g3269293
                     NCBI GI
                                                                                 475
                     BLAST score
                                                                                 3.0e-47
                     E value
                                                                                179
                     Match length
                                                                                 54
                      % identity
                     NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
                                                                                 263261
                     Seq. No.
                                                                                 5227 5.R1011
                     Contig ID
                                                                                dyk700105201.hl
                      5'-most EST
                                                                                 263262
                     Seq. No.
                                                                                 5228 1.R1011
                      Contig ID
                      5'-most EST
                                                                                 uC-zmflb73118b03b1
                                                                                 BLASTX
                     Method
                                                                                 q3176874
                     NCBI GI
                                                                                 1073
                      BLAST score
                                                                                 1.0e-117
                      E value
                                                                                 328
                      Match length
                                                                                  61
                      % identity
                                                                                  (AF065639) cucumisin-like serine protease [Arabidopsis
                NCBI Description
                                                                                 thaliana]
A STATE OF THE STA
                                                                                  263263
                      Seq. No.
                      Contig ID
                                                                                  5229 1.R1011
                                                                                 LIB3180-020-P2-M1-E5
                      5'-most EST
                      Method
                                                                                  BLASTX
                                                                                  q1174470
                      NCBI GI
                      BLAST score
                                                                                  1575
                                                                                  1.0e-176
                      E value
```

Match length 528 58 % identity

OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) NCBI Description

(INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf _2208301A

integral membrane protein [Mus musculus]

263264 Seq. No.

5230 2.R1011 Contig ID

LIB3118-002-Q1-K1-G8 5'-most EST

Method BLASTX g2760323 NCBI GI



183 BLAST score 2.0e-13 E value 73 Match length 45 % identity

NCBI Description (AC002130) F1N21.8 [Arabidopsis thaliana]

263265 Seq. No. Contig ID 5230 3.R1011 fdz701161212.hl 5'-most EST

BLASTX Method g2760323 NCBI GI 274 BLAST score 8.0e-24 E value Match length 108

31 % identity

NCBI Description (AC002130) F1N21.8 [Arabidopsis thaliana]

263266 Seq. No.

Contig ID 5230 4.R1011 ymt700224848.h15'-most EST

263267 Seq. No.

5233 1.R1011 Contig ID

5'-most EST uC-zmflmo17181a12b1

263268 Seq. No.

5238 1.R1011 Contig ID uwc700152532.h1 5'-most EST

Seq. No. 263269

5238 2.R1011 Contig ID

LIB3088-036-Q1-K1-D2 5'-most EST

263270 Seq. No.

5238 3.R1011 Contig ID

LIB3079-023-Q1-K1-A3 5'-most EST

263271 Seq. No.

Contig ID 5238 4.R1011 fdz701161629.hl 5'-most EST

263272 Seq. No.

5240 1.R1011 Contig ID xit700094377.h1 5'-most EST

Method BLASTX g2501005 NCBI GI 167 BLAST score 4.0e-11 E value 147 Match length % identity 33

HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS) NCBI Description

>gi_2137380_pir__JC5223 histidine--tRNA ligase (EC 6.1.1.21) - mouse >gi 1209683 (U39473) histidyl-tRNA

synthetase [Mus musculus]

263273 Seq. No.

5241 1.R1011 Contig ID



5'-most EST

pmx700084060.h1

```
263274
Seq. No.
                   5243 1.R1011
Contig ID
                  LIB36-012-Q1-E1-H2
5'-most EST
                   263275
Seq. No.
                   5245 1.R1011
Contig ID
                   xsy7\overline{0}0212184.h1
5'-most EST
                   BLASTX
Method
                   g2781347
NCBI GI
                   1666
BLAST score
                   0.0e+00
E value
                   514
Match length
                   63
% identity
                  (AC003113) F2401.3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   263276
Contig ID
                   5245 3.R1011
5'-most EST
                   uC-zmflmo17097c10b1
                   BLASTX
Method
                   q2961357
NCBI GI
                   256
BLAST score
E value
                   4.0e-22
                   80
Match length
                   66
% identity
                   (AL022140) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   263277
Contig ID
                   5247 1.R1011
                   ceu700430037.h1
5'-most EST
                   BLASTX
Method
                   q4538939
NCBI GI
BLAST score
                   604
E value
                   3.0e-62
                   283
Match length
                   50
% identity
                   (ALO49483) Col-O casein kinase I-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   263278
Seq. No.
                   5247 2.R1011
Contig ID
                   xsy700211729.hl
5'-most EST
                   263279
Seq. No.
                   5248 1.R1011
Contig ID
                   LIB3150-082-P1-N1-F4
5'-most EST
                   BLASTX
Method
                   g4001720
NCBI GI
                   213
BLAST score
                   7.0e-17
E value
                   91
Match length
                   42
% identity
                   (AB015894) neural specific sr protein NSSR 1 [Mus musculus]
NCBI Description
                   263280
Seq. No.
```

5248 3.R1011

Contig ID

Match length



```
LIB3136-018-Q1-K1-E8
5'-most EST
                  263281
Seq. No.
                   5250 1.R1011
Contig ID
                  uC-zmflb73194a02b2
5'-most EST
                  BLASTX
Method
                   q1654381
NCBI GI
                   186
BLAST score
                   2.0e-13
E value
                   195
Match length
                   27
% identity
                   (U70017) cyclin D-interacting myb-like protein [Mus
NCBI Description
                   musculus]
                   263282
Seq. No.
                   5253 1.R1011
Contig ID
                   LIB3076-036-Q1-K1-B8
5'-most EST
                   BLASTN
Method
                   q3821780
NCBI GI
                   36
BLAST score
E value
                   2.0e-10
Match length
                   48
                   67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   263283
                   5263 1.R1011
Contig ID
                   uC-zmroteosinte018f08b1
5'-most EST
                   BLASTX
Method
                   g3819164
NCBI GI
                   1439
BLAST score
                   1.0e-160
E value
                   321
Match length
                   87
% identity
                   (AJ012318) cytosolic chaperonin, delta-subunit [Glycine
NCBI Description
                   max]
                   263284
Seq. No.
                   5263 2.R1011
Contig ID
                   uC-zmflmo17174f12a1
5'-most EST
                   BLASTX
Method
                   q3819164
NCBI GI
                   217
BLAST score
                   2.0e-17
E value
                   48
Match length
% identity
                   (AJ012318) cytosolic chaperonin, delta-subunit [Glycine
NCBI Description
                   max]
                   263285
Seq. No.
Contig ID
                   5264 1.R1011
                   LIB3076-035-Q1-K1-G7
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3461831
BLAST score
                   262
                   9.0e-23
E value
```



% identity 46 NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]

 Seq. No.
 263286

 Contig ID
 5265_1.R1011

 5'-most EST
 rv1700457671.h1

Seq. No. 263287

Contig ID 5271_1.R1011

5'-most EST uC-zmflmo17001b08b1

Seq. No. 263288 Contig ID 5271_2.R1011

5'-most EST LIB3076-036-Q1-K1-A11

Seq. No. 263289

Contig ID 5272 1.R1011

5'-most EST uC-zmflmo17138f03b1

Method BLASTX
NCBI GI g4160280
BLAST score 503
E value 9.0e-71
Match length 363
% identity 43

NCBI Description (AJ006224) purple acid phosphatase [Ipomoea batatas]

Seq. No. 263290 5273 1

Contig ID 5273_1.R1011 5'-most EST wyr700242562.h1

Method BLASTX
NCBI GI g4531444
BLAST score 1091
E value 1.0e-119
Match length 326
% identity 64

NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No. 263291

Contig ID 5273_2.R1011 5'-most EST fwa700097592.h1

Method BLASTX
NCBI GI g4531444
BLAST score 244
E value 1.0e-20
Match length 121
% identity 47

% identity 47
NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]

 Seq. No.
 263292

 Contig ID
 5277_1.R1011

5'-most EST uC-zmflmo17011b10b1

Method BLASTX
NCBI GI g3617770
BLAST score 848
E value 1.0e-141
Match length 348
% identity 66

5'-most EST

Method



```
NCBI Description
                  (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]
                  263293
Seq. No.
                  5280 1.R1011
Contig ID
5'-most EST
                  LIB143-040-Q1-E1-G4
Method
                  BLASTX
                  g4191778
NCBI GI
BLAST score
                  535
                  2.0e-54
E value
Match length
                  159
% identity
                  67
NCBI Description (AC005917) putative nucleosome assembly protein I
                  [Arabidopsis thaliana]
                  263294
Seq. No.
                  5281 1.R1011
Contig ID
                  LIB84-023-Q1-E1-B10
5'-most EST
                  BLASTX
Method
                  g2244797
NCBI GI
BLAST score
                  331
E value
                  3.0e-30
                  195
Match length
                  39
% identity
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
                  263295
Seq. No.
Contig ID
                  5281 2.R1011
5'-most EST
                  lhp700053318.rl
Seq. No.
                  263296
                  5285 1.R1011
Contig ID
5'-most EST
                  LIB3136-008-Q1-K1-F1
Method
                  BLASTX
                  g1172809
NCBI GI
                  786
BLAST score
E value
                  1.0e-83
Match length
                  149
                  98
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG) >qi 468056
                  (U06108) QM protein [Zea mays]
Seq. No.
                  263297
                  5285 2.R1011
Contig ID
5'-most EST
                  LIB3156-010-Q1-K1-H1
Method
                  BLASTX
NCBI GI
                  q1172809
BLAST score
                  1142
                  1.0e-125
E value
Match length
                  220
                  98
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L10 (2.. PROTEIN HOMOLOG) >gi 468056
                  (U06108) QM protein [Zea mays]
Seq. No.
                  263298
                  5285_3.R1011
Contig ID
```

36517

tfd700571649.h1

BLASTX



```
g1172809
NCBI GI
                  674
BLAST score
                  8.0e-71
E value
                  133
Match length
                  97
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG) >gi_468056
                   (U06108) QM protein [Zea mays]
                  263299
Seq. No.
                  5285 5.R1011
Contig ID
                  LIB3156-007-Q1-K1-F11
5'-most EST
Method
                  BLASTX
                  q1172809
NCBI GI
                   215
BLAST score
                   3.0e-17
E value
                   46
Match length
% identity
                   91
NCBI Description 60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG) >gi_468056
                   (U06108) QM protein [Zea mays]
Seq. No.
                   263300
Contig ID
                   5285 8.R1011
                   LIB3059-009-Q1-K1-E3
5'-most EST
                   BLASTX
Method
                   q4262180
NCBI GI
BLAST score
                   163
                   4.0e-11
E value
                   33
Match length
                   94
% identity
NCBI Description (AC005508) 29621 [Arabidopsis thaliana]
Seq. No.
                   263301
                   5285 10.R1011
Contig ID
                   LIB3150-067-P2-K1-E9
5'-most EST
                   BLASTX
Method
                   q1172809
NCBI GI
                   254
BLAST score
                   1.0e-21
E value
                   58
Match length
                   81
% identity
                   60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG) >gi 468056
NCBI Description
                   (U06108) QM protein [Zea mays]
                   263302
Seq. No.
                   5287 1.R1011
Contig ID
5'-most EST
                   LIB143-037-01-E1-E8
                   BLASTX
Method
                   g2245125
NCBI GI
                   159
BLAST score
                   1.0e-10
E value
Match length
                   52
 % identity
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 263303 Contig ID 5291 1.R1011

5'-most EST uC-zmflmo17312g05b1

NCBI Description

Seq. No.



```
BLASTX
Method
                --- g2833378
NCBI GI
                  658
BLAST score
                  1.0e-68
E value
                  281
Match length
                  49
% identity
                  HEXOKINASE >gi 619928 (U18754) hexokinase [Arabidopsis
NCBI Description
                  thaliana] >gi_1582383_prf__2118367A hexokinase [Arabidopsis
                  thaliana]
                  263304
Seq. No.
                   5291 2.R1011
Contig ID
                  LIB3060-044-Q1-K1-G7
5'-most EST
                  BLASTX
Method
                   g2146739
NCBI GI
BLAST score
                   1033
                   1.0e-112
E value
                   309
Match length
                   65
% identity
                   hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521
NCBI Description
                   (U28214) hexokinase 1 [Arabidopsis thaliana]
                   263305
Seq. No.
                   5291 3.R1011
Contig ID
                   LIB3151-035-Q1-K1-F4
5'-most EST
                   BLASTX
Method
                   g2146739
NCBI GI
                   219
BLAST score
                   1.0e-17
E value
                   65
Match length
                   66
% identity
                   hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521
NCBI Description
                   (U28214) hexokinase 1 [Arabidopsis thaliana]
Seq. No.
                   263306
                   5294 1.R1011
Contig ID
                   dyk700105017.h1
5'-most EST
                   BLASTX
Method
                   q729671
NCBI GI
BLAST score
                   397
                   2.0e-38
E value
                   103
Match length
                   78
 % identity
                  HISTONE H2A >gi_473603 (U08225) histone H2A [Zea mays]
NCBI Description
                   263307
Seq. No.
                   5294 2.R1011
Contig ID
                   LIB3070-008-Q1-N1-D10
 5'-most EST
                   BLASTX
Method
                   g1228074
NCBI GI
 BLAST score
                   253
                   2.0e-21
 E value
Match length
                   51
 % identity
                   96
                   (X95763) histone h2a homologue [Allium cepa]
```



```
Contig ID
                  5295 1.R1011
5'-most EST
                  wty700172093.h1
Method
                  BLASTX
NCBI GI
                  q2369690
BLAST score
                  319
E value
                  3.0e-29
Match length
                  114
% identity
                  54
NCBI Description
                  (Y11988) FPF1 protein [Arabidopsis thaliana]
Seq. No.
                  263309
                  5295 2.R1011
Contig ID
5'-most EST
                  hvj700624095.h1
Seq. No.
                  263310
                  5296 1.R1011
Contig ID
                  xmt700267071.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2981475
BLAST score
                  570
                  1.0e-58
E value
Match length
                  141
                  78
% identity
NCBI Description
                  (AF053084) putative cinnamyl alcohol dehydrogenase [Malus
                  domestica]
Seq. No.
                  263311
Contig ID
                   5298 1.R1011
5'-most EST
                  LIB3078-004-Q1-K1-G12
Method
                  BLASTX
                  g82694
NCBI GI
BLAST score
                  938
E value
                  1.0e-101
                  187
Match length
                   98
% identity
                  glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) 2 -
NCBI Description
                  maize (fragment) >gi_293889 (L13432)
                  glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.
                   263312
Contig ID
                   5298 2.R1011
5'-most EST
                  uC-zmflb73197h05b1
Method
                  BLASTX
NCBI GI
                   g120670
BLAST score
                  758
E value
                   1.0e-80
Match length
                  150
                   99
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 100879 pir S06879 glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) C - maize
                  >gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]
```

Seq. No. 263313

Contig ID 5298 3.R1011

5'-most EST LIB3067-023-Q1-K1-A3

Method BLASTX



q120670 NCBI GI 672 BLAST score 2.0e-70 E value 132 Match length 100 % identity GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description >gi_100879_pir__S06879 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C - maize >gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays] Seq. No. 263314 5298 4.R1011 Contig ID ceu700427662.h1 5'-most EST BLASTX Method g120670 NCBI GI 380 BLAST score 3.0e-36 E value 73 Match length 99 % identity GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description >gi_100879_pir__S06879 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C - maize >gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays] 263315 Seq. No. 5298 5.R1011 Contig ID pmx700083976.h1 5'-most EST BLASTN Method g22237 NCBI GI 86 BLAST score 1.0e-40 E value Match length 222 91 % identity Maize mRNA for cytosolic GAPDH (GapC) NCBI Description glyceraldehyde-3-phosphate dehydrogenase 263316 Seq. No. 5298 8.R1011 Contig ID uC-zmflmo17290a09b15'-most EST BLASTN Method q312178 NCBI GI 135 BLAST score 7.0e-70 E value 163 Match length 97 % identity NCBI Description Z.mays GapC2 gene 263317 Seq. No. 5298 9.R1011 Contig ID uC-zmflmo17331e08a1 5'-most EST BLASTX Method

Method BLASTX
NCBI GI g120670
BLAST score 199
E value 2.0e-15
Match length 38
% identity 97

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC



>gi_100879_pir__S06879 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) C - maize

>gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]

Seq. No. 263318

Contig ID 5300 1.R1011

5'-most EST uC-zmflb73298f12a1

Method BLASTX
NCBI GI g3850576
BLAST score 253
E value 1.0e-21
Match length 49
% identity 96

NCBI Description (AC005278) Strong similarity to gb U04968 nucleotide

excision repair protein (ERCC2) from Cricetulus grisseus.

[Arabidopsis thaliana]

Seq. No. 263319

Contig ID 5302 1.R1011

5'-most EST LIB3076-034-Q1-K1-E1

Method BLASTX
NCBI GI g1168530
BLAST score 651
E value 2.0e-68
Match length 148
% identity 80

NCBI Description SERINE/THREONINE-PROTEIN KINASE ASK2 >gi_99748_pir__S24586

probable serine/threonine-specific protein kinase (EC

2.7.1.-) (clone ASK2) - Arabidopsis thaliana >gi_16443_emb_CAA78106_ (Z12120) protein kinase

[Arabidopsis thaliana]

Seq. No. 263320

Contig ID 5304_1.R1011 5'-most EST gct701176414.h1

Method BLASTN
NCBI GI g3982633
BLAST score 44
E value 2.0e-15
Match length 68
% identity 91

NCBI Description Zea mays disease resistance gene analog PIC21 (pic21) gene,

partial cds

Seq. No. 263321 Contig ID 5305 1.R1011

5'-most EST uC-zmflb73146b02b1

Method BLASTX
NCBI GI g3075399
BLAST score 245
E value 2.0e-20
Match length 176
% identity 35

NCBI Description (AC004484) SF16-like protein [Arabidopsis thaliana]

Seq. No. 263322 Contig ID 5309_1.R1011



LIB3076-034-Q1-K1-C7 5'-most EST BLASTX Method g3402703 NCBI GI 738 BLAST score 2.0e-78 E value 216 Match length 68 % identity (AC004261) hypothetical protein [Arabidopsis thaliana] NCBI Description 263323 Seq. No. 5310 1.R1011 Contig ID LIB3068-029-Q1-K1-A3 5'-most EST BLASTX Method g2583135 NCBI GI 345 BLAST score 5.0e-32 E value 160 Match length % identity 49 (AC002387) hypothetical protein [Arabidopsis thaliana] NCBI Description >qi 3822216 (AF074948) FIL [Arabidopsis thaliana] >qi 4322477 qb AAD16053 (AF087015) abnormal floral organs protein [Arabidopsis thaliana] 263324 Seq. No. 5313 1.R1011 Contig ID amh700026364.f15'-most EST Method BLASTX g3618316 NCBI GI 147 BLAST score 5.0e-09 E value 94 Match length % identity 40 (AB001886) zinc finger protein [Oryza sativa] NCBI Description 263325 Seq. No. Contig ID 5316 1.R1011 uC-zmroteosinte016a10b1 5'-most EST 263326 Seq. No. 5317 1.R1011 Contig ID dhd700197940.h1 5'-most EST BLASTX Method q2821957 NCBI GI 1366 BLAST score 1.0e-151 E value Match length 299 85 % identity (AB006691) spermidine synthase 2 [Hyoscyamus niger] NCBI Description 263327 Seq. No. Contig ID 5317 2.R1011 uC-zmrob73004f10b1 5'-most EST

Method BLASTX
NCBI GI g2821955
BLAST score 414
E value 2.0e-40
Match length 84

E value

Match length % identity

9.0e-45 101

83



% identity NCBI Description (AB006690) spermidine synthase 1 [Hyoscyamus niger] 263328 Seq. No. 5317 3.R1011 Contig ID ceu700423224.h1 5'-most EST BLASTX Method q2821957 NCBI GI BLAST score 333 6.0e - 31E value Match length 76 % identity 80 (AB006691) spermidine synthase 2 [Hyoscyamus niger] NCBI Description 263329 Seq. No. 5320 1.R1011 Contig ID xdb700342185.h1 5'-most EST 263330 Seq. No. 5321 1.R1011 Contig ID 5'-most EST LIB3076-034-Q1-K1-B2 263331 Seq. No. 5326 1.R1011 Contig ID zla700380056.hl 5'-most EST BLASTX Method NCBI GI q3128228 844 BLAST score 1.0e-90 E value 178 Match length 88 % identity (AC004077) putative ribosomal protein L18A [Arabidopsis NCBI Description thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana] 263332 Seq. No. 5326 2.R1011 Contig ID dyk700105573.h1 5'-most EST BLASTX Method g3128228 NCBI GI 837 BLAST score 8.0e-90 E value 178 Match length % identity (AC004077) putative ribosomal protein L18A [Arabidopsis NCBI Description thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana] 263333 Seq. No. 5326 3.R1011 Contig ID 5'-most EST LIB3076-015-Q1-K1-A5 BLASTX Method q3128228 NCBI GI BLAST score 451



NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No. 263334 Contig ID 5326_4.R1011

5'-most EST LIB3150-052-Q1-N1-E10

Method BLASTX
NCBI GI g3128228
BLAST score 718
E value 1.0e-78
Match length 173
% identity 79

NCBI Description (AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi 3337376 (AC004481) putative ribosomal protein

L18A [Arabidopsis thaliana]

Seq. No. 263335
Contig ID 5326_7.R1011

5'-most EST LIB3150-035-Q1-N1-B3

Method BLASTN
NCBI GI g428999
BLAST score 70
E value 4.0e-31
Match length 94

Match length 94 % identity 94

NCBI Description Rice mRNA for ribosomal protein L18a (gene name SS128),

partial cds

Seq. No. 263336 Contig ID 5327_1.R1011

5'-most EST LIB3076-033-Q1-K1-F7

5'-most EST LIB3156-015-Q1-K1-A3

Seq. No. 263338 Contig ID 5330_1.R1011

5'-most EST uC-zmflmo17117a01b1

Method BLASTX
NCBI GI 9485126
BLAST score 150
E value 5.0e-09
Match length 59
% identity 51

NCBI Description (U00052) similar to RNA binding proteins [Caenorhabditis

elegans]

Seq. No. 263339

Contig ID 5330_2.R1011 5'-most EST LIB3150-009-Q1-N1-H5

Method BLASTX
NCBI GI g485126
BLAST score 201
E value 3.0e-15
Match length 85



52 % identity

(U00052) similar to RNA binding proteins [Caenorhabditis NCBI Description

elegans]

263340 Seq. No.

Contig ID 5330 3.R1011 5'-most EST $xdb7\overline{0}0340875.h1$

263341 Seq. No.

Contig ID 5330 4.R1011

5'-most EST uC-zmflmo17287d08a1

263342 Seq. No.

5332 1.R1011 Contig ID

LIB3079-010-Q1-K1-A9 5'-most EST

Method BLASTX g2213594 NCBI GI BLAST score 183 E value 2.0e-16 Match length 70 % identity 67

NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]

263343 Seq. No.

Contig ID 5334 1.R1011

5'-most EST fC-zmle700425457f2

Seq. No. 263344

Contig ID 5336 1.R1011

uC-zmroteosinte088b01b1 5'-most EST

Method BLASTX NCBI GI g3461848 BLAST score 2146 E value 0.0e + 00503 Match length % identity 83

NCBI Description (AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No. 263345

5338 1.R1011 Contig ID

5'-most EST LIB3076-033-Q1-K1-A4

Method BLASTX NCBI GI g2209332 BLAST score 1120 E value 1.0e-123 Match length 248 % identity 86

NCBI Description (U89272) chloroplast membrane protein ALBINO3 [Arabidopsis

thaliana] >gi 3927828 (AC005727) chloroplast membrane

protein ALBINO3 [Arabidopsis thaliana]

Seq. No. 263346

Contig ID 5339 1.R1011

5'-most EST LIB3079-028-Q1-K1-D1

Seq. No. 263347

Contig ID 5340 1.R1011



```
uC-zmflmo17036e11b2
5'-most EST
                  BLASTN
Method
NCBI GI
                  q4416300
                  467
BLAST score
                  0.0e + 00
E value
Match length
                  655
% identity
                  94
NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster
                  region, complete sequence
Seq. No.
                  263348
Contig ID
                  5340 2.R1011
5'-most EST
                  uC-zmflmo17418b01a1
                  263349
Seq. No.
Contig ID
                  5340 3.R1011
5'-most EST
                  uC-zmf1b73027f12b1
Method
                  BLASTX
NCBI GI
                  g4416302
BLAST score
                  1021
E value
                  1.0e-111
Match length
                  196
                  97
% identity
NCBI Description (AF105716) copia-type pol polyprotein [Zea mays]
Seq. No.
                  263350
                  5340 4.R1011
Contig ID
                  gct701174926.h1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g287829
BLAST score
                  163
E value
                  2.0e-86
Match length
                  329
% identity
                  92
NCBI Description Z.mays gene for polygalacturonase
Seq. No.
                  263351
Contig ID
                  5341 1.R1011
5'-most EST
                  uC-zmflb73054d12b1
                  263352
Seq. No.
                  5347 1.R1011
Contig ID
                  LIB3076-033-Q1-K1-C12
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1084476
BLAST score
                  2704
E value
                  0.0e + 00
Match length
                  492
% identity
                  100
NCBI Description catalase (EC 1.11.1.6) - maize >gi 311239 emb CAA42720
                   (X60135) catalase-1 [Zea mays]
                  263353
Seq. No.
                  5347 4.R1011
Contig ID
```

NCBI GI g82677

BLASTX

uC-zmflmo17057c10b1

5'-most EST

Method



```
244
BLAST score
                   8.0e-21
E value
                   45
Match length
                   98
% identity
                   catalase (EC 1.11.1.6) chain 1 - maize
NCBI Description
                   >gi_22232_emb_CAA31056_ (X12538) catalase-1 (AA 1-492) [Zea
Seq. No.
                   263354
                   5352 1.R1011
Contig ID
                   LIB3076-033-Q1-K1-D12
5'-most EST
                   263355
Seq. No.
                   5353_1.R1011
Contig ID
                   uC-z\overline{m}roteosinte043c12b2
5'-most EST
                   BLASTX
Method
                   g121446
NCBI GI
                   2560
BLAST score
                   0.0e + 00
E value
                   517
Match length
                   99
% identity
NCBI Description FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE PRECURSOR
                    (FD-GOGAT) >gi_100877_pir__A38596 glutamate synthase
                    (ferredoxin) (\overline{EC} \ 1.4.\overline{7}.1) - maize >gi_168477 (M59190)
                    ferredoxin-dependent glutamate synthase [Zea mays]
                   263356
Seq. No.
                    5354 1.R1011
Contig ID
                   LIB3076-033-Q1-K1-D4
5'-most EST
                    263357
Seq. No.
                    5356_1.R1011
Contig ID
                    uC-zmflmo17138g12b1
5'-most EST
                    BLASTX
Method
                    g3136311
NCBI GI
BLAST score
                    148
                    3.0e-09
E value
                    25
Match length
                    100
 % identity
                   (AF062734) soluble acid invertase [Saccharum robustum]
 NCBI Description
                    263358
 Seq. No.
                    5358 1.R1011
 Contig ID
                    LIB3076-022-Q1-K1-A10
 5'-most EST
                    263359
 Seq. No.
                    5359 1.R1011
 Contig ID
                    LIB3076-033-Q1-K1-B1
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    g3249066
 BLAST score
                    258
                    5.0e-22
 E value
 Match length
                    113
 % identity
                    54
                    (AC004473) Similar to S. cerevisiae SIK1P protein
 NCBI Description
```

gene. [Arabidopsis thaliana]

gb_984964. ESTs gb_F15433 and gb_AA395158 come from this



263360 Seq. No. 5360 1.R1011 Contig ID

5'-most EST uC-zmflb73226d08b1

263361 Seq. No.

Contig ID 5360 2.R1011

5'-most EST LIB3\overline{1}36-042-P1-K1-F6

BLASTX Method NCBI GI q4581512 BLAST score 253 E value 5.0e-21 Match length 125 % identity 22

(AL049559) putative transcription factor; yeast bdfl-like NCBI Description

[Schizosaccharomyces pombe]

263362 Seq. No.

5360 3.R1011 Contig ID

5'-most EST uC-zmflmo17221d10b1

263363 Seq. No.

5360 4.R1011 Contig ID

5'-most EST uC-zmflmo17047c03a1

263364 Seq. No.

5360 5.R1011 Contig ID uwc700152581.h1 5'-most EST

Seq. No. 263365

Contig ID 5363 1.R1011

5'-most EST uC-zmroteosinte033a04b1

Method BLASTX NCBI GI q3281853 BLAST score 1006 1.0e-109 E value 274 Match length

% identity 76

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

263366 Seq. No.

Contig ID 5363 2.R1011 5'-most EST ypc700805361.h1

Method BLASTX NCBI GI g3281853 BLAST score 410 E value 6.0e-4096 Match length 78 % identity

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

263367 Seq. No.

5363_3.R1011 Contig ID

5'-most EST uC-zmflmo17425g09a1

Method BLASTX q3281853 NCBI GI BLAST score 154



```
4.0e-10
E value
                  66
Match length
% identity
                  50
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  263368
                  5365 1.R1011
Contig ID
                  LIB3076-033-Q1-K1-B8
5'-most EST
                  263369
Seq. No.
                   5366 1.R1011
Contig ID
                  wty700171432.hl
5'-most EST
                  BLASTX
Method
                   q4104931
NCBI GI
BLAST score
                   478
                   1.0e-47
E value
Match length
                   160
% identity
                  (AF042196) auxin response factor 8 [Arabidopsis thaliana]
NCBI Description
                   263370
Seq. No.
                   5366 4.R1011
Contig ID
                   pmx700082827.hl
5'-most EST
                   BLASTX
Method
                   q4104931
NCBI GI
BLAST score
                   252
                   4.0e-21
E value
                   115
Match length
                   50
% identity
                   (AF042196) auxin response factor 8 [Arabidopsis thaliana]
NCBI Description
                   263371
Seq. No.
                   5367 1.R1011
Contig ID
                   cyk700050522.fl
5'-most EST
                   BLASTX
Method
                   q3482914
NCBI GI
                   565
BLAST score
                   5.0e-58
E value
                   240
Match length
                   47
 % identity
                   (AC003970) Similar to nodulins and lipase [Arabidopsis
NCBI Description
                   thaliana]
                   263372
 Seq. No.
                   5368 1.R1011
 Contig ID
                   xmt700258092.h1
 5'-most EST
                   BLASTX
Method
                   g3047090
 NCBI GI
                   401
 BLAST score
                   2.0e-38
 E value
                   136
 Match length
                    53
 % identity
                   (AF058826) T26D22.18 gene product [Arabidopsis thaliana]
 NCBI Description
```

263373 Seq. No. 5368 2.R1011 Contig ID

uC-zmflmo17099g05b1 5'-most EST



75

NCBI Description small GTP-binding protein - garden pea

Match length % identity

```
263374
Seq. No.
                  5368 3.R1011
Contig ID
5'-most EST
                  xmt700259116.h2
                  263375
Seq. No.
Contig ID
                  5368 6.R1011
5'-most EST
                  uC-zmflb73032b07a1
                  263376
Seq. No.
Contig ID
                  5368 8.R1011
5'-most EST
                  ymt700220704.h1
                  BLASTX
Method
NCBI GI
                  q3047090
BLAST score
                  154
E value
                  8.0e-10
Match length
                  78
% identity
                  40
NCBI Description (AF058826) T26D22.18 gene product [Arabidopsis thaliana]
Seq. No.
                  263377
                  5370 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73169h10b2
Method
                  BLASTX
                  g4507075
NCBI GI
                  2009
BLAST score
E value
                  0.0e+00
                  683
Match length
                  59
% identity
NCBI Description SWI/SNF related, matrix associated, actin dependent
                  regulator of chromatin, subfamily a, member 5
                  >gi_2967452_dbj_BAA25173_ (AB010882) hSNF2H [Homo sapiens]
Seq. No.
                  263378
Contig ID
                  5373 1.R1011
5'-most EST
                  LIB3079-017-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g1362066
BLAST score
                  841
                  5.0e-90
E value
                  201
Match length
                  83
% identity
NCBI Description
                  small GTP-binding protein - garden pea
                  >gi 871510 emb CAA90080 (Z49900) small GTP-binding protein
                  [Pisum sativum]
Seq. No.
                  263379
Contig ID
                  5373 2.R1011
5'-most EST
                  LIB3067-033-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g1362066
BLAST score
                  212
E value
                  1.0e-16
```

36531

>gi_871510_emb_CAA90080 (Z49900) small GTP-binding protein



```
[Pisum sativum]
```

```
263380
Seq. No.
                  5373 4.R1011
Contig ID
                  wyr700240836.hl
5'-most EST
                  BLASTN
Method
                  g974775
NCBI GI
                  34
BLAST score
                  2.0e-09
E value
                  50
Match length
                   92
% identity
NCBI Description B.vulgaris mRNA for small G protein (clone 1S3)
                   263381
Seq. No.
                   5375 1.R1011
Contig ID
                   ymt700221810.hl
5'-most EST
                   263382
Seq. No.
                   5376 1.R1011
Contig ID
                   cyk700049814.f1
5'-most EST
Method
                   BLASTX
                   g1613900
NCBI GI
                   194
BLAST score
                   2.0e-14
E value
                   150
Match length
                   35
% identity
                   (U73168) partial CDS, human putative tumor suppressor
NCBI Description
                   (U23946) [Homo sapiens]
                   263383
Seq. No.
                   5376 2.R1011
Contig ID
                   LIB3076-033-Q1-K1-A2
5'-most EST
                   263384
Seq. No.
Contig ID
                   5378 1.R1011
                   xyt700343035.h1
5'-most EST
                   BLASTX
Method
                   q4371285
NCBI GI
                   815
BLAST score
                   5.0e-87
E value
                   259
Match length
 % identity
                   (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   263385
 Seq. No.
                   5382 1.R1011
 Contig ID
                   wyr700235242.h1
 5'-most EST
                   BLASTX
 Method
                   g136125
 NCBI GI
 BLAST score
                   1600
                   1.0e-180
 E value
 Match length
                   530
                   60
 % identity
 NCBI Description PUTATIVE AC TRANSPOSASE (ORFA) >gi_22113_emb_CAA29005_
                   (X05424) ORFa [Zea mays]
```

Seq. No.



```
5385 1.R1011
Contig ID
                   uC-z\overline{m}flb73056h01b1
5'-most EST
                   BLASTX
Method
                   g2961107
NCBI GI
BLAST score
                   204
                   2.0e-15
E value
Match length
                   91
                   43
% identity
                   (AF042383) TLS-associated protein with SR repeats [Mus
NCBI Description
                   musculus] >gi_2961149 (AF047448) TLS-associated protein
                   TASR [Homo sapiens]
```

 Seq. No.
 263388

 Contig ID
 5386_1.R1011

 5'-most EST
 uC-zmflb73202c01b1

 Method
 BLASTX

 NCBI GI
 g2688824

 BLAST score
 227

BLAST score 227 E value 3.0e-18 Match length 132 % identity 45 NCRI Description (193273)

NCBI Description (U93273) putative auxin-repressed protein [Prunus

armeniaca]

Seq. No. 263389 Contig ID 5386 2.R1011

5'-most EST LIB3137-036-Q1-K1-D10

Method BLASTX
NCBI GI g2688824
BLAST score 148
E value 4.0e-09
Match length 78
% identity 49

NCBI Description (U93273) putative auxin-repressed protein [Prunus

armeniaca]

Seq. No. 263390 Contig ID 5386_3.R1011

5'-most EST uC-zmflmo17078h06b1

Method BLASTX
NCBI GI g2688824
BLAST score 228
E value 3.0e-18
Match length 132
% identity 45

NCBI Description (U93273) putative auxin-repressed protein [Prunus

armeniaca]

Seq. No. 263391 Contig ID 5386_4.R1011

5'-most EST LIB3076-032-Q1-K1-F9

Seq. No. 263392

Match length

% identity

94



```
5387 1.R1011
Contig ID
                  LIB3076-032-Q1-K1-G3
5'-most EST
                  263393
Seq. No.
                  5387 2.R1011
Contig ID
                  LIB3069-015-Q1-K1-C6
5'-most EST
                  263394
Seq. No.
                   5388 1.R1011
Contig ID
                  uC-zmflb73060h05b1
5'-most EST
                   263395
Seg. No.
                   5390 1.R1011
Contig ID
                  xsy700212664.h1
5'-most EST
                   263396
Seq. No.
                   5391 1.R1011
Contig ID
                   uC-zmflb73033c03b1
5'-most EST
                   BLASTX
Method
                   g3135543
NCBI GI
BLAST score
                   1296
                   1.0e-143
E value
                   289
Match length
% identity
                   85
NCBI Description (AF062393) aquaporin [Oryza sativa]
                   263397
Seq. No.
                   5391 2.R1011
Contig ID
                   dyk7\overline{0}0106980.h1
5'-most EST
                   BLASTX
Method
                   q2662310
NCBI GI
                   1139
BLAST score
                   1.0e-125
E value
                   276
Match length
                   77
 % identity
NCBI Description (AB009307) bpw1 [Hordeum vulgare]
                   263398
 Seq. No.
                   5391 3.R1011
 Contig ID
                   ntr700072854.h1
 5'-most EST
                   BLASTX
Method
 NCBI GI
                   q3395673
 BLAST score
                   495
                   1.0e-114
 E value
 Match length
                   280
 % identity
                   80
 NCBI Description (AB016623) RWC-3 [Oryza sativa]
                    263399
 Seq. No.
                    5391 4.R1011
 Contig ID
                   LIB143-006-Q1-E1-E3
 5'-most EST
                    BLASTX
 Method
                    q3135543
 NCBI GI
 BLAST score
                    445
                    3.0e-44
 E value
                    89
```

NCBI Description



```
NCBI Description (AF062393) aquaporin [Oryza sativa]
                  263400
Seq. No.
                  5391 5.R1011
Contig ID
                  uC-zmflmo17054g07b1
5'-most EST
                  BLASTX
Method
                  g3135543
NCBI GI
                  327
BLAST score
                  7.0e-55
E value
                  123
Match length
% identity
                  88
NCBI Description (AF062393) aquaporin [Oryza sativa]
                  263401
Seq. No.
                   5391 6.R1011
Contia ID
                  ntr700072060.hl
5'-most EST
                  BLASTX
Method
                   g3135543
NCBI GI
                   513
BLAST score
                   3.0e-52
E value
Match length
                   113
% identity
                   88
NCBI Description (AF062393) aquaporin [Oryza sativa]
                   263402
Seq. No.
                   5391 9.R1011
Contig ID
                   uC-zmroteosinte029b02b1
5'-most EST
                   BLASTX
Method
                   g3395673
NCBI GI
                   317
BLAST score
                   4.0e-29
E value
                   63
Match length
                   90
% identity
NCBI Description (AB016623) RWC-3 [Oryza sativa]
                   263403
Seq. No.
                   5391 10.R1011
Contig ID
5'-most EST
                   uC-zmromo17017f03a1
                   BLASTN
Method
                   q1848280
NCBI GI
                   38
BLAST score
                   7.0e-12
E value
                   78
Match length
                   87
 % identity
                   Sorghum bicolor membrane intrinsic protein (Mip1) mRNA,
NCBI Description
                   partial cds
                   263404
 Seq. No.
                   5391 11.R1011
 Contig ID
                   uC-zmflmo17180e07b1
 5'-most EST
                   BLASTX
 Method
                   g1657948
 NCBI GI
 BLAST score
                   404
                   4.0e-39
 E value
                   95
 Match length
                   78
 % identity
                   (U73466) MipC [Mesembryanthemum crystallinum]
```

E value

Match length

NCBI Description

% identity

460

90

```
263405
Seq. No.
                  5391 12.R1011
Contig ID
                  uwc700152183.h1
5'-most EST
                  BLASTX
Method
                  q3135543
NCBI GI
                  322
BLAST score
                  5.0e-30
E value
                  77
Match length
% identity
NCBI Description (AF062393) aquaporin [Oryza sativa]
                   263406
Seq. No.
                   5391 13.R1011
Contig ID
                   LIB3078-027-Q1-K1-H9
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2662310
                   467
BLAST score
                   1.0e-46
E value
                   94
Match length
                   93
% identity
NCBI Description (AB009307) bpw1 [Hordeum vulgare]
                   263407
Seq. No.
                   5391 16.R1011
Contig ID
                   cyk700048109.f1
5'-most EST
                   BLASTX
Method
                   g2662310
NCBI GI
                   355
BLAST score
                   2.0e-33
E value
                   79
Match length
                   89
% identity
NCBI Description (AB009307) bpw1 [Hordeum vulgare]
                   263408
Seq. No.
                   5391 17.R1011
Contig ID
                   uC-zmroteosinte074f07b1
5'-most EST
                   BLASTX
Method
                   g2662310
NCBI GI
                   372
BLAST score
                   2.0e-35
E value
                   73
Match length
                   97
 % identity
 NCBI Description (AB009307) bpw1 [Hordeum vulgare]
                   263409
 Seq. No.
                    5393 1.R1011
 Contig ID
                   LIB3180-044-P2-M2-C11
 5'-most EST
                   BLASTX
 Method
                    g3142294
 NCBI GI
 BLAST score
                    2161
                    0.0e + 00
```

36536

(AC002411) Strong similarity to initiation factor eIF-2,

gb_U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and gb_N37529 come from this gene. [Arabidopsis thaliana]

Seq. No.

Contig ID

5'-most EST

263415

5397 5.R1011

kem700612257.hl



```
263410
Seq. No.
                  5393 3.R1011
Contig ID
                  LIB3159-018-Q1-K1-E3
5'-most EST
                  BLASTX
Method
                  q2832707
NCBI GI
                  330
BLAST score
                  9.0e-31
E value
                  75
Match length
                  91
% identity
                  (AL021713) translation initiation factor eIF-2 gamma
NCBI Description
                  chain-like protein [Arabidopsis thaliana]
                  263411
Seq. No.
                  5394 1.R1011
Contig ID
                  uC-zmflmo17286e09b1
5'-most EST
Method
                  BLASTX
                  q2339980
NCBI GI
                   907
BLAST score
                   5.0e-98
E value
                   267
Match length
% identity
NCBI Description (Y11337) RGA2 protein [Arabidopsis thaliana]
                   263412
Seq. No.
                   5397 1.R1011
Contig ID
                   uC-zmflmo17223a09b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3273243
                   2322
BLAST score
E value
                   0.0e + 00
                   516
Match length
                   89
% identity
                   (AB004660) NLS receptor [Oryza sativa]
NCBI Description
                   >gi_3273245_dbj_BAA31166_ (AB004814) NLS receptor [Oryza
                   sativa]
 Seq. No.
                   263413
                   5397 2.R1011
 Contig ID
                   LIB3079-013-Q1-K1-D8
 5'-most EST
                   BLASTX
Method
                   g3273243
 NCBI GI
                   264
 BLAST score
                   1.0e-22
 E value
                   65
 Match length
                   78
 % identity
                   (AB004660) NLS receptor [Oryza sativa]
 NCBI Description
                   >gi_3273245_dbj_BAA31166_ (AB004814) NLS receptor [Oryza
                   sativa]
                   263414
 Seq. No.
                   5397 3.R1011
 Contig ID
                   uC-zmflm017092e08b1
 5'-most EST
```



```
263416
Seq. No.
                  5397 7.R1011
Contig ID
                  LIB3069-033-Q1-K1-F10
5'-most EST
                  BLASTX
Method
                  g3273243
NCBI GI
                  338
BLAST score
                  1.0e-31
E value
Match length
                  92
                  78
% identity
                  (AB004660) NLS receptor [Oryza sativa]
NCBI Description
                  >qi 3273245 dbj BAA31166 (AB004814) NLS receptor [Oryza
                  sativa]
                  263417
Seq. No.
                  5401 1.R1011
Contig ID
                  pmx700082514.h1
5'-most EST
                  263418
Seq. No.
                  5402 1.R1011
Contig ID
5'-most EST
                  yyf700352106.hl
                  263419
Seq. No.
                  5402 3.R1011
Contig ID
                  pmx700084055.hl
5'-most EST
                   263420
Seq. No.
                   5405 1.R1011
Contig ID
                  LIB3076-032-Q1-K1-E1
5'-most EST
                  BLASTX
Method
                   g3283072
NCBI GI
                   329
BLAST score
                   2.0e-30
E value
                   122
Match length
                   55
% identity
NCBI Description (AF056022) p60 katanin [Homo sapiens]
                   263421
Seq. No.
                   5405 2.R1011
Contig ID
5'-most EST
                   uC-zmflb73068c11a1
Seq. No.
                   263422
                   5411 1.R1011
Contig ID
                   nbm700478024.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3834307
                   1101
BLAST score
                   1.0e-120
E value
                   350
Match length
% identity
                   (AC005679) Strong similarity to gene T10I14.120 gi_2832679
NCBI Description
                   putative protein from Arabidopsis thaliana BAC gb_AL021712.
                   ESTs gb_N65887 and gb_N65627 come from this gene.
```

Seq. No. 263423 Contig ID 5411_2.R1011

[Arabidopsis thaliana]



LIB3062-049-Q1-K1-C3 5'-most EST BLASTX Method g3834307 NCBI GI 503 BLAST score 1.0e-50 E value Match length 133 % identity (AC005679) Strong similarity to gene T10I14.120 gi_2832679 NCBI Description putative protein from Arabidopsis thaliana BAC gb_AL021712. ESTs qb N65887 and qb N65627 come from this gene. [Arabidopsis thaliana] 263424 Seq. No. 5414 1.R1011 Contig ID LIB3115-029-P1-K1-D2 5'-most EST BLASTX Method NCBI GI q4455194 243 BLAST score 3.0e-20 E value 67 Match length 67 % identity NCBI Description (AL035440) putative protein [Arabidopsis thaliana] 263425 Seq. No. 5414 2.R1011 Contig ID rvt700551565.hl 5'-most EST BLASTX Method NCBI GI q4455194 240 BLAST score 5.0e-20 E value 67 Match length % identity NCBI Description (AL035440) putative protein [Arabidopsis thaliana] 263426 Seq. No. 5420 1.R1011 Contig ID uC-zmflmo17067d10b1 5'-most EST 263427 Seq. No. 5423 1.R1011 Contig ID uC-zmf1B73010b04b1 5'-most EST ${\tt BLASTX}$ Method g542175 NCBI GI 1364 BLAST score 1.0e-151 E value 272 Match length % identity 91 NCBI Description endoxyloglucan transferase - wheat >gi 469511 dbj BAA03924 (D16457) endo-xyloglucan transferase [Triticum aestivum] 263428 Seq. No. 5423 3.R1011 Contig ID

5'-most EST uC-zmflB73004g09b1

Method BLASTX
NCBI GI g542175
BLAST score 702
E value 5.0e-74



```
138
Match length
% identity
                  endoxyloglucan transferase - wheat >gi_469511_dbj_BAA03924_
NCBI Description
                  (D16457) endo-xyloglucan transferase [Triticum aestivum]
                  263429
Seq. No.
                  5425 1.R1011
Contig ID
                  LIB3067-039-Q1-K1-C11
5'-most EST
                  BLASTX
Method
                  g1679794
NCBI GI
BLAST score
                  146
                  6.0e-09
E value
Match length
                  51
                  57
% identity
NCBI Description (U77627) Allele: hi2 [Danio rerio]
                   263430
Seq. No.
                   5425 2.R1011
Contig ID
                  nbm700466694.hl
5'-most EST
                  BLASTX
Method
                   q3080524
NCBI GI
BLAST score
                   907
                   1.0e-97
E value
                   576
Match length
                   37
% identity
NCBI Description (AL022599) hypothetical protein [Schizosaccharomyces pombe]
                   263431
Seq. No.
                   5425 3.R1011
Contig ID
                   uC-zmroteosinte082c07b1
5'-most EST
                   BLASTX
Method
                   g2462749
NCBI GI
                   320
BLAST score
                   2.0e-29
E value
                   90
Match length
                   71
% identity
                   (AC002292) Putative Serine/Threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   263432
Seq. No.
                   5426 1.R1011
Contig ID
                   rvt700548505.h1
5'-most EST
                   BLASTX
Method
                   a2980777
NCBI GI
BLAST score
                   534
                   4.0e-55
E value
                   215
Match length
 % identity
                  (AL022198) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 263433
Contig ID 5428_1.R1011
5'-most EST LIB189-012-Q1-E1-D11

~

 Seq. No.
 263434

 Contig ID
 5431_1.R1011

5'-most EST LIB3067-056-Q1-K1-C8

% identity



```
Method
                   BLASTX
NCBI GI
                   g2245020
BLAST score
                  223
E value
                  1.0e-17
Match length
                  331
                  29
% identity
NCBI Description (Z97341) growth regulator homolog [Arabidopsis thaliana]
                  263435
Seq. No.
                  5431_2.R1011
Contig ID
5'-most EST
                  nbm7\overline{0}0477245.h1
Seq. No.
                   263436
                   5433 1.R1011
Contig ID
                  LIB3076-031-Q1-K1-H5
5'-most EST
Seq. No.
                   263437
                   5435 1.R1011
Contig ID
5'-most EST
                   ymt700218905.h1
Method
                   BLASTX
NCBI GI
                   g3236250
BLAST score
                   629
E value
                   3.0e-65
Match length
                  193
                   62
% identity
NCBI Description (AC004684) hypothetical protein [Arabidopsis thaliana]
                   263438
Seq. No.
Contig ID
                   5435 2.R1011
5'-most EST
                  LIB3060-023-Q1-K1-B11
Seq. No.
                   263439
                   5435 3.R1011
Contig ID
5'-most EST
                  LIB3059-010-Q1-K1-B5
Method
                  BLASTX
NCBI GI
                  g3236250
BLAST score
                   323
E value
                   1.0e-29
                   88
Match length
% identity
                   69
NCBI Description (AC004684) hypothetical protein [Arabidopsis thaliana]
                   263440
Seq. No.
                   5435 4.R1011
Contig ID
5'-most EST
                   LIB3136-008-Q1-K1-B10
                   263441
Seq. No.
                   5435 5.R1011
Contig ID
5'-most EST
                   zla700380126.h1
Method
                  BLASTX
                  q3236250
NCBI GI
BLAST score
                  184
E value
                   6.0e-14
Match length
                   42
```

NCBI Description (AC004684) hypothetical protein [Arabidopsis thaliana]



```
263442
Seq. No.
                  5436 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17336f10b1
Method
                  BLASTN
                  g2760170
NCBI GI
BLAST score
                  40
E value
                  5.0e-13
Match length
                  56
                  93
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIO24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  263443
Contig ID
                  5438 1.R1011
                  LIB3088-010-Q1-K1-D11
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2407800
BLAST score
                  415
E value
                  3.0e-45
Match length
                  107
                  92
% identity
NCBI Description
                 (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
Seq. No.
                  263444
                  5443 1.R1011
Contig ID
                  uC-zmflb73300b11b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1350969
BLAST score
                  348
E value
                  1.0e-32
Match length
                  66
% identity
                  94
NCBI Description 40S RIBOSOMAL PROTEIN S26 (S31) >gi 971284 dbj BAA07208
                  (D38011) ribosomal protein S31 [Oryza sativa]
Seq. No.
                  263445
                  5443 2.R1011
Contig ID
5'-most EST
                  LIB3150-052-Q1-N1-A5
Method
                  BLASTX
NCBI GI
                  g1350969
BLAST score
                  348
E value
                  1.0e-32
Match length
                  66
% identity
                  94
                  40S RIBOSOMAL PROTEIN S26 (S31) >gi 971284 dbj BAA07208
NCBI Description
                  (D38011) ribosomal protein S31 [Oryza sativa]
Seq. No.
                  263446
Contig ID
                  5443 3.R1011
5'-most EST
                  LIB3136-001-P1-K1-D7
```

Seq. No. 263447 5443 4.R1011 Contig ID 5'-most EST LIB3059-013-Q1-K1-F4 Method BLASTX NCBI GI g1350969 BLAST score 226



```
E value
                  1.0e-39
Match length
                  91
                  88
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S26 (S31) >gi 971284 dbj BAA07208
                  (D38011) ribosomal protein S31 [Oryza sativa]
Seq. No.
                  263448
Contig ID
                  5445 1.R1011
5'-most EST
                  uC-zmflb73238f08b2
                  263449
Seq. No.
Contig ID
                  5446 1.R1011
5'-most EST
                  uC-zmflb73140e10b1
Method
                  BLASTX
NCBI GI
                  g3128186
BLAST score
                  392
                  3.0e-37
E value
Match length
                  332
% identity
                  36
NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]
                  263450
Seq. No.
Contig ID
                  5446 4.R1011
5'-most EST
                  uC-zmflb73387h11a1
Seq. No.
                  263451
Contig ID
                  5446 5.R1011
5'-most EST
                  gct701177041.h1
                  263452
Seq. No.
                  5450 1.R1011
Contig ID
5'-most EST
                  LIB189-020-Q1-E1-C10
Method
                  BLASTX
                  g1747294
NCBI GI
BLAST score
                  1109
E value
                  1.0e-122
Match length
                  250
% identity
                  89
NCBI Description (D45383) vacuolar H+-pyrophosphatase [Oryza sativa]
Seq. No.
                  263453
Contig ID
                  5459 1.R1011
5'-most EST
                  xmt700263164.h1
Method
                  BLASTX
NCBI GI
                  q2104681
BLAST score
                  377
E value
                  2.0e-35
Match length
                  223
                  43
% identity
NCBI Description (X97907) transcription factor [Vicia faba]
```

Seq. No. 263455 Contig ID 5459_6.R1011



5'-most EST LIB3150-001-Q1-N1-G12

Seq. No. 263456 Contig ID 5465_1.R

Contig ID 5465_1.R1011 5'-most EST tfd700575158.h1

Seq. No. 263457

Contig ID 5472 1.R1011 5'-most EST kem700611966.h1

Method BLASTX
NCBI GI g1362615
BLAST score 643
E value 8.0e-67
Match length 319
% identity 44

NCBI Description iswi protein - fruit fly (Drosophila melanogaster)

>gi_439197 (L27127) ISWI protein [Drosophila melanogaster]

Seq. No. 263458 Contig ID 5472_2.R1011

5'-most EST LIB3088-034-Q1-K1-B12

Seq. No. 263459

Contig ID 5472_3.R1011

5'-most EST LIB3115-034-P1-K2-G11

Method BLASTX
NCBI GI g4507067
BLAST score 330
E value 8.0e-35
Match length 141
% identity 56

NCBI Description SWI/SNF related, matrix associated, actin dependent

regulator of chromatin, subfamily a, member 1 >gi 134584 sp P28370 SN21 HUMAN POSSIBLE GLOBAL

TRANSCRIPTION ACTIVATOR SNF2L1 >gi 479804 pir S35457 SNF2 protein homolog - human >gi 292496 (M88163) transcription

activator [Homo sapiens]

 Seq. No.
 263460

 Contig ID
 5478_1.R1011

 5'-most EST
 cyk700050415.f1

Method BLASTX
NCBI GI g1850546
BLAST score 284
E value 5.0e-25
Match length 160
% identity 43

NCBI Description (U88045) syntaxin related protein AtVam3p [Arabidopsis

thaliana]

Seq. No. 263461 Contig ID 5478_2.R1011

5'-most EST uC-zmflmo17204b12b1

Seq. No. 263462 Contig ID 5482_1.R1011

5'-most EST LIB3076-030-Q1-K1-C8



Method BLASTX
NCBI GI g122007
BLAST score 407
E value 2.0e-39
Match length 105
% identity 76

NCBI Description HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley >gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1

- 149) [Petroselinum crispum]

Method BLASTX
NCBI GI g729671
BLAST score 205
E value 4.0e-31
Match length 81
% identity 91

NCBI Description HISTONE H2A >gi_473603 (U08225) histone H2A [Zea mays]

Seq. No. 263464 Contig ID 5486_1.R1011

5'-most EST uC-zmflmo17165h04b1

Seq. No. 263465 Contig ID 5487_1.R1011

5'-most EST uC-zmflMo17003d08b1

Method BLASTX
NCBI GI g4126809
BLAST score 1344
E value 1.0e-149
Match length 289
% identity 89

NCBI Description (AB017042) glyoxalase I [Oryza sativa]

 Seq. No.
 263466

 Contig ID
 5487_8.R1011

 5'-most EST
 xsy700207685.h1

Method BLASTX
NCBI GI g4126809
BLAST score 590
E value 3.0e-62
Match length 140
% identity 59

NCBI Description (AB017042) glyoxalase I [Oryza sativa]

Seq. No. 263467 Contig ID 5491_1.R1011 5'-most EST rv1700454105.h1

Seq. No. 263468 Contig ID 5491_2.R1011

5'-most EST uC-zmflb73246b08b3

Method BLASTX
NCBI GI g4586107
BLAST score 351



E value 1.0e-32 Match length 256 % identity 15

NCBI Description (AL049638) putative disease resistance protein [Arabidopsis

thaliana]

Seq. No. 263469 Contig ID 5495_1.R1011

5'-most EST LIB3076-029-Q1-K1-H7

Method BLASTX
NCBI GI g2462749
BLAST score 162
E value 2.0e-11
Match length 49
% identity 67

NCBI Description (AC002292) Putative Serine/Threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 263470

Contig ID 5497_1.R1011 5'-most EST wty700167476.h1

Seq. No. 263471

Contig ID 5504_1.R1011

5'-most EST LIB3150-065-P2-K1-G1

Method BLASTX
NCBI GI g3695403
BLAST score 596
E value 2.0e-61
Match length 162
% identity 72

NCBI Description (AF096373) contains similarity to the pfkB family of

carbohydrate kinases (Pfam: PF00294, E=1.6e-75) [Arabidopsis thaliana] >gi_4538955_emb_CAB39779.1

(AL049488) fructokinase-like protein [Arabidopsis thaliana]

Seq. No. 263472

Contig ID 5504_2.R1011

5'-most EST LIB83-008-Q1-E1-G3

Method BLASTX
NCBI GI g2501189
BLAST score 1584
E value 1.0e-177
Match length 340
% identity 93

NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR

>gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
- maize >gi_596078 (U17350) thiamine biosynthetic enzyme

[Zea mays]

Seq. No. 263473

Contig ID 5504_3.R1011

5'-most EST uC-zmflb73016g04b1

Method BLASTX
NCBI GI g3695403
BLAST score 973
E value 1.0e-105



Match length 253 % identity 74

NCBI Description (AF096373) contains similarity to the pfkB family of

carbohydrate kinases (Pfam: PF00294, E=1.6e-75) [Arabidopsis thaliana] >gi 4538955 emb CAB39779.1

(AL049488) fructokinase-like protein [Arabidopsis thaliana]

263474 Seq. No.

5504 4.R1011 Contig ID

LIB3180-008-P2-M1-A5 5'-most EST

Method BLASTX g2501190 NCBI GI 575 BLAST score 2.0e-59 E value Match length 120 97 % identity

THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR NCBI Description

>gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2 - maize >gi 596080 (U17351) thiamine biosynthetic enzyme

[Zea mays]

263475 Seq. No.

5504 5.R1011 Contig ID

5'-most EST LIB83-009-Q1-E1-D10

BLASTX Method NCBI GI g2501189 BLAST score 548 E value 7.0e-56 Match length 130 % identity 86

NCBI Description

THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR

>gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi 596078 (U17350) thiamine biosynthetic enzyme

[Zea mays]

263476 Seq. No.

Contig ID 5504 6.R1011 5'-most EST fwa700098096.hl

Method BLASTX NCBI GI q2501189 BLAST score 240 E value 7.0e-20 Match length 48 100 % identity

THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR NCBI Description

>gi 2130146 pir S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi 596078 (U17350) thiamine biosynthetic enzyme

[Zea mays]

263477 Seq. No.

Contig ID 5506 1.R1011 5'-most EST $fdz7\overline{0}1159729.h2$

Seq. No. 263478

Contig ID 5508 1.R1011

uC-zmf1b73022d12b1 5'-most EST

Method BLASTX

```
q3935185
NCBI GI
                   202
BLAST score
                   1.0e-15
E value
                   90
Match length
                   46
% identity
                 (AC004557) F17L21.28 [Arabidopsis thaliana]
NCBI Description
                   263479
Seq. No.
                   5512 1.R1011
Contig ID
                   uC-zmflb73295d02b2
5'-most EST
                   BLASTX
Method
                   q1209703
NCBI GI
                   1717
BLAST score
                   0.0e + 00
E value
                   620
Match length
                   51
% identity
                  (U40489) maize gll homolog [Arabidopsis thaliana]
NCBI Description
                   263480
Seq. No.
                   5512 2.R1011
Contig ID
                   LIB3159-007-Q1-K1-F5
5'-most EST
                   BLASTX
Method
                   g1418317
NCBI GI
                                                                    ---
                   298
BLAST score
                   9.0e-27
E value
                   94
Match length
                   55
% identity
                   (X95964) CER1-like [Arabidopsis thaliana]
NCBI Description
                   263481
Seq. No.
                   5512 3.R1011
Contig ID
                   LIB3068-035-Q1-K1-C9
5'-most EST
Seq. No.
                    263482
                    5512 7.R1011
Contig ID
                   LIB3076-029-Q1-K1-F12
5'-most EST
                    BLASTX
Method
                    g2317910
NCBI GI
BLAST score
                    365
                    2.0e-34
E value
Match length
                    93
                    69
 % identity
                   (U89959) CER1 protein [Arabidopsis thaliana]
 NCBI Description
                    263483
 Seq. No.
                    5513 1.R1011
 Contig ID
                    dhd7\overline{0}0198083.h1
 5'-most EST
                    BLASTX
 Method
                    g2344894
 NCBI GI
```

990 BLAST score

1.0e-107 E value Match length 317 33 % identity

(AC002388) hypothetical protein [Arabidopsis thaliana] NCBI Description

263484 Seq. No. 5515_1.R1011 Contig ID



```
LIB3076-028-Q1-K1-A11
5'-most EST
                  263485
Seq. No.
                  5517 1.R1011
Contig ID
                  xsy700214923.h1
5'-most EST
                  BLASTX
Method
                  g99801
NCBI GI
                  210
BLAST score
                  4.0e-25
E value
                  97
Match length
                  67
% identity
NCBI Description chaperonine 60K alpha chain - rape plastid (fragment)
                  263486
Seq. No.
                   5519 1.R1011
Contig ID
                  LIB3137-058-Q1-K1-H1
5'-most EST
                  BLASTX
Method
                   g3150410
NCBI GI
                   204
BLAST score
                   7.0e-29
E value
                   184
Match length
                   25
% identity
NCBI Description (AC004165) unknown protein [Arabidopsis thaliana]
                   263487
Seq. No.
                   5521 1.R1011
Contig ID
                   LIB3076-029-Q1-K1-B5
5'-most EST
                   BLASTX
Method
                   g4337206
NCBI GI
BLAST score
                   210
                   1.0e-16
E value
                   95
Match length
                   47
% identity
                   (AC006403) putative replication factor-A protein
NCBI Description
                   [Arabidopsis thaliana]
                   263488
Seq. No.
Contig ID
                   5524 1.R1011
                   mwy700441177.h1
5'-most EST
                   BLASTX
Method
                   g2191175
NCBI GI
BLAST score
                   898
                   2.0e-96
E value
                   649
Match length
                   37
 % identity
                   (AF007270) A_IG002P16.24 gene product [Arabidopsis
NCBI Description
                   thaliana]
 Seq. No.
                   263489
                   5525 1.R1011
 Contig ID
                   LIB3076-029-Q1-K1-C12
 5'-most EST
                   BLASTX
Method
                   g4567279
 NCBI GI
                   349
 BLAST score
                   6.0e-33
 E value
                   130
 Match length
                   57
 % identity
```



```
(AC006841) putative serine/threonine protein kinase
NCBI Description
                  [Arabidopsis thaliana]
                  263490
Seq. No.
                  5527 1.R1011
Contig ID
                  xsy700213778.h1
5'-most EST
                  BLASTX
Method
                  q4586255
NCBI GI
BLAST score
                  956
                  1.0e-103
E value
                  266
Match length
                  70
% identity
                  (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
                  263491
Seq. No.
                  5528 1.R1011
Contig ID
                  fwa700097470.h1
5'-most EST
                  263492
Seq. No.
Contig ID
                   5531 1.R1011
                  LIB3076-028-Q1-K1-F9
5'-most EST
                  BLASTX
Method
                   q3643599
NCBI GI
                   208
BLAST score
                   2.0e-16
E value
                   49
Match length
                   82
% identity
                  (AC005395) putative trytophanyl-tRNA synthetase
NCBI Description
                   [Arabidopsis thaliana]
                   263493
Seq. No.
                   5537 1.R1011
Contig ID
                   LIB3076-028-Q1-K1-G9
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4091117
                   268
BLAST score
                   1.0e-45
E value
                   112
Match length
                   84
% identity
                  (AF047428) nucleic acid binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   263494
                   5538 1.R1011
Contig ID
5'-most EST
                   pmx700083219.hl
                   263495
Seq. No.
                   5542 1.R1011
Contig ID
                   uC-zmflB73042f12b1
 5'-most EST
                   BLASTX
Method
NCBI GI
                   q3582333
```

Method BLASTX
NCBI GI g3582333
BLAST score 243
E value 2.0e-20
Match length 155
% identity 34

NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No. 263496



```
5545 1.R1011
Contig ID
                  LIB3061-040-Q1-K1-F2
5'-most EST
                  263497
Seq. No.
                   5548 1.R1011
Contig ID
                  LIB3076-028-Q1-K1-C8
5'-most EST
                   263498
Seq. No.
                   5561 1.R1011
Contig ID
                   uC-zmflMo17092c07b1
5'-most EST
                   BLASTX
Method
                   q2809326
NCBI GI
                   1004
BLAST score
                   1.0e-109
E value
                   311
Match length
                   61
% identity
NCBI Description (U72663) uricase II [Phaseolus vulgaris]
Seq. No.
                   263499
                   5565 1.R1011
Contig ID
                   LIB3076-028-Q1-K1-A1
5'-most EST
                   263500
Seq. No.
                   5566 1.R1011
Contig ID
                   ntr700075375.hl
5'-most EST
                   BLASTX
Method
                   q2388564
NCBI GI
                   287
BLAST score
                   8.0e-25
E value
Match length
                   494
% identity
                   24
                   (AC000098) ESTs gb_AA042402,gb_ATTS1380 come from this
NCBI Description
                   gene. [Arabidopsis thaliana]
                   263501
Seq. No.
                   5566 2.R1011
Contig ID
                   uC-z\overline{m}flMo17086f04b1
5'-most EST
                   BLASTX
Method
                   g3212866
NCBI GI
BLAST score
                   486
                   1.0e-48
E value
Match length
                   265
                    40
 % identity
                   (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                    263502
                    5566 3.R1011
 Contig ID
                   LIB3156-010-Q1-K1-B10
 5'-most EST
                    BLASTX
Method
                    q1663724
 NCBI GI
                    412
 BLAST score
                    4.0e-74
 E value
                    223
 Match length
 % identity
                    65
                   (U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
 NCBI Description
```

36551

263503

Seq. No.



```
5566 4.R1011
Contig ID
                  cyk700047986.f1
5'-most EST
                  BLASTX
Method
                  g1663722
NCBI GI
                  1037
BLAST score
                  1.0e-131
E value
                   316
Match length
                  71
% identity
NCBI Description (U50845) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
                   263504
Seq. No.
                   5566 5.R1011
Contig ID
                   LIB189-013-Q1-E1-F12
5'-most EST
                   BLASTX
Method
                   q3212866
NCBI GI
                   165
BLAST score
                   3.0e-11
E value
                   135
Match length
                   33
% identity
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                   263505
Seq. No.
                   5566 8.R1011
Contig ID
                   LIB3062-002-Q1-K2-D3
5'-most EST
                   BLASTN
Method
                   g1154858
NCBI GI
                   41
BLAST score
                   8.0e-14
E value
                   45
Match length
                   98
% identity
NCBI Description H.vulgare mRNA for L24 ribosomal protein
Seq. No.
                   263506
                   5567 1.R1011
Contig ID
                   uC-zmflb73134d03b1
 5'-most EST
                   BLASTX
Method
                   g2081612
NCBI GI
                   1737
BLAST score
                   0.0e + 00
E value
Match length
                   433
                   80
 % identity
                   (D49714) deltal-pyrroline-5-carboxylate synthetase [Oryza
 NCBI Description
                   sativa]
                   263507
 Seq. No.
                   5572_1.R1011
 Contig ID
                   LIB3076-027-Q1-K1-E2
 5'-most EST
                   BLASTX
 Method
                   g2244998
 NCBI GI
                    283
 BLAST score
                    8.0e-25
 E value
 Match length
                   165
                    40
 % identity
                   (Z97341) similarity to probable transcriptional adaptor
 NCBI Description
                    ADA2 [Arabidopsis thaliana]
```

Seq. No. 263508



5582 1.R1011 Contig ID uC-zmroteosinte018g03b1 5'-most EST BLASTX Method g1703380 NCBI GI 927 BLAST score 1.0e-100 E value 181 Match length % identity NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760) ADP-ribosylation factor [Oryza sativa] 263509 Seq. No. 5582 4.R1011 Contig ID LIB3076-027-Q1-K1-C4 5'-most EST BLASTX Method g1703380 NCBI GI 247 BLAST score 1.0e-20 E value Match length 69 % identity ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760) NCBI Description ADP-ribosylation factor [Oryza sativa] 263510 Seq. No. 5582 6.R1011 Contig ID uwc700151493.h1 5'-most EST BLASTX Method q2129946 NCBI GI 257 BLAST score 3.0e-22 E value 53 Match length % identity ADP-ribosylation factor homolog GTP-binding protein NTGB1 -NCBI Description common tobacco (fragment) >gi_1184987 (U46927) NTGB1 [Nicotiana tabacum] 263511 Seq. No. 5592 1.R1011 Contig ID LIB36-009-Q1-E1-B9 5'-most EST BLASTX Method q3123264 NCBI GI BLAST score 572 8.0e-59 E value 137 Match length 82 % identity NCBI Description 60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279 (Z97337) hypothetical protein [Arabidopsis thaliana] 263512 Seq. No. 5592 2.R1011 Contig ID LIB3069-057-Q1-K1-A5 5'-most EST BLASTX Method g3123264 NCBI GI 526 BLAST score 2.0e-53 E value

137

74

Match length

% identity



```
NCBI Description 60S RIBOSOMAL PROTEIN L27 >gi_2244857 emb_CAB10279
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
                  263513
Seq. No.
                  5592 3.R1011
Contig ID
                  LIB3059-042-Q1-K1-B9
5'-most EST
                  BLASTX
Method
                  g3123264
NCBI GI
                  488
BLAST score
                  5.0e-49
E value
                  129
Match length
                  74
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L27 >gi 2244857 emb CAB10279
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
                  263514
Seq. No.
                  5592 4.R1011
Contig ID
                  LIB3078-030-Q1-K1-C3
5'-most EST
                  BLASTX
Method
                  g3123264
NCBI GI
                  419
BLAST score
                   3.0e-41
E value
                   96
Match length
                   81
% identity
                  60S RIBOSOMAL PROTEIN L27 >gi 2244857 emb CAB10279
NCBI Description
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
                   263515
Seq. No.
                   5594 1.R1011
Contig ID
5'-most EST
                   LIB3076-026-Q1-K1-H3
                   263516
Seq. No.
                   5596 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17101b06b1
                   BLASTX
Method
                   q3005931
NCBI GI
                   1826
BLAST score
                   0.0e + 00
E value
                   533
Match length
                   66
% identity
                  (AJ005016) ABC transporter [Homo sapiens]
NCBI Description
                   263517
Seq. No.
                   5597 1.R1011
Contig ID
                   rv1700454861.h1
 5'-most EST
Method
                   BLASTX
                   g530088
NCBI GI
BLAST score
                   1006
                   1.0e-109
E value
Match length
                   251
 % identity
                   72
                  (U12735) aminoalcoholphosphotransferase [Glycine max]
NCBI Description
```

 Seq. No.
 263518

 Contig ID
 5599_1.R1011

 5'-most EST
 LIB3180-022-P2-M1-H7

Method BLASTX



NCBI GI g3297809 BLAST score 176 E value 2.0e-14 Match length 160 % identity 39

NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 263519

Contig ID 5599_2.R1011

5'-most EST LIB3076-026-Q1-K1-G1

Seq. No. 263520

Contig ID 5600 1.R1011

5'-most EST LIB3\overline{1}37-040-Q1-K1-F2

Seq. No. 263521

Contig ID 5600 2.R1011

5'-most EST LIB3076-027-Q1-K1-A9

Seq. No. 263522

Contig ID 5613_1.R1011

5'-most EST uC-zmflb73192a05b1

Seq. No. 263523

Contig ID 5613 2.R1011

5'-most EST LIB3076-026-Q1-K1-G6

Seq. No. 263524

Contig ID 5614_1.R1011

5'-most EST LIB3076-026-Q1-K1-A12

Method BLASTX
NCBI GI g1363492
BLAST score 610
E value 1.0e-103
Match length 268
% identity 68

NCBI Description outer envelope membrane protein OEP75 precursor - garden

pea >gi_576507 (L36858) outer membrane protein [Pisum sativum] >gi_633607_emb_CAA58720_ (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]

Seq. No. 263525

Contig ID 5619 1.R1011

5'-most EST uC-zmflmo17108a08b1

Method BLASTX
NCBI GI g2460124
BLAST score 193
E value 2.0e-14
Match length 200
% identity 28

NCBI Description (AF017789) putative transcription factor CA150 [Homo

sapiens]

Seq. No. 263526 Contig ID 5622 1.R1011



Seq. No. 263527 5626 1.R1011 Contig ID 5'-most EST uC-zmflmo17313g12b1 BLASTX Method NCBI GI q3953471 BLAST score 285 2.0e-25 E value Match length 69 72 % identity (AC002328) F2202.16 [Arabidopsis thaliana] NCBI Description 263528 Seq. No. Contig ID 5626 2.R1011 LIB3150-030-Q1-N1-E8 5'-most EST BLASTX Method NCBI GI q3953471 BLAST score 1404 E value 1.0e-156 Match length 409 65 % identity (AC002328) F2202.16 [Arabidopsis thaliana] NCBI Description Seq. No. 263529 5626 3.R1011 Contig ID LIB3151-019-Q1-K1-D1 5'-most EST Method BLASTX g3953471 NCBI GI BLAST score 291 E value 7.0e-26 118 Match length 52 % identity (AC002328) F2202.16 [Arabidopsis thaliana] NCBI Description 263530 Seq. No. 5635 1.R1011 Contig ID 5'-most EST LIB3279-009-P1-K1-B12 Method BLASTX NCBI GI q1632831 617 BLAST score 5.0e-64E value Match length 142 83 % identity (Z49698) orf [Ricinus communis] NCBI Description 263531 Seq. No. 5635 2.R1011 Contig ID 5'-most EST LIB3150-077-P2-N2-B12 Method BLASTX NCBI GI q1632831 BLAST score 562 E value 1.0e-57 140 Match length % identity 78 (Z49698) orf [Ricinus communis] NCBI Description

263532

5635_3.R1011

Seq. No. Contig ID

Contig ID

5'-most EST



5'-most EST uC-zmflmo17259a06b1 Method BLASTX g1632831 NCBI GI BLAST score 617 5.0e-64 E value 142 Match length 83 % identity NCBI Description (Z49698) orf [Ricinus communis] 263533 Seq. No. 5635 5.R1011 Contig ID LIB143-063-Q1-E1-B10 5'-most EST BLASTX Method q1632831 NCBI GI BLAST score 253 3.0e-36 E value Match length 103 77 % identity NCBI Description (Z49698) orf [Ricinus communis] 263534 Seq. No. 5637 1.R1011 Contig ID LIB3059-044-Q1-K1-A5 5'-most EST 263535 Seq. No. 5639 1.R1011 Contig ID LIB3076-024-Q1-K1-G5 5'-most EST BLASTX Method NCBI GI q2702273 BLAST score 166 2.0e-11 E value Match length 100 48 % identity (AC003033) carrot B2 protein-like [Arabidopsis thaliana] NCBI Description 263536 Seq. No. 5641_1.R1011 Contig ID uC-zmflmo17068c11b2 5'-most EST 263537 Seq. No. 5643 1.R1011 Contig ID $uC-z\overline{m}flb73039d12b1$ 5'-most EST BLASTX Method q4582488 NCBI GI BLAST score 1112 1.0e-122 E value 386 Match length 66 % identity (AL021768) putative protein [Arabidopsis thaliana] NCBI Description 263538 Seq. No. 5643 2.R1011 Contig ID 5'-most EST LIB3062-038-Q1-K1-F12 263539 Seq. No.

36557

5643 4.R1011

LIB3136-008-Q1-K1-G6

5'-most EST

BLAST score

Method

NCBI GI

E value

```
263540
Seq. No.
                     5643 6.R1011
Contig ID
                     uC-z\overline{m}flb73245f04a1
5'-most EST
Seq. No.
                     263541
                     5643 13.R1011
Contig ID
                     gw1700613781.h1
5'-most EST
Seq. No.
                     263542
                     5643 14.R1011
Contig ID
5'-most EST
                     qmh700029852.fl
                     263543
Seq. No.
                     5646 1.R1011
Contig ID
                     uC-z\overline{m}flMo17004e01b1
5'-most EST
Method
                     BLASTX
NCBI GI
                     q550429
BLAST score
                     305
                     2.0e-27
E value
Match length
                     182
                     39
% identity
NCBI Description (X81635) RAD26 [Saccharomyces cerevisiae]
Seq. No.
                     263544
                     5647 1.R1011
Contig ID
                     LIB3076-025-Q1-K1-A6
5'-most EST
                     263545
Seq. No.
                     5648 1.R1011
Contig ID
                     LIB3076-025-Q1-K1-B1
5'-most EST
                     263546
Seq. No.
                     5655 1.R1011
Contig ID
                     LIB3076-024-Q1-K1-F8
5'-most EST
                     263547
Seq. No.
                     5656 1.R1011
Contig ID
                     LIB3078-040-Q1-K1-H12
5'-most EST
                     BLASTX
Method
                     q1169871
NCBI GI
                     408
BLAST score
                     1.0e-39
E value
                     145
Match length
                      52
 % identity
NCBI Description GCN20 PROTEIN >gi_1363661_pir__S56146 GCN20 protein - yeast (Saccharomyces cerevisiae) >gi_643479 (U19971) Gcn20p [Saccharomyces cerevisiae] >gi_836764_dbj_BAA09248.1_
                      (D50617) YFR009W [Saccharomyces cerevisiae]
                      263548
 Seq. No.
                      5656 2.R1011
 Contig ID
```

36558

LIB3078-057-Q1-K1-D7

BLASTX g3006145

2.0e-66



Match length 248 % identity 50

NCBI Description (AL022299) ABC transporter [Schizosaccharomyces pombe]

Seq. No. 263549 Contig ID 5656_3.R1011

5'-most EST LIB3137-023-Q1-K1-A6

Method BLASTX
NCBI GI g500734
BLAST score 334
E value 4.0e-31
Match length 142
% identity 49

NCBI Description (U10414) similar to ATP-binding transport protein family

(ABC transporters) [Caenorhabditis elegans]

Seq. No. 263550

Contig ID 5658_1.R1011

5'-most EST uC-zmflmo17321a01b1

Method BLASTX
NCBI GI g3046696
BLAST score 833
E value 4.0e-89
Match length 206
% identity 74

NCBI Description (AL022224) CTP synthase like protein [Arabidopsis thaliana]

Seq. No. 263551

Contig ID 5658_2.R1011

5'-most EST uC-zmflB73047a09b1

Seq. No. 263552

Contig ID 5662_1.R1011

5'-most EST LIB3076-046-Q1-K1-F7

 Seq. No.
 263553

 Contig ID
 5662_4.R1011

 5'-most EST
 xyt700345015.h1

 Seq. No.
 263554

 Contig ID
 5664_1.R1011

5'-most EST uC-zmflmo17078b08b1

Method BLASTX
NCBI GI g3980397
BLAST score 420
E value 7.0e-41
Match length 184
% identity 49

NCBI Description (AC004561) putative protein phosphatase 2C [Arabidopsis

thaliana]

Seq. No. 263555

Contig ID 5664_2.R1011

5'-most EST LIB3076-024-Q1-K1-H6

Seq. No. 263556 Contig ID 5667_1.R1011

Contig ID

5'-most EST



```
5'-most EST
                  LIB3067-053-Q1-K1-G9
Method
                  BLASTX
                  g1518113
NCBI GI
BLAST score
                  737
                  7.0e-78
E value
                   332
Match length
                   50
% identity
NCBI Description (U66193) SLL2 [Brassica napus]
                   263557
Seq. No.
                   5670 1.R1011
Contig ID
                  LIB3076-026-Q1-K1-D11
5'-most EST
                   263558
Seq. No.
                   5674 1.R1011
Contig ID
                   LIB3076-024-Q1-K1-E8
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4538948
BLAST score
                   343
                   5.0e-32
E value
                   126
Match length
                   53
% identity
NCBI Description (AL049483) putative protein [Arabidopsis thaliana]
                   263559
Seq. No.
                   5677 1.R1011
Contig ID
                   uC-zmflm017233d02b1
5'-most EST
Seq. No.
                   263560
Contig ID
                   5679 1.R1011
                   LIB3069-028-Q1-K1-D4
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2829897
BLAST score
                   190
                   9.0e-14
E value
Match length
                   115
                   44
% identity
                  (AC002311) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   263561
                   5679 2.R1011
Contig ID
                   nbm7\overline{0}0470257.h1
5'-most EST
                   263562
Seq. No.
                   5682 1.R1011
Contig ID
                   uC-zmflb73183d04b1
5'-most EST
                   BLASTX
Method
                   g3859570
NCBI GI
BLAST score
                   580
                   2.0e-59
E value
                   188
Match length
                   63
% identity
                   (AF098753) unknown [Oryza sativa]
NCBI Description
                   263563
Seq. No.
                   5682 2.R1011
```

36560 *.

LIB3067-017-Q1-K1-G5



```
BLASTX
Method
NCBI GI
                  q3859570
                  305
BLAST score
                  2.0e-27
E value
Match length
                  109
% identity
                   63
                  (AF098753) unknown [Oryza sativa]
NCBI Description
                  263564
Seq. No.
                   5682 3.R1011
Contig ID
                  LIB143-051-Q1-E1-B8
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3859570
                   273
BLAST score
                   7.0e-24
E value
                   78
Match length
% identity
                   67
                  (AF098753) unknown [Oryza sativa]
NCBI Description
                   263565
Seq. No.
                   5685 1.R1011
Contig ID
                  LIB3076-024-Q1-K1-B10
5'-most EST
Seq. No.
                   263566
                   5691 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17139f09b1
                   BLASTX
Method
                   q4584527
NCBI GI
BLAST score
                   192
E value
                   4.0e-14
Match length
                   149
% identity
                   35
NCBI Description (AL049607) putative protein [Arabidopsis thaliana]
                   263567
Seq. No.
                   5694 1.R1011
Contig ID
                   uC-zmflb73199a11b1
5'-most EST
                   BLASTX
Method
                   g3021357
NCBI GI
                   1475
BLAST score
                   1.0e-164
E value
Match length
                   346
                   78
% identity
                  (AJ005082) UDP-galactose 4-epimerase [Cyamopsis
NCBI Description
                   tetragonoloba]
                   263568
Seq. No.
                   5696_1.R1011
Contig ID
5'-most EST
                   pmx700083858.hl
Method
                   BLASTX
                   g417360
NCBI GI
                   378
BLAST score
                   7.0e-36
E value
Match length
                   128
% identity
                   55
NCBI Description HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2
```

36561

>gi_2131280_pir__S67767 high mobility group-like protein

Seq. No.



NHP2 - yeast (Saccharomyces cerevisiae)
>gi_666101_emb_CAA40885_ (X57714) high mobility group-like
nuclear protein 2 [Saccharomyces cerevisiae]
>gi_1429348_emb_CAA67483_ (X99000) high-mobility-group-like
protein [Saccharomyces cerevisiae]
>gi_1431346_emb_CAA98786_ (Z74256) ORF YDL208w
[Saccharomyces cerevisiae]

5696 2.R1011 Contig ID LIB143-011-Q1-E1-D2 5'-most EST BLASTX Method g417360 NCBI GI BLAST score 260 2.0e-22 E value 128 Match length 41 % identity

263569

NCBI Description HIGH MOBILITY GROUP-LIKE NUCLEAR PROTEIN 2

>gi_2131280_pir__S67767 high mobility group-like protein

NHP2 - yeast (Saccharomyces cerevisiae)

>gi_666101_emb_CAA40885_ (X57714) high mobility group-like

nuclear protein 2 [Saccharomyces cerevisiae]

>gi 1429348_emb_CAA67483_ (X99000) high-mobility-group-like

protein [Saccharomyces cerevisiae]

>qi 1431346 emb CAA98786 (Z74256) ORF YDL208w

[Saccharomyces cerevisiae]

 Seq. No.
 263570

 Contig ID
 5696_5.R1011

 5'-most EST
 rvt700550925.h1

Seq. No. 263571
Contig ID 5701_1.R1011
5'-most EST uer700578664.h1

Method BLASTX
NCBI GI g3080437
BLAST score 514
E value 1.0e-51
Match length 181
% identity 59

NCBI Description (AL022605) putative protein [Arabidopsis thaliana]

 Seq. No.
 263572

 Contig ID
 5701_2.R1011

 5'-most EST
 uC-zmflb73158a10b2

Seq. No. 263573 Contig ID 5701_3.R1011 5'-most EST wuj700282002.h1

Seq. No. 263574 Contig ID 5707_1.R1011

5'-most EST LIB3070-007-Q1-N1-C8

Method BLASTX
NCBI GI g3860323
BLAST score 329
E value 2.0e-30



Match length 75 % identity 80

NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]

 Seq. No.
 263575

 Contig ID
 5707_2.R1011

 5'-most EST
 qmh700027778.f1

Method BLASTX
NCBI GI g3860323
BLAST score 153
E value 3.0e-10
Match length 49
% identity 65

NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]

Seq. No. 263576 Contig ID 5708_1.R1011

5'-most EST LIB3068-010-Q1-K1-B3

Method BLASTX
NCBI GI g3618320
BLAST score 697
E value 4.0e-77
Match length 230
% identity 67

NCBI Description (AB001888) zinc finger protein [Oryza sativa]

Seq. No. 263577
Contig ID 5712_1.R1011

5'-most EST uC-zmflmo17270h12b1

Method BLASTX
NCBI GI g3149952
BLAST score 315
E value 1.0e-30
Match length 149
% identity 67

NCBI Description (AB010259) DRH1 [Arabidopsis thaliana]

Seq. No. 263578

Contig ID 5712_2.R1011

5'-most EST uC-zmflm017025b06b1

Method BLASTX
NCBI GI g3149952
BLAST score 203
E value 9.0e-16
Match length 52
% identity 73

NCBI Description (AB010259) DRH1 [Arabidopsis thaliana]

Seq. No. 263579 Contig ID 5718_1.R1011

5'-most EST LIB3076-022-Q1-K1-H6

Method BLASTX
NCBI GI g3913366
BLAST score 313
E value 8.0e-29
Match length 128
% identity 52



NCBI Description PUTATIVE RECEPTOR PROTEIN KINASE CRINKLY4 PRECURSOR >qi 1597723 (U67422) CRINKLY4 precursor [Zea mays] Seq. No. 263580 Contig ID 5720 1.R1011 dyk700103247.h1 5'-most EST BLASTX Method NCBI GI g2132388 BLAST score 321 6.0e-29 E value 255 Match length 40 % identity PHO85 protein - yeast (Saccharomyces cerevisiae) NCBI Description >gi 1163103 (U43503) Lph16p [Saccharomyces cerevisiae] 263581 Seq. No. Contig ID 5720 2.R1011 qmh700026931.f1 5'-most EST Seq. No. 263582 5721 1.R1011 Contig ID $xmt7\overline{0}0265444.h1$ 5'-most EST BLASTX Method NCBI GI g2842689 BLAST score 167 1.0e-11 E value Match length 105 33 % identity HYPOTHETICAL 50.4 KD PROTEIN C1F8.04C IN CHROMOSOME I NCBI Description >gi_1638851_emb_CAB03598_ (Z81312) unknown [Schizosaccharomyces pombe] 263583 Seq. No. 5724 1.R1011 Contig ID LIB3136-052-Q1-K1-G6 5'-most EST BLASTX Method q483412 NCBI GI 456 BLAST score 1.0e-120 E value 280 Match length 80 % identity (L01497) calmodulin-binding protein [Zea mays] NCBI Description

263584 Seq. No. 5724 2.R1011 Contig ID uC-zmrob73055e07b1 5'-most EST BLASTX Method NCBI GI g4185141 198 BLAST score 3.0e-15E value

106 Match length 56 % identity

(AC005724) putative calmodulin-binding protein [Arabidopsis NCBI Description

thaliana]

263585 Seq. No.

Contig ID 5724_3.R1011



uC-zmflb73119b05b1 5'-most EST BLASTX Method g4185141 NCBI GI 1258 BLAST score 1.0e-139 E value 320 Match length 76 % identity (AC005724) putative calmodulin-binding protein [Arabidopsis NCBI Description thaliana] 263586 Seq. No. 5724 4.R1011 Contig ID LIB3181-014-P1-M1-A6 5'-most EST BLASTX Method g1698548 NCBI GI BLAST score 306 5.0e-28 E value 71 Match length 82 % identity (U58971) calmodulin-binding protein [Nicotiana tabacum] NCBI Description Seq. No. 263587 5724 6.R1011 Contig ID qct701177518.h1 5'-most EST BLASTN Method q483411 NCBI GI BLAST score 67 3.0e-29 E value 209 Match length 84 % identity NCBI Description Zea Mays calmodulin-binding protein mRNA, 3'end 263588 Seq. No. 5727 1.R1011 Contig ID zuv700354762.h1 5'-most EST 263589 Seq. No. 5730 1.R1011 Contig ID ntr700075434.h15'-most EST BLASTX Method q4557229 NCBI GI BLAST score 581 2.0e-59 E value 343 Match length 36 % identity angio-associated, migratory cell protein NCBI Description >gi 3121739 sp_Q13685 AAMP HUMAN ANGIO-ASSOCIATED MIGRATORY CELL PROTEIN >gi_2134759 pir__139383 angio-associated migratory cell protein - human >gi_870803 (M95627) angio-associated migratory cell protein [Homo sapiens] 263590 Seq. No. 5740 1.R1011 Contig ID 5'-most EST LIB3076-022-Q1-K1-G8

36565

263591

5743 1.R1011

Seq. No. Contig ID



5'-most EST wyr700240855.h1 Method BLASTX NCBI GI g3212848 BLAST score 401 5.0e-39 E value Match length 119 60 % identity (AC004005) putative inositol polyphosphate-5-phosphatase NCBI Description [Arabidopsis thaliana] 263592 Seq. No. Contig ID 5745 1.R1011 LIB3076-022-Q1-K1-H11 5'-most EST Seq. No. 263593 Contig ID 5750 1.R1011 LIB3067-049-Q1-K1-E6 5'-most EST Method BLASTX NCBI GI q729668 BLAST score 254 2.0e-21 E value Match length 71 66 % identity HISTONE H1 >gi 2147479 pir S65059 histone H1, NCBI Description drought-inducible - Lycopersicon pennellii >gi 436823 (U01890) Solanum pennellii histone H1 [Solanum pennellii] Seq. No. 263594 Contig ID 5750 2.R1011 LIB3069-047-Q1-K1-B6 5'-most EST 263595 Seq. No. 5751 1.R1011 Contig ID LIB3060-016-Q1-K1-G3 5'-most EST BLASTX Method g3334320 NCBI GI BLAST score 1083 1.0e-118 E value Match length 287 77 % identity 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553) NCBI Description ribosome-associated protein p40 [Glycine max] 263596 Seq. No. 5751 2.R1011 Contig ID 5'-most EST LIB3069-025-Q1-K1-G5 Seq. No. 263597 5751 3.R1011 Contig ID 5'-most EST uC-zmrob73075e12b1 BLASTX Method NCBI GI q3334320 BLAST score 672 1.0e-70 E value Match length 136

36566

NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)

95

% identity



ribosome-associated protein p40 [Glycine max]

Seq. No. 263598 5751 4.R1011 Contig ID 5'-most EST uC-zmflb73256c06b1 BLASTX Method NCBI GI q3334320 BLAST score 541 2.0e-55 E value Match length 112 94 % identity NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553) ribosome-associated protein p40 [Glycine max] Seq. No. 263599 Contig ID 5751 5.R1011 5'-most EST uer700577040.h1 BLASTX Method NCBI GI q3334320 BLAST score 479 E value 3.0e-48 Match length 99 94 % identity NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553) ribosome-associated protein p40 [Glycine max] 263600 Seq. No. Contig ID 5751 7.R1011 5'-most EST tzu700203089.h1 263601 Seq. No. 5751 8.R1011 Contig ID 5'-most EST uC-zmflmo17027e01a1 263602 Seq. No. 5751 9.R1011 Contig ID 5'-most EST uC-zmflmo17058e04a1 263603 Seq. No. 5751 13.R1011 Contig ID LIB3150-101-P1-N1-B3 5'-most EST BLASTX Method g3551245 NCBI GI BLAST score 607 1.0e-62 E value 222 Match length % identity 61 NCBI Description (AB012702) P40-like protein [Daucus carota] Seq. No. 263604 5755_1.R1011 Contig ID 5'-most EST uC-zmflmo17052c02b1 Method BLASTX NCBI GI q2129636 BLAST score 663

36567

4.0e-69

338

E value Match length



43 % identity lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase NCBI Description [Arabidopsis thaliana] 263605 Seq. No. 5755 2.R1011 Contig ID LIB3062-058-Q1-K1-F5 5'-most EST BLASTX Method NCBI GI g4314378 157 BLAST score 2.0e-10 E value 63 Match length 52 % identity NCBI Description (AC006232) putative lipase [Arabidopsis thaliana] 263606 Seq. No. 5756 1.R1011 uC-zmflmo17108d02b1

Contig ID 5'-most EST BLASTX Method g2134794 NCBI GI BLAST score 161 E value 3.0e-10 234 Match length 23

-% identity autoantigen - human >gi_533202 (L26339) autoantigen [Homo NCBI Description

sapiens]

263607 Seq. No. 5756 2.R1011 Contig ID uC-zmflmo17313g11b15'-most EST

Seq. No. 263608 5756 3.R1011 Contig ID LIB84-013-Q1-E1-B7 5'-most EST

263609 Seq. No. 5757 1.R1011 Contig ID uC-zmroB73020h11b1 5'-most EST

263610 Seq. No. 5764_1.R1011 Contig ID 5'-most EST uC-zmflb73053a04b2

BLASTX Method NCBI GI q4454477 234 BLAST score 2.0e-19 E value

112 Match length % identity 42

(AC006234) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 263611 5766 1.R1011 Contig ID 5'-most EST gwl700612991.h1 Method BLASTX NCBI GI g4467152

BLAST score 796 1.0e-85 E value



238 Match length % identity (AL035540) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 263612 5769 1.R1011 Contig ID 5'-most EST rvt700549568.h1 263613 Seq. No. 5790 1.R1011 Contig ID $yyf7\overline{0}0349988.h1$ 5'-most EST BLASTX Method NCBI GI q2832641 1515 BLAST score 1.0e-169 E value 357 Match length 82 % identity (AL021710) glycolate oxidase - like protein [Arabidopsis NCBI Description thaliana] 263614 Seq. No. 5790 2.R1011 Contig ID LIB3137-010-Q1-K1-C7 5'-most EST Method BLASTX q2832641 NCBI GI BLAST score 203 8.0e-33 E value 90 Match length % identity 83 (AL021710) glycolate oxidase - like protein [Arabidopsis NCBI Description thaliana] 263615 Seq. No. Contiq ID 5790 6.R1011 hbs701181905.hl 5'-most EST Method BLASTX g1063400 NCBI GI 243 BLAST score E value 1.0e-20 Match length 115 % identity 52 (X92888) glycolate oxidase [Lycopersicon esculentum] NCBI Description 263616 Seq. No. 5795 1.R1011 Contig ID wyr700242418.h1 5'-most EST BLASTX Method

g2911058 NCBI GI 270 BLAST score 3.0e-23E value

Match length

% identity

(AL021961) putative protein [Arabidopsis thaliana] NCBI Description

263617 Seq. No. 5811 1.R1011 Contig ID uC-zmf1b73226a10b1 5'-most EST

184

NCBI Description



```
Method
                  BLASTX
NCBI GI
                  g3337352
BLAST score
                  1350
                   1.0e-149
E value
Match length
                   597
                   50
% identity
                   (AC004481) putative chromatin structural protein Supt5hp
NCBI Description
                   [Arabidopsis thaliana]
                   263618
Seq. No.
Contig ID
                   5811 2.R1011
                   uC-zmflmo17001d09b1
5'-most EST
Method
                   BLASTX
                   g3786010
NCBI GI
BLAST score
                   175
                   1.0e-11
E value
Match length
                   202
% identity
                   31
                   (AC005499) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   263619
Seq. No.
Contig ID
                   5819 1.R1011
                   LIB3069-026-Q1-K1-G11
5'-most EST
                   BLASTX
Method
                   g629829
NCBI GI
BLAST score
                   1320
E value
                   1.0e-146
Match length
                   387
                   70
% identity
                   protochlorophyllide reductase (EC 1.3.1.33) - wheat
NCBI Description
                   >gi 510677 emb CAA54042_ (X76532) protochlorophyilide
                   reductase [Triticum aestivum]
                   263620
Seq. No.
                   5819 2.R1011
Contig ID
5'-most EST
                   fwa700101540.h1
Method
                   BLASTX
                   g1076725
NCBI GI
BLAST score
                   1127
                   1.0e-124
E value
                   282
Match length
                   82
% identity
                   NADPH dehydrogenase (EC 1.6.99.1) - barley
NCBI Description
                   >gi 683476 emb_CAA59228_ (X84738) NADPH dehydrogenase
                   [Hordeum vulgare]
                   263621
Seq. No.
                   5819 3.R1011
Contig ID
                   LIB3068-012-Q1-K1-C6
5'-most EST
Method
                   BLASTN
                   q19060
NCBI GI
BLAST score
                   51
                   1.0e-19
E value
                   111
Match length
% identity
```

Barley mRNA for NADPH-protochlorophyllide oxidoreductase



(PCR)

NCBI GI g1076725
BLAST score 333
E value 5.0e-31
Match length 69
% identity 91

NCBI Description NADPH dehydrogenase (EC 1.6.99.1) - barley

>gi 683476 emb CAA59228 (X84738) NADPH dehydrogenase

[Hordeum vulgare]

Seq. No. 263623

Contig ID 5823_1.R1011 5'-most EST cjh700193805.h1

Seq. No. 263624

Contig ID 5828_1.R1011

5'-most EST uC-zmflb73173a10b1

Method BLASTX
NCBI GI g465898
BLAST score 246
E value 1.0e-20
Match length 148
% identity 43

NCBI Description HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III

>gi_630692_pir__S44849 K12H4.8 protein - Caenorhabditis
elegans >gi_289703 (L14331) homology with eukaryotic
initiation factor-4A (eIF-4A) and E. coli Ribonuclease III;

coded for by C. elegans cDNA GenBank: T02268; putative

[Caenorhabditis elegans]

Seq. No. 263625

Contig ID 5828_2.R1011

5'-most EST uC-zmflmo17273a07b1

Method BLASTX
NCBI GI g4589488
BLAST score 191
E value 4.0e-14
Match length 88
% identity 43

NCBI Description (AB023145) KIAA0928 protein [Homo sapiens]

Seq. No. 263626 Contig ID 5831_1.R1011

5'-most EST LIB3076-006-Q1-K1-B3

Seq. No. 263627

Contig ID 5835 1.R1011

5'-most EST uC-zmflmo17212b07a1

Method BLASTX
NCBI GI g422023
BLAST score 3249
E value 0.0e+00



```
Match length
                   657
% identity
                   95
                  acetyl-CoA carboxylase (EC 6.4.1.2) - maize (fragment)
NCBI Description
                  >gi_629836_pir__S42659 acetyl-CoA carboxylase (EC 6.4.1.2)
                   - maize
                  263628
Seq. No.
                  5835 4.R1011
Contig ID
                  wty700165250.hl
5'-most EST
                  BLASTN
Method
                  g1335965
NCBI GI
BLAST score
                   317
                   1.0e-178
E value
                   402
Match length
                   95
% identity
                  Zea mays acetyl CoA carboxylase mRNA, partial cds
NCBI Description
                   263629
Seq. No.
Contig ID
                   5835 5.R1011
5'-most EST
                   ntr700076413.hl
                   BLASTN
Method
                   g1045304
NCBI GI
                   372
BLAST score
                   0.0e+00
E value
                   443
Match length
                   95
% identity
                  Zea mays acetyl-coenzyme A carboxylase mRNA, complete cds
NCBI Description
Seq. No.
                   263630
                   5845 1.R1011
Contig ID
                   LIB3150-008-Q1-N1-F2
5'-most EST
                   BLASTX
Method
                   q1854386
NCBI GI
BLAST score
                   197
                   7.0e-15
E value
Match length
                   60
% identity
                   67
                   (AB001375) similar to soluble NSF attachment protein [Vitis
NCBI Description
                   vinifera]
                   263631
Seq. No.
                   5845 2.R1011
Contig ID
                   {\tt uC-zmroteosinte062f01b1}
5'-most EST
                   263632
Seq. No.
                   5845 3.R1011
Contig ID
                   LIB3115-005-Q1-K1-C7
5'-most EST
                   BLASTX
Method
                   g1854386
NCBI GI
```

Method BLASTX
NCBI GI g1854386
BLAST score 591
E value 1.0e-71
Match length 239
% identity 54

NCBI Description (AB001375) similar to soluble NSF attachment protein [Vitis

vinifera]

Seq. No. 263633



Contig ID 5852_1.R1011 5'-most EST LIB3066-054-Q1-K1-B10

Seq. No. 263634

Contig ID 5854_1.R1011

5'-most EST LIB3151-044-Q1-K1-D6

Method BLASTX
NCBI GI g1172635
BLAST score 1933
E value 0.0e+00
Match length 445
% identity 91

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING

PROTEIN HOMOLOG 2) >gi_556558_dbj_BAA04615_ (D17789) rice

homologue of Tat binding protein [Oryza sativa]

Seq. No. 263635

Contig ID 5854_2.R1011

5'-most EST LIB84-016-Q1-E1-B4

Method BLASTX
NCBI GI g1172635
BLAST score 511
E value 1.0e-51
Match length 118
% identity 86

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING

PROTEIN HOMOLOG 2) >gi_556558_dbj_BAA04615_ (D17789) rice

homologue of Tat binding protein [Oryza sativa]

Seq. No. 263636

Contig ID 5854_3.R1011

5'-most EST LIB3078-029-Q1-K1-B7

Method BLASTX
NCBI GI g1172635
BLAST score 290
E value 5.0e-33
Match length 91
% identity 83

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING

PROTEIN HOMOLOG 2) >gi 556558 dbj BAA04615 (D17789) rice

homologue of Tat binding protein [Oryza sativa]

Seq. No. 263637

Contig ID 5854 5.R1011 5'-most EST zuv700356649.h1

Method BLASTX
NCBI GI g1172635
BLAST score 337
E value 1.0e-31
Match length 94
% identity 77

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING

PROTEIN HOMOLOG 2) >gi_556558_dbj_BAA04615_ (D17789) rice

homologue of Tat binding protein [Oryza sativa]

Seq. No. 263638

Contig ID 5856 1.R1011



LIB3078-016-Q1-K1-H10 5'-most EST BLASTX Method q439879 NCBI GI BLAST score 220 4.0e-25 E value 94 Match length 67 % identity (L15194) [Golden delicious apple fruit expressed mRNA, NCBI Description complete cds.], gene product [Malus domestica] 263639 Seq. No. 5856 2.R1011 Contig ID 5'-most EST uC-zmroteosinte032c02b1 Method BLASTX q1707011 NCBI GI 207 BLAST score 3.0e-16 E value Match length 47 % identity 79 (U78721) auxin-repressed protein isolog [Arabidopsis NCBI Description thaliana] 263640 Seq. No. 5856 3.R1011 Contig ID LIB143-064-Q1-E1-H12 5'-most EST BLASTN Method q439878 NCBI GI 35 BLAST score E value 5.0e-10 Match length 55 91 % identity Golden delicious apple fruit expressed mRNA, complete cds NCBI Description 263641 Sea. No. 5856 4.R1011 Contig ID uC-zmflmo17171c08b1 5'-most EST BLASTX Method g439879 NCBI GI BLAST score 185 3.0e-13 E value Match length 40 80 % identity (L15194) [Golden delicious apple fruit expressed mRNA, NCBI Description complete cds.], gene product [Malus domestica] 263642 Seq. No. 5856 5.R1011 Contig ID LIB3\overline{1}37-018-Q1-K1-D10 5'-most EST BLASTX Method g1707011 NCBI GI BLAST score 245 2.0e-20 E value 109 Match length 50 % identity (U78721) auxin-repressed protein isolog [Arabidopsis NCBI Description thaliana]

NCBI Description



```
263643
Seq. No.
Contig ID
                  5856 6.R1011
                  xsy700217159.h1
5'-most EST
Seq. No.
                  263644
                  5856 12.R1011
Contig ID
                  LIB3067-039-Q1-K1-D4
5'-most EST
                   263645
Seq. No.
                   5857 1.R1011
Contig ID
                  uC-zmrob73039a10a1
5'-most EST
                   BLASTX
Method
                   g3559805
NCBI GI
                   1447
BLAST score
                   1.0e-161
E value
                   334
Match length
                   77
% identity
                   (AJ006787) putative phytochelatin synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   263646
Seq. No.
                   5857 2.R1011
Contig ID
                   uC-zmflb73177g04a1
5'-most EST
                   BLASTX
Method
                   q2058284
NCBI GI
                   599
BLAST score
                   1.0e-61
E value
                   157
Match length
                   72
% identity
NCBI Description (X97378) atranbp1b [Arabidopsis thaliana]
                   263647
Seq. No.
                   5857 3.R1011
Contig ID
                   uC-zmroteosinte061c09b2
5'-most EST
                   BLASTX
Method
                   g3559805
NCBI GI
                   818
BLAST score
                   1.0e-94
E value
                   227
Match length
                   73
% identity
                   (AJ006787) putative phytochelatin synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   263648
Seq. No.
                   5857 4.R1011
Contig ID
                   LIB3076-009-Q1-K1-F3
5'-most EST
                   263649
Seq. No.
                   5857 5.R1011
Contig ID
                   LIB3118-012-Q1-K1-B10
 5'-most EST
                   BLASTX
Method
                   g2058284
NCBI GI
                   235
 BLAST score
                   2.0e-19
 E value
Match length
                    68
                    68
 % identity
```

36575

(X97378) atranbp1b [Arabidopsis thaliana]



263650 Seq. No. 5857 7.R1011 Contig ID 5'-most EST LIB3088-012-Q1-K1-A1 263651 Seq. No. 5857 11.R1011 Contig ID 5'-most EST xjt700094994.h1 BLASTN Method q1042260 NCBI GI 128 BLAST score 9.0e-66 E value 136 Match length % identity {Mu1 element insertion site, clone 10} [maize, Transposon, NCBI Description 285 nt] 263652 Seq. No. Contig ID 5859 1.R1011 wty700170201.h1 5'-most EST BLASTX Method g2384956 NCBI GI 367 BLAST score E value 2.0e-34 199 Match length 38 % identity (AF022985) No definition line found [Caenorhabditis NCBI Description elegans] Seq. No. 263653 5859 3.R1011 Contig ID LIB3078-030-Q1-K1-G5 5'-most EST Seq. No. 263654 5859 4.R1011 Contig ID vux700156830.h1 5'-most EST BLASTX Method g2072393 NCBI GI BLAST score 231 E value 4.0e-19 Match length 110 45 % identity (U29168) similar to human Xeroderma pigmentosum group B DNA NCBI Description repair protein, Swiss-Prot Accession Number P19447 [Arabidopsis thaliana] 263655 Seq. No. 5859 5.R1011 Contig ID pmx700091450.h15'-most EST 263656 Seq. No. 5862 1.R1011 Contig ID

5'-most EST uC-zmflMo17004c12b1

Method BLASTX
NCBI GI 94432859
BLAST score 497
E value 1.0e-49



Match length 318 % identity 40

NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]

Seq. No. 263657

Contig ID 5862_2.R1011 5'-most EST pmx700082695.h1

Seq. No. 263658

Contig ID 5862 3.R1011 5'-most EST ntr700075628.h1

Seq. No. 263659

Contig ID 5873_1.R1011

5'-most EST LIB3076-012-Q1-K1-D12

Method BLASTX
NCBI GI g2664214
BLAST score 193
E value 2.0e-14
Match length 134
% identity 42

NCBI Description (AJ222646) G2484-1 [Arabidopsis thaliana]

Seq. No. 263660

Contig ID 5876 1.R1011

5'-most EST LIB3076-012-Q1-K1-G5

Seq. No. 263661

Contig ID 5877_1.R1011

5'-most EST LIB3076-013-Q1-K1-D3

Seq. No. 263662

Contig ID 5877_2.R1011 5'-most EST xmt700267707.h1

Seq. No. 263663

Contig ID 5885_1.R1011 5'-most EST gct701177172.h1

Seq. No. 263664

Contig ID 5888_1.R1011 5'-most EST pmx700087503.h1

Method BLASTX
NCBI GI g3024501
BLAST score 845
E value 1.0e-90
Match length 210
% identity 79

NCBI Description RAS-RELATED PROTEIN RAB11C >gi_1370146_emb_CAA98179_

(Z73951) RAB11C [Lotus japonicus]

Seq. No. 263665

Contig ID 5888_2.R1011 5'-most EST xjt700093660.h1

Method BLASTX NCBI GI g452357 BLAST score 293

365.77



```
5.0e-26
E value
Mátch length
                  115
% identity
                  (Z29591) guanine nucleotide regulatory protein [Vicia faba]
NCBI Description
                  >gi 1098294 prf 2115367B small GTP-binding protein [Vicia
                   faba]
                   263666
Seq. No.
                   5888 3.R1011
Contig ID
                   wen7\overline{0}0334258.h1
5'-most EST
                   BLASTX
Method
                   g303742
NCBI GI
BLAST score
                   875
                   2.0e-94
E value
                   217
Match length
% identity
                   (D12544) GTP-binding protein [Pisum sativum]
NCBI Description
                   >gi 738936 prf 2001457D GTP-binding protein [Pisum
                   sativum]
                   263667
Seq. No.
                   5888 4.R1011
Contig ID
                   uC-zmflB73004h07b1
5'-most EST
                   BLASTX
Method
                   q730512
NCBI GI
BLAST score
                   616
                   4.0e-64
E value
                   134
Match length
                   90
% identity
                   RAS-RELATED PROTEIN RIC2 >gi 481506 pir S38741 GTP-binding
NCBI Description
                   protein ric2 - rice >gi_218228_dbj_BAA02904_ (D13758)
                   ras-related GTP binding protein [Oryza sativa]
                   263668
Seq. No.
                   5888 5.R1011
Contig ID
                   fC-zmf1700342858f4
5'-most EST
                   BLASTX
Method
NCBI GI
                   q452357
BLAST score
                   615
E value
                   5.0e-64
                   134
Match length
% identity
                   90
                   (Z29591) guanine nucleotide regulatory protein [Vicia faba]
NCBI Description
                   >gi_1098294_prf__2115367B small GTP-binding protein [Vicia
                   fabal
                   263669
Seq. No.
                   5888 6.R1011
Contig ID
                   LIB3137-039-Q1-K1-C7
5'-most EST
                   BLASTX
Method
```

Method BLASTX
NCBI GI 9730512
BLAST score 640
E value 5.0e-67
Match length 126
% identity 99

NCBI Description RAS-RELATED PROTEIN RIC2 >gi_481506_pir__ \$38741 GTP-binding protein ric2 - rice >gi_218228_dbj_BAA02904_ (D13758)

Contig ID

5'-most EST



ras-related GTP binding protein [Oryza sativa]

```
263670
Seq. No.
                   5888 7.R1011
Contig ID
                   LIB3079-006-Q1-K1-G5
5'-most EST
Method
                   BLASTX
                   g303742
NCBI GI
                   373
BLAST score
                   9.0e-42
E value
                   97
Match length
% identity
                   96
                   (D12544) GTP-binding protein [Pisum sativum]
NCBI Description
                   >qi 738936 prf 2001457D GTP-binding protein [Pisum
                   sativum]
                   263671
Seq. No.
                   5888 8.R1011
Contig ID
                   fdz701161793.hl
5'-most EST
                   BLASTX
Method
                   g730512
NCBI GI
BLAST score
                   553
E value
                   8.0e-57
Match length
                   114
                   93
% identity
                   RAS-RELATED PROTEIN RIC2 >gi 481506 pir S38741 GTP-binding
NCBI Description
                   protein ric2 - rice >gi 21\overline{8}2\overline{2}8 dbj \overline{BAA}0\overline{29}04 (D13758)
                   ras-related GTP binding protein [Oryza sativa]
                   263672
Seq. No.
                   5888 9.R1011
Contig ID
                   gwl700617007.hl
5'-most EST
                   BLASTX
Method
                   g3024528
NCBI GI
                   381
BLAST score
                   2.0e-54
E value
                   157
Match length
                   73
% identity
NCBI Description RAS-RELATED PROTEIN RAB2BV >gi 974778 emb CAA89049
                   (Z49190) small G protein [Beta vulgaris]
                   263673
Seq. No.
                    5888 11.R1011
Contig ID
                   ntr700072965.h1
5'-most EST
                   BLASTX
Method
                   g303742
NCBI GI
BLAST score
                    403
                    3.0e-39
E value
                    81
Match length
                    98
% identity
                   (D12544) GTP-binding protein [Pisum sativum]
NCBI Description
                    >qi 738936 prf 2001457D GTP-binding protein [Pisum
                    satīvum]
                    263674
Seq. No.
```

36579

5892 1.R1011

LIB3076-015-Q1-K1-C10

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263675 Seq. No. 5893 1.R1011 Contig ID uC-zmrob73080e05b1 5'-most EST BLASTX Method g1769895 NCBI GI BLAST score 1233 1.0e-136 E value 396 Match length 62 % identity NCBI Description (X96598) CaLB protein [Arabidopsis thaliana] Seq. No. 263676 5901 1.R1011 Contig ID LIB3116-017-P1-K1-E7 5'-most EST BLASTX Method g1871182 NCBI GI BLAST score 997 1.0e-108 E value 253 Match length 74 % identity NCBI Description (U90439) phospholipase D isolog [Arabidopsis thaliana] 263677 Seq. No. 5902 1.R1011 Contig ID LIB3076-015-Q1-K1-E5 5'-most EST 263678 Seq. No. 5912 1.R1011 Contig ID LIB3158-012-Q1-K1-H7 5'-most EST 263679 Seq. No. 5916 1.R1011 Contig ID LIB3078-034-Q1-K1-F9 5'-most EST 263680 Seq. No. 5918 1.R1011 Contig ID LIB3150-075-P2-N2-G12 5'-most EST 263681 Seq. No. 5919 1.R1011 Contig ID 5'-most EST vux700157911.h1 263682 Seq. No. 5923 1.R1011 Contig ID uer700582157.hl 5'-most EST 263683 Seq. No. 5925 1.R1011 Contig ID LIB3076-018-Q1-K1-D6 5'-most EST BLASTX Method NCBI GI q4220527

Method BLASTX
NCBI GI g4220527
BLAST score 276
E value 3.0e-24
Match length 90

% identity 58

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Method

NCBI GI BLAST score BLASTX q2257756

337



```
Seq. No.
                   263684
                   5928 1.R1011
Contig ID
                   wty700171701.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2130123
                   470
BLAST score
                   1.0e-46
E value
                   126
Match length
                   75
% identity
                   DNA-binding factor LIP 15 - maize >gi_1060935_dbj_BAA05617
NCBI Description
                   (D26563) mLIP15 [Zea mays]
                   263685
Seq. No.
                   5935 1.R1011
Contig ID
                   xsy700217963.h1
5'-most EST
                   BLASTX
Method
                   g464621
NCBI GI
                   743
BLAST score
                   1.0e-78
E value
                   214
Match length
% identity
                   71
                   60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586
NCBI Description
                   ribosomal protein ML16 - common ice plant >gi 19539 emb_CAA49175_ (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
Seq. No.
                   263686
                   5935 2.R1011
Contig ID
                   LIB36-009-Q1-E1-B7
5'-most EST
                   BLASTX
Method
                   g464621
NCBI GI
BLAST score
                   281
                   1.0e-24
E value
                   103
Match length
                   57
% identity
                   60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586
NCBI Description
                   ribosomal protein ML16 - common ice plant
                   >gi 19539 emb CAA49175 (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
                   263687
Seq. No.
                   5948 1.R1011
Contig ID
                   LIB148-047-Q1-E1-H12
5'-most EST
Method
                   BLASTX
                   q3978474
NCBI GI
BLAST score
                   203
                   1.0e-15
E value
                   147
Match length
                   37
% identity
NCBI Description (AF092918) MetZ homolog [Pseudomonas alcaligenes]
                   263688
Seq. No.
                   5959 1.R1011
Contig ID
5'-most EST
                   LIB3076-020-Q1-K1-B6
```



```
2.0e-31
E value
                  96
Match length
                  69
% identity
                   (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays]
NCBI Description
                  >gi 3650466 (AF026917) histone deacetylase HD2-p39 [Zea
                  mays]
                  263689
Seq. No.
                   5961 1.R1011
Contig ID
                  LIB3076-020-Q1-K1-C7
5'-most EST
                  BLASTX
Method
                   g2632254
NCBI GI
                   742
BLAST score
                   9.0e-79
E value
                   177
Match length
% identity
                   80
                  (Y12465) serine/threonine kinase [Sorghum bicolor]
NCBI Description
                   263690
Seq. No.
                   5965 1.R1011
Contig ID
                   uC-zmf1b73265a02b4
5'-most EST
Method
                   BLASTX
                   q4455242
NCBI GI
                   295
BLAST score
                   4.0e-26
E value
                   111
Match length
                   53
% identity
                   (AL035523) geranylgeranylated protein ATGP4 [Arabidopsis
NCBI Description
                   thaliana]
                   263691
Seq. No.
                   5965 2.R1011
Contig ID
                   uC-zmflb73220f08b2
5'-most EST
Seq. No.
                   263692
                   5979 1.R1011
Contig ID
                   LIB3076-022-Q1-K1-C9
5'-most EST
                   263693
Seq. No.
                   5983 1.R1011
Contig ID
                   uC-zmflb73079f10b2
5'-most EST
                   263694
Seq. No.
                   5983 2.R1011
Contig ID
                   LIB3069-029-Q1-K1-B11
 5'-most EST
                   263695
Seq. No.
                   5984 1.R1011
 Contig ID
                   LIB3076-023-Q1-K1-B2
 5'-most EST
                   BLASTX
Method
                   g2190992
 NCBI GI
 BLAST score
                    353
                    3.0e-33
 E value
                   97
 Match length
                    64
 % identity
                   (AF004358) glutathione S-transferase TSI-1 [Aegilops
 NCBI Description
```

36582

tauschii]

% identity

NCBI Description

83



```
263696
Seq. No.
                  5990 1.R1011
Contig ID
                  LIB3076-024-Q1-K1-A2
5'-most EST
                  BLASTX
Method
                  g4263722
NCBI GI
                  870
BLAST score
                  7.0e-94
E value
                  195
Match length
                  85
% identity
                  (AC006223) putative glucan synthase [Arabidopsis thaliana]
NCBI Description
                  263697
Seq. No.
                   6000 1.R1011
Contig ID
5'-most EST
                  LIB3076-024-Q1-K1-H11
Method
                  BLASTN
                   g2065239
NCBI GI
                   35
BLAST score
                   1.0e-09
E value
                   39
Match length
% identity
                   97
                  M.musculus mRNA for coxsackie and adenovirus receptor
NCBI Description
                  homologue
                   263698
Seq. No.
                   6000 2.R1011
Contig ID
                   wty700171838.hl
5'-most EST
                   BLASTX
Method
                   g4584527
NCBI GI
BLAST score
                   212
E value
                   7.0e-17
                   81
Match length
                   51
% identity
                  (AL049607) putative protein [Arabidopsis thaliana]
NCBI Description
                   263699
Seq. No.
                   6004 1.R1011
Contiq ID
                   tfd700572929.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1931647
                   884
BLAST score
E value
                   3.0e-95
                   248
Match length
% identity
                   (U95973) endomembrane protein EMP70 precusor isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   263700
Contig ID
                   6006 1.R1011
5'-most EST
                   LIB3076-025-Q1-K1-A5
Method
                   BLASTX
NCBI GI
                   g4586253
BLAST score
                   548
                   4.0e-56
E value
Match length
                   123
```

36583

(AL049640) auxilin-like protein [Arabidopsis thaliana]



```
263701
Seq. No.
                  6009 1.R1011
Contig ID
                  LIB3076-025-Q1-K1-B9
5'-most EST
                  BLASTX
Method
                  g4165861
NCBI GI
                  442
BLAST score
                  8.0e-44
E value
                  160
Match length
                  27
% identity
NCBI Description (AF006603) histone deacetylase mHDA2 [Mus musculus]
                  263702
Seq. No.
                   6010 1.R1011
Contig ID
                  pmx700086588.h1
5'-most EST
Method
                  BLASTX
                   g3128209
NCBI GI
                   1265
BLAST score
                   1.0e-139
E value
                   341
Match length
% identity
                   69
NCBI Description (AC004077) unknown protein [Arabidopsis thaliana]
                   263703
Seq. No.
                   6013 1.R1011
Contig ID
                   uC-zmflb73080c03b2
5'-most EST
                   263704
Seq. No.
                   6017 2.R1011
Contig ID
                   LIB3076-026-Q1-K1-A6
5'-most EST
                   BLASTN
Method
                   g2062705
NCBI GI
                   38
BLAST score
                   9.0e-12
E value
                   42
Match length
                   98
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                   263705
Seq. No.
                   6024 1.R1011
Contig ID
                   LIB3076-026-Q1-K1-E9
5'-most EST
                   BLASTX
Method
                   q3882211
NCBI GI
                   232
BLAST score
                   5.0e-19
E value
Match length
                   117
                   44
% identity
                  (AB018288) KIAA0745 protein [Homo sapiens]
NCBI Description
Seq. No.
                   263706
                   6028 1.R1011
Contig ID
                   fwa700097846.hl
 5'-most EST
                   BLASTX
Method
                   q3063698
NCBI GI
                   815
BLAST score
```

36584

6.0e-87

369

E value

Match length



% identity (AL022537) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 263707 6029 1.R1011 Contig ID uC-zmflb73080e06b25'-most EST BLASTX Method g4512705 NCBI GI 876 BLAST score 3.0e-94 E value 222 Match length 77 % identity (AC006569) putative serine/threonine protein kinase NCBI Description [Arabidopsis thaliana] 263708 Seq. No. 6029 2.R1011 Contig ID xjt700096986.h15'-most EST BLASTX Method g4322327 NCBI GI BLAST score 630 1.0e-65 E value 239 Match length 49 % identity (AF080545) peptide transporter [Nepenthes alata] NCBI Description 263709 Seq. No. 6029 3.R1011 Contig ID uC-zmflmo17077d09b1 5'-most EST BLASTX Method q1076331 NCBI GI 581 BLAST score 9.0e-60 E value 223 Match length 48 % identity histidine transport protein - Arabidopsis thaliana NCBI Description >gi 510238 emb CAA54634 (X77503) oligopeptide transporter 1-1 [Arabidopsis thaliana] >gi 744157 prf 2014244A His transporter [Arabidopsis thaliana] 263710 Seq. No. 6040 1.R1011 Contig ID LIB3076-027-Q1-K1-E11 5'-most EST BLASTX Method q1086833 NCBI GI BLAST score 414 5.0e-40 E value 214 Match length 40 % identity (U41264) coded for by C. elegans cDNA CEESN26F; coded for NCBI Description

by C. elegans cDNA CEESI89F; similar to 60S acidic

ribosomal protein Po (L10) [Caenorhabditis elegans]

263711 Seq. No. 6040 2.R1011 Contig ID

LIB3137-038-Q1-K1-E3 5'-most EST



263712 Seq. No. 6042 1.R1011 Contiq ID mwy700441170.hl 5'-most EST BLASTX Method NCBI GI g2497492 702 BLAST score 4.0e-74E value 205 Match length % identity 67 URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP NCBI Description KINASE) >gi 1653646 dbj BAA18558_ (D90915) uridine monophosphate kinase [Synechocystis sp.] Seq. No. 263713 6044 1.R1011 Contia ID 5'-most EST fC-zmle700427941r3 263714 Seq. No. 6049 1.R1011 Contig ID 5'-most EST LIB3076-027-Q1-K1-H9 Seq. No. 263715 6071 1.R1011 Contig ID ymt700220141.hl 5'-most EST 263716 Seq. No. 6073 1.R1011 Contig ID LIB3076-030-Q1-K1-E11 5'-most EST BLASTX Method g1588589 NCBI GI BLAST score 1614 0.0e + 00E value 352 Match length 89 % identity NCBI Description dihydrodipicolinate synthase [Zea mays] Seq. No. 263717 6079 1.R1011 Contig ID dyk700104366.h1 5'-most EST BLASTX Method NCBI GI g4454468 BLAST score 1397 1.0e-155 E value 393 Match length 68 % identity (AC006234) putative NADH dehydrogenase [Arabidopsis NCBI Description thaliana] 263718 Seq. No.

 Seq. No.
 263718

 Contig ID
 6079_2.R1011

 5'-most EST
 dyk700103167.h1

 Method
 BLASTX

 NCBI GI
 g4006893

 BLAST score
 1649

E value 0.0e+00 Match length 447 % identity 69



NCBI Description (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No. 263719

Contig ID 6082 1.R1011

5'-most EST LIB3076-030-Q1-K1-H3

Seq. No. 263720

Contig ID 6086_1.R1011

5'-most EST LIB3079-045-Q1-K1-A11

Seq. No. 263721

Contig ID 6086_2.R1011

5'-most EST uC-zmflm017207d01b1

Seq. No. 263722

Contig ID 6087_1.R1011

5'-most EST LIB3076-031-Q1-K1-A4

Seq. No. 263723

Contig ID 6092_1.R1011

5'-most EST LIB3137-017-Q1-K1-D8

Seq. No. 263724

Contig ID 6095 1.R1011

5'-most EST LIB3076-031-Q1-K1-E3

Seq. No. 263725

Contig ID 6097_1.R1011

5'-most EST LIB3069-039-Q1-K1-B8

Method BLASTX
NCBI GI g3892051
BLAST score 993
E value 1.0e-108
Match length 228

% identity 78

NCBI Description (AC002330) predicted NADH dehydrogenase 24 kD subunit

[Arabidopsis thaliana]

Seq. No. 263726

Contig ID 6097_2.R1011

5'-most EST LIB3059-003-Q1-K1-G7

Method BLASTX
NCBI GI g3892051
BLAST score 171
E value 6.0e-12
Match length 43
% identity 70

NCBI Description (AC002330) predicted NADH dehydrogenase 24 kD subunit

[Arabidopsis thaliana]

Seq. No. 263727

Contig ID 6099_1.R1011

5'-most EST uC-zmflb73014f09b1

Method BLASTX
NCBI GI g4567207
BLAST score 191
E value 3.0e-14



```
44
Match length
% identity
NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]
                  263728
Seq. No.
                  6099_2.R1011
Contig ID
                  uC-zmflb73173h09b1
5'-most EST
                  BLASTX
Method
                  g3080442
NCBI GI
                   448
BLAST score
                   4.0e-44
E value
                   143
Match length
                   57
% identity
                  (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
                   263729
Seq. No.
                   6099 3.R1011
Contig ID
                   LIB3068-023-Q1-K1-G7
5'-most EST
                   BLASTX
Method
                   g4567207
NCBI GI
                   344
BLAST score
                   2.0e-32
E value
                   110
Match length
                   55
% identity
NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]
                   263730
Seq. No.
                   6100 1.R1011
Contig ID
                   LIB3076-031-Q1-K1-F3
5'-most EST
                   263731
Seq. No.
                   6102 1.R1011
Contig ID
                   LIB3076-031-Q1-K1-G7
5'-most EST
                   BLASTX
Method
                   q600855
NCBI GI
                   406
BLAST score
                   2.0e-39
E value
                   172
Match length
                   45
% identity
                   (U17887) bZIP protein [Arabidopsis thaliana]
NCBI Description
                   263732
Seq. No.
                   6104 1.R1011
Contig ID
                   LIB3076-031-Q1-K1-H1
5'-most EST
Seq. No.
                   263733
                   6107 1.R1011
Contig ID
                   LIB3060-023-Q1-K1-D2
 5'-most EST
                   BLASTX
Method
NCBI GI
                   g2914703
BLAST score
                   813
                   8.0e-87
E value
                   295
Match length
                   51
 % identity
                   (AC003974) unknown protein [Arabidopsis thaliana]
NCBI Description
```

36588

263734

Seq. No.



Contig ID 6107_2.R1011

5'-most EST uC-zmflmo17073g11b1

Method BLASTX
NCBI GI g2914703
BLAST score 406
E value 5.0e-39

Match length 157 % identity 54

NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]

Seq. No. 263735

Contig ID 6107_3.R1011

5'-most EST LIB189-011-Q1-E1-C10

Seq. No. 263736

Contig ID 6107_4.R1011 5'-most EST xjt700095125.h1

Seq. No. 263737

Contig ID 6117_1.R1011 5'-most EST nbm700467990.h1

Method BLASTX
NCBI GI g4587514
BLAST score 1755
E value 0.0e+00
Match length 393
% identity 83

NCBI Description (AC007060) Similar to WO8E3.3 gi_3880615 putative

GTP-binding protein from C. elegans cosmid gb_Z92773. EST gb_AA597331 comes from this gene. [Arabidopsis thaliana]

Seq. No. 263738
Contig ID 6117_2.R1011
5'-most EST xtj700377291.h1

Seq. No. 263739 Contig ID 6117_3.R1011 5'-most EST rvt700549928.h1

Seq. No. 263740 Contig ID 6117_5.R1011 5'-most EST nbm700469754.h1

Seq. No. 263741 Contig ID 6121 1.R1011

5'-most EST LIB3076-033-Q1-K1-D11

Seq. No. 263742 Contig ID 6121_2.R1011

5'-most EST LIB3115-018-P1-K1-E1

 Seq. No.
 263743

 Contig ID
 6121_3.R1011

 5'-most EST
 yyf700350665.h1

Seq. No. 263744 Contig ID 6121_5.R1011

NCBI GI BLAST score

E value

1020 1.0e-111



```
5'-most EST
                  vux700157369.h1
                  263745
Seq. No.
                  6123 1.R1011
Contig ID
                  LIB3\overline{1}36-017-Q1-K1-G4
5'-most EST
                  BLASTX
Method
                  g2052383
NCBI GI
BLAST score
                  1052
                  1.0e-115
E value
Match length
                  281
                  70
% identity
NCBI Description (U66345) calreticulin [Arabidopsis thaliana]
                  263746
Seq. No.
                  6123 2.R1011
Contig ID
                  LIB3069-008-Q1-K1-E12
5'-most EST
                  BLASTX
Method
                  g2052383
NCBI GI
                  245
BLAST score
E value
                  2.0e-20
Match length
                  59
                  75
% identity
NCBI Description (U66345) calreticulin [Arabidopsis thaliana]
                  263747
Seq. No.
                  6123 3.R1011
Contig ID
5'-most EST
                  uC-zmroteosinte072a08b2
                  BLASTX
Method
                  g2052383
NCBI GI
BLAST score
                  958
E value
                  1.0e-104
                  219
Match length
                  78
% identity
NCBI Description (U66345) calreticulin [Arabidopsis thaliana]
Seq. No.
                  263748
                   6125 1.R1011
Contig ID
                  LIB3076-033-Q1-K1-D8
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2655098
BLAST score
                  1095
E value
                  1.0e-120
                   283
Match length
% identity
NCBI Description (AF023472) peptide transporter [Hordeum vulgare]
                   263749
Seq. No.
                   6130 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17112f07a1
Seq. No.
                   263750
Contig ID
                   6134 1.R1011
5'-most EST
                  LIB189-007-Q1-E1-E1
Method
                   BLASTX
                   g2911075
```



270

95

Match length

NCBI Description

% identity

```
Match length
                  321
% identity
                  (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                  263751
Seq. No.
Contig ID
                  6135 1.R1011
                  uC-zmflmo17113b10b1
5'-most EST
                  263752
Seq. No.
                  6138 1.R1011
Contig ID
                  LIB143-038-Q1-E1-F10
5'-most EST
                  BLASTX
Method
                  g3004950
NCBI GI
BLAST score
                  1137
                  1.0e-125
E value
                  250
Match length
                  88
% identity
NCBI Description (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]
                  263753
Seq. No.
Contig ID
                  6138 2.R1011
                  xmt7\overline{0}0262322.h1
5'-most EST
                  BLASTX
Method
                  q1709619
NCBI GI
BLAST score
                   2282
                  0.0e + 00
E value
                   485
Match length
                   76
% identity
                  PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /
NCBI Description
                   DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
                   (GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)
                   >gi 2146814 pir S69181 protein disulfide isomerase (EC
                   5.3.4.1) precursor - maize >gi 625148 (L39014) protein
                   disulfide isomerase [Zea mays]
                   263754
Seq. No.
                   6138 3.R1011
Contig ID
5'-most EST
                   xsy700209388.h1
                   BLASTX
Method
NCBI GI
                   q3004950
BLAST score
                   600
E value
                   9.0e-64
Match length
                   127
                   98
% identity
                  (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]
NCBI Description
                   263755
Seq. No.
Contig ID
                   6138 4.R1011
                   LIB3150-066-P2-K1-E4
5'-most EST
Method
                   BLASTN
NCBI GI
                   q625147
                   135
BLAST score
E value
                   9.0e-70
```

36591

Zea mays protein disulfide isomerase (pdi) mRNA, complete

```
263756
Seq. No.
                  6138 6.R1011
Contig ID
                  uC-zmflmo17398q12a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3004950
                  196
BLAST score
                  4.0e-15
E value
Match length
                  35
% identity
                  100
NCBI Description
                  (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]
                  263757
Seq. No.
                  6138 8.R1011
Contig ID
                  LIB3059-005-01-K1-G2
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1709619
                  624
BLAST score
                  1.0e-64
E value
                  173
Match length
% identity
                  48
NCBI Description
                  PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /
                  DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
                  (GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)
                  >gi_2146814_pir__S69181 protein disulfide isomerase (EC
                  5.3.4.1) precursor - maize >gi_625148 (L39014) protein
                  disulfide isomerase [Zea mays]
                  263758
Seq. No.
                  6138 12.R1011
Contig ID
5'-most EST
                  uC-zmflb73155e10b2
Method
                  BLASTN
                  q625147
NCBI GI
BLAST score
                  103
                  2.0e-50
E value
Match length
                  118
                  98
% identity
                  Zea mays protein disulfide isomerase (pdi) mRNA, complete
NCBI Description
                  cds
                  263759
Seq. No.
                  6138 14.R1011
Contig ID
                  LIB3180-017-P2-M1-G2
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1709619
BLAST score
                  225
                  2.0e-24
E value
                  97
Match length
                  67
% identity
                  PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) /
NCBI Description
                  DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
                   (GLYCOSYLATION SITE-BINDING CHAIN) (GSBP)
                  >gi_2146814_pir__S69181 protein disulfide isomerase (EC
                   5.3.4.1) precursor - maize >gi 625148 (L39014) protein
```

Seq. No. 263760

36592

disulfide isomerase [Zea mays]



Contig ID 6141_1.R1011

5'-most EST uC-zmflMo17063d11b1

Method BLASTX
NCBI GI g129731
BLAST score 308
E value 2.0e-27
Match length 329
% identity 30

NCBI Description PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (PROLYL

4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (THYROXINE DEIODINASE) (IODOTHYRONINE

> -

5'-MONODEIODINASE) (5'-MD)

Seq. No. 263761

Contig ID 6143 1.R1011

5'-most EST LIB3079-021-Q1-K1-F3

Method BLASTX
NCBI GI g2809246
BLAST score 734
E value 2.0e-77
Match length 296
% identity 49

NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana]

Seq. No. 263762

Contig ID 6143_2.R1011

5'-most EST LIB3076-034-Q1-K1-G8

Method BLASTN
NCBI GI g4140643
BLAST score 127
E value 7.0e-65
Match length 335
% identity 68

NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

Seq. No. 263763

Contig ID 6143_5.R1011 5'-most EST hvj700624405.h1

Method BLASTX
NCBI GI g3786015
BLAST score 148
E value 2.0e-09
Match length 41
% identity 66

NCBI Description (AC005499) hypothetical protein [Arabidopsis thaliana]

Seq. No. 263764 Contig ID 6143_7.R1011 5'-most EST fwa700099017.h1

Seq. No. 263765

Contig ID 6145_1.R1011

5'-most EST LIB3076-035-Q1-K1-C11

Method BLASTX NCBI GI g584893 BLAST score 1284



E value 1.0e-142 Match length 283 % identity 86

NCBI Description SERINE CARBOXYPEPTIDASE III PRECURSOR

>gi 283002_pir__S22530 carboxypeptidase III (EC 3.4.16.-) -

rice >gi 218153 dbj_BAA01757_ (D10985) serine

carboxypeptidase III [Oryza sativa]

Seq. No. 263766

Contig ID 6149_1.R1011 5'-most EST clt700044645.f1

Seq. No. 263767

Contig ID 6149_2.R1011

5'-most EST LIB189-001-Q1-E1-G6

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 263768

Contig ID 6149_3.R1011

5'-most EST LIB3067-007-Q1-K1-G6

Seq. No. 263769 Contig ID 6153_1.R1011

5'-most EST LIB3150-059-Q1-N1-D2

Method BLASTX
NCBI GI g100293
BLAST score 355
E value 4.0e-65
Match length 180
% identity 38

NCBI Description ribonucleoprotein A, 29K - wood tobacco

>gi 19754 emb CAA43427_ (X61113) 29kD A ribonucleoprotein

[Nicotiana sylvestris]

 Seq. No.
 263770

 Contig ID
 6153_2.R1011

 5'-most EST
 1hp700053401.r1

 Method
 BLASTX

Method BLASIX
NCBI GI g4056477
BLAST score 639
E value 2.0e-66
Match length 190
% identity 67

NCBI Description (AC005896) putative RNA binding protein [Arabidopsis

thaliana]

Seq. No. 263771 Contig ID 6153_3.R1011

5'-most EST LIB3136-056-Q1-K1-H7

Method BLASTX NCBI GI g1350821



343 BLAST score 4.0e-32 E value 89 Match length 38 % identity

CHLOROPLAST 31 KD RIBONUCLEOPROTEIN PRECURSOR NCBI Description

>gi 280403_pir__S26204 RNA-binding protein 31 curled-leaved tobacco >gi 19710 emb_CAA46233_ (X65117) RNA

binding protein 31 [Nicotiana plumbaginifolia]

263772 Seq. No.

6156 1.R1011 Contig ID

uC-zmflmo17235e12b1 5'-most EST

BLASTX Method g2506174 NCBI GI 446 BLAST score E value 1.0e-43 Match length 243 41 % identity

TAGATOSE-BISPHOSPHATE ALDOLASE GATY NCBI Description

>gi 1736822 dbj_BAA15966_ (D90848) Tagatose-bisphosphate aldolase Gaty (EC 4.1.2.-). [Escherichia coli] >gi_1788412 (AE000298) tagatose-bisphosphate aldolase 1 [Escherichia

coli]

263773 Seq. No.

6157 1.R1011 Contia ID

5'-most EST LIB3076-035-Q1-K1-H4

263774 Seq. No. 6160 1.R1011 Contig ID

 $uC\text{-}z\overline{m}flmo17153b11b1$ 5'-most EST

263775 Seq. No.

6164 1.R1011 Contig ID pmx700089468.h1 5'-most EST

BLASTX Method g3132825 NCBI GI 2084 BLAST score 0.0e+00E value 387 Match length 99 % identity

(AF063403) putative cytosine-5 DNA methyltransferase [Zea NCBI Description

mays]

263776 Seq. No. 6167 1.R1011 Contig ID

LIB3069-008-Q1-K1-C9 5'-most EST

BLASTX Method NCBI GI q4454042 725 BLAST score E value 1.0e-76 204 Match length % identity

(AL035394) putative protein [Arabidopsis thaliana] NCBI Description

263777 Seq. No. Contig ID 6167 2.R1011



xmt700264114.h1 5'-most EST BLASTX Method NCBI GI g2501555 526 BLAST score 1.0e-53 E value 150 Match length 68 % identity POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi 549984 (U13148) NCBI Description possible apospory-associated protein [Pennisetum ciliare] 263778 Seq. No. 6174 1.R1011 Contig ID $wen7\overline{0}0333728.h1$ 5'-most EST BLASTX Method g3219858 NCBI GI 504 BLAST score 8.0e-51 E value 115 Match length 82 % identity DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE NCBI Description >gi_2129724_pir__S71204 RNA polymerase II 13.6 kDa chain -Arabidopsis thaliana >gi 881501 (U28048) RNA polymerase II 13.6 kDa subunit [Arabidopsis thaliana] 263779 Seq. No. 6174 2.R1011 Contig ID uC-zmflMo17006g10b1 5'-most EST BLASTX Method g3914621 NCBI GI BLAST score 225 E value 1.0e-17 373 Match length 20 % identity RAN GTPASE ACTIVATING PROTEIN 1 >qi 2062660 (U88155) NCBI Description RanGTPase activating protein [Xenopus laevis] 263780 Seq. No. 6174 3.R1011 Contig ID xit700094182.h15'-most EST Method BLASTX q551428 NCBI GI BLAST score 1256 1.0e-138 E value Match length 376 65 % identity (X78996) tetrafunctional protein [Cucumis sativus] NCBI Description 263781 Seq. No. Contig ID 6174 4.R1011

5'-most EST LIB143-024-Q1-E1-D1

Seq. No. 263782 Contig ID 6175 1.R1011

uC-zmroteosinte092e05b2 5'-most EST

Method BLASTX NCBI GI q2984157 BLAST score 312



```
3.0e-28
E value
                  125
Match length
                  52
% identity
                  (AE000761) ribosomal protein L13 [Aquifex aeolicus]
NCBI Description
                  263783
Seq. No.
                  6175 3.R1011
Contig ID
                  kem700611748.h1
5'-most EST
Method
                  BLASTX
                  g2500257
NCBI GI
                  147
BLAST score
                  1.0e-09
E value
                  49
Match length
                  53
% identity
                  50S RIBOSOMAL PROTEIN L13 >gi 1652400 dbj BAA17322
NCBI Description
                   (D90905) 50S ribosomal protein L13 [Synechocystis sp.]
                  263784
Seq. No.
Contig ID
                   6175 4.R1011
5'-most EST
                   vux700160981.h1
                  BLASTX
Method
                   g2500257
NCBI GI
                   184
BLAST score
                   1.0e-13
E value
                   55
Match length
                   56
% identity
                   50S RIBOSOMAL PROTEIN L13 >gi 1652400 dbj BAA17322
NCBI Description
                   (D90905) 50S ribosomal protein L13 [Synechocystis sp.]
                   263785
Seq. No.
Contig ID
                   6178 1.R1011
                   uC-zmflmo17060d03b1
5'-most EST
Method
                   BLASTX
                   q2244785
NCBI GI
BLAST score
                   873
                   6.0e-94
E value
                   312
Match length
% identity
                   61
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   263786
Contig ID
                   6183 1.R1011
5'-most EST
                   LIB3180-053-P2-M1-C6
                   BLASTX
Method
NCBI GI
                   q4539292
BLAST score
                   304
                   4.0e-36
E value
Match length
                   95
                   81
% identity
NCBI Description
                   (AL049480) putative ribosomal protein S10 [Arabidopsis
                   thaliana]
Seq. No.
                   263787
```

Contig ID 6183_2.R1011 5'-most EST LIB3059-009-Q1-K1-A9 Method BLASTX NCBI GI 94539292



```
BLAST score
                  426
E value
                  7.0e-42
Match length
                  96
% identity
                  81
                  (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                  thaliana]
                  263788
Seq. No.
Contig ID
                  6183 3.R1011
5'-most EST
                  uC-zmflb73012e11b1
Method
                  BLASTX
                  g4539292
NCBI GI
BLAST score
                  335
E value
                  7.0e-31
                  76
Match length
                  80
% identity
```

NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

 Seq. No.
 263789

 Contig ID
 6183_4.R1011

 5'-most EST
 LIB3069-045-Q1-K1-B4

Seq. No. 263791
Contig ID 6187_1.R1011
5'-most EST uC-zmflb73275d10a1

 Seq. No.
 263792

 Contig ID
 6203_1.R1011

5'-most EST LIB3076-040-Q1-K1-A1

Method BLASTX
NCBI GI g4138265
BLAST score 265
E value 7.0e-23
Match length 98

% identity 59

NCBI Description (AJ006228) Avr9 elicitor response protein [Nicotiana

tabacum]

Seq. No. 263794 Contig ID 6218_1.R1011

5'-most EST uC-zmroteosinte070h03b1

Method BLASTX
NCBI GI g1174613
BLAST score 775
E value 1.0e-82
Match length 162
% identity 96

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING



PROTEIN HOMOLOG 1) (TBP-1) >gi_556560_dbj_BAA04614_ (D17788) rice homologue of Tat binding protein [Oryza sativa]

Seq. No. 263795

Contig ID 6219_1.R1011

5'-most EST LIB3067-045-Q1-K1-C3

Seq. No. 263796

Contig ID 6219_3.R1011 5'-most EST uwc700153437.h1

Seq. No. 263797

Contig ID 6219_4.R1011

5'-most EST LIB3076-041-Q1-K1-B8

Seq. No. 263798

Contig ID 6219_5.R1011 5'-most EST qmh700025724.f1

Seq. No. 263799

Contig ID 6222_1.R1011

5'-most EST LIB3279-060-P1-K1-B4

Method BLASTX
NCBI GI g3236249
BLAST score 617
E value 7.0e-64
Match length 294
% identity 48

NCBI Description (AC004684) hypothetical protein [Arabidopsis thaliana]

Seq. No. 263800

Contig ID 6222_2.R1011

5'-most EST uC-zmflmo17235e06b1

Seq. No. 263801

Contig ID 6225_1.R1011 5'-most EST pwr700449356.h1

Method BLASTX
NCBI GI g3298548
BLAST score 830
E value 8.0e-89
Match length 210
% identity 74

NCBI Description (AC004681) putative spliceosomal protein [Arabidopsis

thaliana]

Seq. No. 263802

Contig ID 6225 2.R1011

5'-most EST LIB189-017-Q1-E1-C11

Seq. No. 263803
Contig ID 6235_1.R1011
5'-most EST fwa700101110.h1

Seq. No. 263804 Contig ID 6238 1.R1011



```
uC-zmroteosintel18c01b1
5'-most EST
                  BLASTX
Method
                  g3063708
NCBI GI
                  242
BLAST score
                  4.0e-20
E value
                  172
Match length
                  37
% identity
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
                  263805
Seq. No.
                  6245 1.R1011
Contig ID
                  LIB36-012-Q1-E1-C10
5'-most EST
                  BLASTX
Method
                  g2760362
NCBI GI
                  190
BLAST score
                  8.0e-14
E value
                  126
Match length
                  35
% identity
NCBI Description (AF016511) 15.9 kDa subunit of RNA polymerase II
                  [Arabidopsis thaliana]
                  263806
Seq. No.
                  6250 1.R1011
Contig ID
                  LIB3076-044-Q1-K1-A6
5'-most EST
                  263807
Seq. No.
                   6252 1.R1011
Contig ID
                  LIB3076-044-Q1-K1-D8
5'-most EST
Seq. No.
                   263808
                   6252 2.R1011
Contig ID
                  pmx700084295.h1
5'-most EST
                   263809
Seq. No.
Contig ID
                   6260 1.R1011
                   fC-zmle700447381a1
5'-most EST
                   BLASTX
Method
                   q4455311
NCBI GI
BLAST score
                   288
E value
                   1.0e-25
Match length
                   167
% identity
                   38
                  (AL035528) putative disease resistance protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   263810
                   6265 1.R1011
Contig ID
                   LIB3076-046-Q1-K1-C10
 5'-most EST
                   263811
 Seq. No.
                   6265 2.R1011
 Contig ID
                   hbs701183353.h1
 5'-most EST
                   263812
 Seq. No.
                   6268 1.R1011
 Contig ID
```

xjt700096664.h1

5'-most EST



```
263813
Seq. No.
                  6271 1.R1011
Contig ID
                  hbs701181036.hl
5'-most EST
                  263814
Seq. No.
                  6272 1.R1011
Contig ID
                  fdz701165603.h1
5'-most EST
                  BLASTX
Method
                  g2244939
NCBI GI
                   402
BLAST score
                   1.0e-38
E value
                  196
Match length
                   43
% identity
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   263815
Seq. No.
                   6275 1.R1011
Contig ID
                   LIB3076-047-Q1-K1-A4
5'-most EST
                   BLASTX
Method
                   g1619300
NCBI GI
                   864
BLAST score
                   7.0e-93
E value
                   190
Match length
                   86
% identity
                  (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
                   263816
Seq. No.
                   6275 2.R1011
Contig ID
                   uC-zmflb73361d03a2
5'-most EST
                   BLASTX
Method
                   g1619300
NCBI GI
                   758
BLAST score
                   1.0e-80
E value
                   167
Match length
                   86
% identity
                  (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
                   263817
Seq. No.
                   6275 3.R1011
Contig ID
5'-most EST
                   LIB3060-043-Q1-K1-D5
                   BLASTX
Method
NCBI GI
                   q1619300
                   266
BLAST score
                   1.0e-29
E value
                   117
Match length
% identity
                  (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
                   263818
Seq. No.
                   6275 4.R1011
Contig ID
                   uC-zmflb73254f02a1
5'-most EST
                   BLASTX
Method
                   g1619300
NCBI GI
BLAST score
                   319
                   2.0e-29
E value
Match length
                   69
                   87
% identity
```

Method

BLASTX



```
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
                  263819
Seq. No.
                  6275 5.R1011
Contig ID
                  LIB3180-020-P2-M1-B8
5'-most EST
                  BLASTX
Method
                  q1619300
NCBI GI
                  168
BLAST score
E value
                  6.0e-12
                  38
Match length
% identity
                  82
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
                  263820
Seq. No.
                  6276 1.R1011
Contig ID
                  uwc700155332.h1
5'-most EST
                  BLASTX
Method
                  g2191194
NCBI GI
                  324
BLAST score
                  2.0e-29
E value
                  133
Match length
% identity
                   51
                   (AF007271) contains weak to the SAPB protein (TR:E236624)
NCBI Description
                   [Arabidopsis thaliana]
                   263821
Seq. No.
                   6279 1.R1011
Contig ID
                   LIB3076-047-Q1-K1-B5
5'-most EST
                   263822
Seq. No.
                   6289 1.R1011
Contig ID
                   LIB3076-048-Q1-E1-C12
5'-most EST
                   BLASTX
Method
                   g4204793
NCBI GI
                   309
BLAST score
                   3.0e-39
E value
                   198
Match length
                   43
% identity
NCBI Description (U52079) P-glycoprotein [Solanum tuberosum]
                263823
Seq. No.
                   6290 1.R1011
Contig ID
                   LIB3066-012-Q1-K1-F3
5'-most EST
                   BLASTX
Method
                   g3913811
NCBI GI
BLAST score
                   1074
                   1.0e-117
E value
                   264
Match length
                   82
 % identity
                   GLUTAMYL-TRNA REDUCTASE PRECURSOR (GLUTR)
NCBI Description
                   >gi_2920320_dbj_BAA25003_ (AB011416) glutamyl-tRNA
                   reductase [Oryza sativa]
                   263824
 Seq. No.
 Contig ID
                   6290 2.R1011
                   uC-zmflmo17154e08b1
 5'-most EST
```



```
NCBI GI
                  g3913811
BLAST score
                  583
                  5.0e-60
E value
                  143
Match length
                  82
% identity
                  GLUTAMYL-TRNA REDUCTASE PRECURSOR (GLUTR)
NCBI Description
                  >gi_2920320_dbj_BAA25003_ (AB011416) glutamyl-tRNA
                  reductase [Oryza sativa]
                  263825
Seq. No.
                  6291 1.R1011
Contig ID
                  LIB3136-017-Q1-K1-A6
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4584546
                   235
BLAST score
                   2.0e-19
E value
                   91
Match length
                   57
% identity
                  (AL049608) putative protein [Arabidopsis thaliana]
NCBI Description
                   263826
Seq. No.
                   6295 2.R1011
Contig ID
                   ymt700219411.h1
5'-most EST
                   263827
Seq. No.
                   6302 1.R1011
Contig ID
                   LIB3060-018-Q1-K1-C9
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3746791
BLAST score
                   341
                   2.0e-31
E value
                   205
Match length
                   36
% identity
                   (AF081788) putative spliceosome associated protein [Homo
NCBI Description
                   sapiens] >gi 3985930_dbj_BAA34863_ (AB020623) DAM1 [Homo
                   sapiens]
Seq. No.
                   263828
Contig ID
                   6306 1.R1011
                   uC-zmroteosinte003e10b1
5'-most EST
Method
                   BLASTX
                   q4454464
NCBI GI
                   282
BLAST score
                   9.0e-25
E value
                   79
Match length
                   71
% identity
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   263829
Seq. No.
                   6306 2.R1011
Contig ID
5'-most EST
                   nbm700470983.h1
                   BLASTX
Method
                   g4454464
NCBI GI
                   287
BLAST score
                   2.0e-25
E value
```

36603

62

81

Match length

% identity



```
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
                  263830
Seq. No.
                  6306 3.R1011
Contig ID
5'-most EST
                  LIB3076-049-Q1-K1-G11
Method
                  BLASTX
                  q4454464
NCBI GI
BLAST score
                  839
E value
                  5.0e-90
Match length
                  198
% identity
                  77
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                  263831
Seq. No.
                  6306 4.R1011
Contig ID
                  LIB3079-037-Q1-K1-F7
5'-most EST
Method
                  BLASTX
                  q4454464
NCBI GI
                  209
BLAST score
                  2.0e-16
E value
Match length
                  49
% identity
                  80
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                  263832
Seq. No.
                  6306 5.R1011
Contig ID
                  LIB189-023-Q1-E1-E1
5'-most EST
                  263833
Seq. No.
                  6308 1.R1011
Contig ID
                  LIB3076-052-Q1-E1-A10
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1363488
BLAST score
                  205
                  1.0e-33
E value
Match length
                  113
                  63
% identity
                  IAA8 protein - Arabidopsis thaliana >gi 972919 (U18410)
NCBI Description
                  IAA8 [Arabidopsis thaliana] >gi 4314364 gb AAD15575
                   (AC006340) auxin-induced IAA8 protein [Arabidopsis
                  thaliana]
                  263834
Seq. No.
                  6308 2.R1011
Contig ID
                  uC-zmflMo17010a04b1
5'-most EST
Method
                  BLASTX
                  g1363488
NCBI GI
BLAST score
                  357
                  2.0e-33
E value
                  139
Match length
% identity
                  51
                  IAA8 protein - Arabidopsis thaliana >gi 972919 (U18410)
NCBI Description
                  IAA8 [Arabidopsis thaliana] >gi 4314364 gb AAD15575
```

Seq. No. 263835

thaliana]

36604

(AC006340) auxin-induced IAA8 protein [Arabidopsis



```
6311 1.R1011
Contig ID
5'-most EST
                  wty700164815.hl
                  BLASTX
Method
NCBI GI
                  q123183
BLAST score
                  900
                  4.0e-97
E value
                  224
Match length
                  83
% identity
                  HOMEOTIC PROTEIN KNOTTED-1 >qi 100888 pir S14283 homeotic
NCBI Description
                  protein Kn-1 - maize >gi 22351 emb CAA43605 (X61308) Kn1
                  [Zea mays] >gi_227607_prf 1707304A Knotted-1 gene [Zea
                  mays]
                  263836
Seq. No.
                  6316 1.R1011
Contig ID
                  LIB3076-052-Q1-E1-D1
5'-most EST
Method
                  BLASTX
                  q129350
NCBI GI
BLAST score
                  192
                  2.0e-14
E value
                  60
Match length
                  57
% identity
                  PROBABLE PROTEASE INHIBITOR P322 PRECURSOR
NCBI Description
                  >gi 82278 pir S05594 pseudothionin St1 - potato (strain
                  cv. Bintje) >gi 21394 emb CAA31577_ (X13180) put.
                  preprotein (AA -27 to 47) [Solanum tuberosum]
                  263837
Seq. No.
Contig ID
                  6316 3.R1011
5'-most EST
                  uwc700152342.h1
                  BLASTX
Method
NCBI GI
                  q129350
BLAST score
                  186
E value
                   6.0e-14
Match length
                   57
                   58
% identity
                  PROBABLE PROTEASE INHIBITOR P322 PRECURSOR
NCBI Description
                  >gi_82278_pir__S05594 pseudothionin St1 - potato (strain
                   cv. Bintje) >gi 21394 emb CAA31577_ (X13180) put.
                  preprotein (AA -27 to 47) [Solanum tuberosum]
                   263838
Seq. No.
                   6317 1.R1011
Contig ID
5'-most EST
                  LIB3076-052-Q1-E1-D11
                  BLASTX
Method
NCBI GI
                   g2245134
BLAST score
                   211
                   8.0e-17
E value
Match length
                   62
                   63
% identity
                  (Z97344) heat shock transcription factor HSF1 [Arabidopsis
NCBI Description
```

thaliana]
Seq. No. 263839

Contig ID 6318_1.R1011 5'-most EST uC-zmflmo17d04b1



```
Seq. No. 263840
Contig ID 6321_1.R1011
5'-most EST LIB3076-052-Q1-E1-G2
Seq. No. 263841
Contig ID 6334_2.R1011
5'-most EST xjt700095434.h1
Seq. No. 263842
```

Contig ID 6336_1.R1011
5'-most EST pmx700088746.h1
Method BLASTX
NCBI GI g1817584
BLAST score 308
E value 2.0e-27

BLAST score 308
E value 2.0e-27
Match length 416
% identity 26

NCBI Description (Y08991) adaptor protein [Homo sapiens]

Seq. No. 263843

Contig ID 6337_1.R1011 5'-most EST uC-zmflb73159h09b2

Seq. No. 263844 Contig ID 6340_1.R1011

5'-most EST LIB3076-053-Q1-E1-E3

Method BLASTX
NCBI GI g3928758
BLAST score 212
E value 6.0e-17
Match length 54
% identity 72

NCBI Description (AB007987) Lipoic acid synthase [Arabidopsis thaliana]

>gi 4454462 gb AAD20909 (AC006234) putative lipoic acid

synthase [Arabidopsis thaliana]

Seq. No. 263845 Contig ID 6344_1.R1011

5'-most EST uC-zmflb73245a09b2

Method BLASTX
NCBI GI g3668089
BLAST score 1068
E value 1.0e-118
Match length 404
% identity 59

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

 Seq. No.
 263846

 Contig ID
 6344_2.R1011

 5'-most EST
 gwl700618160.h1

Seq. No. 263847

Contig ID 6347_1.R1011 5'-most EST nbm700468870.h1

Method BLASTX
NCBI GI g3142303
BLAST score 1958



0.0e+00E value 463 Match length % identity 56 (ACO02411) Strong similarity to MRP-like ABC transporter NCBI Description gb U92650 from A. thaliana and canalicular multi-drug resistance protein gb_L49379 from Rattus norvegicus. [Arabidopsis thaliana] 263848 Seq. No.

Contig ID uC-zmflmo17001h05b1 5'-most EST BLASTX Method g4510345 NCBI GI BLAST score 373 3.0e-35 E value 175 Match length 44 % identity

6348 1.R1011

(AC006921) unknown protein [Arabidopsis thaliana] NCBI Description

263849 Seq. No. 6348 2.R1011 Contig ID LIB189-019-Q1-E1-F1 5'-most EST BLASTX Method

q169363 NCBI GI BLAST score 244 2.0e-20 E value 62 Match length 65 % identity

(M75856) PVPR3 [Phaseolus vulgaris] NCBI Description

Seq. No. 263850 6351 1.R1011 Contig ID uC-zmflB73025b12b2 5'-most EST

Method BLASTX

NCBI GI q1483150 BLAST score 1628 0.0e + 00E value 443 Match length 70 % identity

NCBI Description (D84417) monodehydroascorbate reductase [Arabidopsis

thaliana]

Seq. No. 263851 Contig ID 6355 1.R1011

5'-most EST uC-zmflmo17240f03b1

Method BLASTX NCBI GI g132567 733 BLAST score 4.0e-77 E value Match length 551 % identity 35

NCBI Description RICIN PRECURSOR (RRNA N-GLYCOSIDASE) >gi 476541_pir RLCSD ricin D precursor - castor bean >gi 21083 emb CAA26939_

(X03179) ricin precursor [Ricinus communis]

>gi_21085_emb_CAA37095_ (X52908) pre-propolypeptide (AA -35

to 541) [Ricinus communis]



```
263852
Seq. No.
                  6355 3.R1011
Contig ID
5'-most EST
                  LIB3068-028-Q1-K1-A2
                  263853
Seq. No.
                  6355 7.R1011
Contig ID
                  LIB3136-059-Q1-K1-B4
5'-most EST
                  BLASTX
Method
NCBI GI
                  g21078
BLAST score
                  197
                   3.0e-15
E value
                  110
Match length
                   41
% identity
                  (X02388) preproricin [Ricinus communis]
NCBI Description
                   263854
Seq. No.
                   6385 1.R1011
Contig ID
5'-most EST
                  mwy700442802.h1
                  BLASTX
Method
                   g129915
NCBI GI
BLAST score
                   1837
                   0.0e + 00
E value
                   403
Match length
                   91
% identity
                   PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi 66912 pir _TVWTGC phosphoglycerate kinase (EC 2.7.2.3)
                   precursor, chloroplast - wheat >gi_21833_emb_CAA33303_
                   (X15233) phosphoglycerate kinase (\overline{AA}\ 1\ -\ 480) [Triticum
                   aestivum] >gi_3293043_emb_CAA51931_ (X73528)
                   phosphoglycerate kinase [Triticum aestivum]
                   263855
Seq. No.
Contig ID
                   6385 2.R1011
                   uC-zmflb73264f02b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g129915
                   245
BLAST score
                   2.0e-32
E value
                   85
Match length
% identity
                   PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi 66912 pir TVWTGC phosphoglycerate kinase (EC 2.7.2.3)
                   precursor, chloroplast - wheat >gi 21833 emb CAA33303
                   (X15233) phosphoglycerate kinase (AA 1 - 480) [Triticum
                   aestivum] >qi 3293043 emb CAA51931 (X73528)
                   phosphoglycerate kinase [Triticum aestivum]
                   263856
Seq. No.
                   6388 1.R1011
Contig ID
5'-most EST
                   LIB3180-049-P2-M1-B7
Method
                   BLASTX
NCBI GI
                   q168586
BLAST score
                   4459
```

E value 0.0e+00
Match length 880
% identity 98

NCBI Description (M58656) pyruvate, orthophosphate dikinase [Zea mays]

Match length

% identity

208 92



263857 Seq. No. 6388 2.R1011 Contig ID 5'-most EST LIB3150-051-Q1-N1-H12 BLASTX Method g168586 NCBI GI 3739 BLAST score 0.0e + 00E value Match length 767 94 % identity (M58656) pyruvate, orthophosphate dikinase [Zea mays] NCBI Description 263858 Seq. No. Contig ID 6388 4.R1011 5'-most EST LIB3060-051-Q1-K1-C1 BLASTX Method NCBI GI q67155 BLAST score 584 E value 2.0e-60 Match length 116 99 % identity pyruvate, orthophosphate dikinase (EC 2.7.9.1) precursor -NCBI Description maize 263859 Seq. No. 6388 5.R1011 Contig ID LIB3115-039-P1-K2-G9 5'-most EST Method BLASTX NCBI GI q4249413 BLAST score 240 6.0e-39 E value Match length 105 72 % identity NCBI Description (AC006072) unknown protein [Arabidopsis thaliana] Seq. No. 263860 Contig ID 6388 6.R1011 LIB3116-009-Q1-K1-C3 5'-most EST Method BLASTX NCBI GI g168586 BLAST score 397 2.0e-38 E value Match length 101 82 % identity (M58656) pyruvate, orthophosphate dikinase [Zea mays] NCBI Description 263861 Seq. No. 6388 7.R1011 Contig ID LIB3078-047-Q1-K1-D4 5'-most EST Method BLASTX g168586 NCBI GI BLAST score 929 1.0e-100 E value

36609

NCBI Description (M58656) pyruvate, orthophosphate dikinase [Zea mays]

Match length

NCBI Description

% identity

124 97



```
263862
Seq. No.
                   6388 9.R1011
Contig ID
5'-most EST
                  fwa700099229.hl
                  BLASTX
Method
                   g168586
NCBI GI
BLAST score
                   645
E value
                   1.0e-101
                   288
Match length
                   96
% identity
                  (M58656) pyruvate, orthophosphate dikinase [Zea mays]
NCBI Description
                   263863
Seq. No.
                   6388 10.R1011
Contig ID
5'-most EST
                   LIB36-021-Q1-E1-G7
                  BLASTX
Method
NCBI GI
                   g168586
                   455
BLAST score
E value
                   3.0e-45
Match length
                   164
% identity
                   45
NCBI Description
                  (M58656) pyruvate, orthophosphate dikinase [Zea mays]
Seq. No.
                   263864
                   6388 14.R1011
Contig ID
5'-most EST
                   LIB3150-044-Q1-N1-A10
                   BLASTX
Method
NCBI GI
                   q82717
BLAST score
                   372
E value
                   1.0e-38
Match length
                   83
                   90
% identity
                  pyruvate, orthophosphate dikinase (EC 2.7.9.1) 1, cytosolic
NCBI Description
                   - maize (fragment) >gi 257808 bbs 117085 (S46966)
                   orthophosphate dikinase, PPDK {N-terminal} [maize, Peptide
                   Partial, 89 aa] [Zea mays]
Seq. No.
                   263865
Contig ID
                   6388 27.R1011
5'-most EST
                   uer700578768.hl
Method
                   BLASTN
NCBI GI
                   q168584
BLAST score
                   140
E value
                   9.0e-73
Match length
                   396
% identity
                   94
                  Corn pyruvate, orthophosphate dikinase gene, exons 2-19
NCBI Description
                   263866
Seq. No.
                   6388 30.R1011
Contig ID
5'-most EST
                   nwy7\overline{0}0448312.h1
Method
                   BLASTN
NCBI GI
                   g168579
BLAST score
                   111
                   9.0e-56
E value
```

36610

Maize pyruvate, orthophosphate dikinase mRNA, complete cds



```
263867
Seq. No.
                   6392 1.R1011
Contig ID
                   LIB3\overline{1}37-050-Q1-K1-G10
5'-most EST
                   BLASTX
Method
                   g126888
NCBI GI
BLAST score
                   2046
                   0.0e+00
E value
                   432
Match length
                   92
% identity
                   MALATE DEHYDROGENASE (NADP), CHLOROPLAST PRECURSOR
NCBI Description
                    (NADP-MDH) >gi_319840_pir__DEMZMC malate dehydrogenase
                    (NADP+) (EC 1.1.1.82) precursor, chloroplast - maize
                   >gi 22368 emb CAA34213 (X16084) precursor protein (AA -57 to 375) [Zea mays] >gi 226766 prf 1604473A NADP malate
                   dehydrogenase [Zea mays]
                   263868
Seq. No.
                   6399 1.R1011
Contig ID
5'-most EST
                   LIB189-017-Q1-E1-C8
Method
                   BLASTX
                   g2191138
NCBI GI
                   417
BLAST score
                   1.0e-40
E value
                   108
Match length
                   71
% identity
                   (AF007269) A IG002N01.18 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   263869
Seq. No.
Contig ID
                    6399 2.R1011
5'-most EST
                   LIB36-014-Q1-E1-B11
                   BLASTX
Method
                   g2191138
NCBI GI
BLAST score
                    418
                   1.0e-40
E value
                   109
Match length
% identity
                   (AF007269) A IG002N01.18 gene product [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                    263870
Contig ID
                    6399 4.R1011
5'-most EST
                   LIB83-009-Q1-E1-C4
Seq. No.
                    263871
Contig ID
                    6413 1.R1011
                   LIB3078-018-Q1-K1-G9
5'-most EST
```

Seq. No. 263872 Contig ID 6415 1.R1011

5'-most EST uC-zmflb73019c03b1

Seq. No. 263873 Contig ID 6415_2.R1011

5'-most EST uC-zmflMo17012g07b1



```
263874
Seq. No.
                  6416 1.R1011
Contig ID
                  LIB3078-018-Q1-K1-H6
5'-most EST
                  263875
Seq. No.
                  6417 1.R1011
Contig ID
                  xsy700217025.h1
5'-most EST
                  BLASTX
Method
                  g131773
NCBI GI
                  614
BLAST score
                  8.0e-64
E value
                  140
Match length
                   91
% identity
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
NCBI Description
                   >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) -
                  maize
                   263876
Seq. No.
                   6417 2.R1011
Contig ID
                   uC-zmroteosinte025b11b1
5'-most EST
                   BLASTN
Method
                   q3821780
NCBI GI
                   36
BLAST score
                   1.0e-10
E value
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   263877
Seq. No.
                   6418 1.R1011
Contig ID
                   uC-zmroteosinte018c11b1
5'-most EST
                   263878
Seq. No.
                   6418 2.R1011
Contig ID
5'-most EST
                   uC-zmflmo17073c06b1
                   BLASTX
Method
                   q2499570
NCBI GI
                   880
BLAST score
                   9.0e-95
E value
Match length
                   226
                   72
% identity
                   PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE
NCBI Description
                   (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN
                   L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN
                   CARBOXYL METHYLTRANSFERASE) >gi 414332 (L07941)
                   L-isoaspartyl methyltransferase [Triticum aestivum]
                   263879
Seq. No.
                   6418 3.R1011
Contig ID
                   uC-z\overline{m}f1b73344h02a2
 5'-most EST
                   BLASTX
Method
                   g2499569
NCBI GI
                   303
BLAST score
                   3.0e-27
E value
                   70
Match length
```

NCBI Description PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE

79

% identity



(PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) >gi 2129700 pir S66344 protein-L-isoaspartate(D-aspartate) O-methyltransferase (EC 2.1.1.77) - Arabidopsis thaliana >gi 1322021 (U31288) L-isoaspartyl methyltransferase [Arabidopsis thaliana]

Seq. No. 6420 1.R1011 Contiq ID LIB3078-018-Q1-K1-F10 5'-most EST Method BLASTX q1175453 NCBI GI 158 BLAST score 1.0e-10 E value 68 Match length % identity 41

263880

HYPOTHETICAL 11.4 KD PROTEIN C13G6.04 IN CHROMOSOME I NCBI Description >gi 2130268_pir__S62433 hypothetical protein SPAC13G6.04 -

fission yeast (Schizosaccharomyces pombe)

>gi 1008989_emb CAA91097 (Z54308) hypothetical protein

[Schizosaccharomyces pombe]

263881 Seq. No. 6421 1.R1011 Contig ID tzu700206492.h1 5'-most EST BLASTX Method g3236259 NCBI GI

977 BLAST score 1.0e-106 E value 283 Match length 65 % identity

(AC004684) putative alcohol dehydrogenase [Arabidopsis NCBI Description

thaliana]

263882 Seq. No. 6422 1.R1011 Contig ID

LIB3078-018-Q1-K1-F12 5'-most EST

BLASTX Method q4557018 NCBI GI BLAST score 667 3.0e-70E value 123 Match length 100 % identity

chitinase 3-like 1 >gi 544413 sp P36222 C3L1 HUMAN NCBI Description

CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL

PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1)

>gi 1082278_pir__A49562 cartilage glycoprotein gp39 precursor - human >gi_348912 (M80927) glycoprotein [Homo sapiens] >gi_2121310_emb_CAA69661_ (Y08374) GP-39 cartilage

protein [Homo sapiens]

263883 Seq. No. 6423 1.R1011 Contig ID xyt700347054.h1 5'-most EST Method BLASTX NCBI GI q3914386

164 BLAST score



```
1.0e-17
E value
                  124
Match length
                   41
% identity
NCBI Description ALLERGEN MF1 >gi_3445490_dbj_BAA32435_ (AB011804) MF1
                   [Malassezia furfur]
                  263884
Seq. No.
                   6425 1.R1011
Contig ID
                  LIB3060-043-Q1-K1-E5
5'-most EST
                  BLASTX
Method
                   g2494264
NCBI GI
                   827
BLAST score
                   1.0e-88
E value
                   309
Match length
                   54
% identity
                  HYPOTHETICAL 66.0 KD GTP-BINDING PROTEIN SLR1105
NCBI Description
                   >gi 1651837_dbj BAA16764_ (D90900) elongation factor EF-G
                   [Synechocystis sp.]
                   263885
Seq. No.
                   6426 1.R1011
Contig ID
                   wty7\overline{0}0172702.h1
5'-most EST
                   BLASTX
Method
                   g1710551
NCBI GI
                   281
BLAST score
                   8.0e-25
E value
                   51
Match length
                   100
% identity
                   60S RIBOSOMAL PROTEIN L39 >gi 1177369 emb CAA64728
NCBI Description
                   (X95458) ribosomal protein L39 [Zea mays]
                   263886
Seq. No.
                   6426 2.R1011
Contig ID
                   LIB3070-016-Q1-N1-D5
 5'-most EST
                   BLASTX
Method
                   q1710551
NCBI GI
                   281
BLAST score
                   6.0e-25
E value
                   51
Match length
                   100
 % identity
                   60S RIBOSOMAL PROTEIN L39 >gi 1177369 emb_CAA64728_
 NCBI Description
                   (X95458) ribosomal protein L39 [Zea mays]
                   263887
 Seq. No.
                   6426 3.R1011
 Contig ID
                   fdz701161110.h1
 5'-most EST
                   BLASTX
 Method
                   g1710551
 NCBI GI
 BLAST score
                   281
                   7.0e-25
 E value
 Match length
                   51
                   100
 % identity
 NCBI Description 60S RIBOSOMAL PROTEIN L39 >gi_1177369_emb_CAA64728_
                    (X95458) ribosomal protein L39 [Zea mays]
```

263888

6426 6.R1011

Seq. No.

Contig ID



```
xdb700338211.h1
5'-most EST
                  BLASTX
Method
                  g1710551
NCBI GI
                  227
BLAST score
                  7.0e-19
E value
                  41
Match length
                  100
% identity
                  60S RIBOSOMAL PROTEIN L39 >gi_1177369_emb_CAA64728_
NCBI Description
                   (X95458) ribosomal protein L39 [Zea mays]
                  263889
Seq. No.
                  6427 1.R1011
Contig ID
                  LIB3078-018-Q1-K1-G10
5'-most EST
                  BLASTX
Method
                  g1711550
NCBI GI
                   551
BLAST score
                  1.0e-56
E value
                  108
Match length
                   99
% identity
                  TRANSLOCON-ASSOCIATED PROTEIN, DELTA SUBUNIT PRECURSOR
NCBI Description
                   (TRAP-DELTA) (SIGNAL SEQUENCE RECEPTOR DELTA SUBUNIT)
                   (SSR-DELTA) >gi_2136318_pir__S59865 TRAP-like protein
                   precursor (clone H0286) - human >gi 1071681 emb_CAA62211
                   (X90583) unnamed protein product [Homo sapiens] >gi 1302656
                   (U52111) translocon-associated protein delta [Homo sapiens]
                   >gi 1673433 emb CAA92215 (Z68129) translocon-associated
                   protein delta subunit precursor [Homo sapiens]
                   >gi 2398657 emb CAA93157 (Z69043) translocon-associated
                   protein delta subunit precursor [Homo sapiens]
                   263890
Seq. No.
                   6430 1.R1011
Contig ID
                   qw1700614754.h1
5'-most EST
                   BLASTX
Method
                   q4226128
NCBI GI
                   149
BLAST score
                   4.0e-09
E value
                   143
Match length
                   34
% identity
                   (AF125459) No definition line found [Caenorhabditis
NCBI Description
                   elegans]
                   263891
Seq. No.
                   6431 1.R1011
Contig ID
                   uC-zmroteosinte074a03b1
5'-most EST
Method
                   BLASTX
                   q3757521
NCBI GI
BLAST score
                   911
                   2.0e-98
E value
Match length
                   327
 % identity
                   56
                  (AC005167) unknown protein [Arabidopsis thaliana]
NCBI Description
                   263892
Seq. No.
```

36615

6432 1.R1011

BLASTX

 $qmh7\overline{0}0028452.f1$

Contig ID

Method

5'-most EST



```
g4263787
NCBI GI
BLAST score
                   207
                  6.0e-16
E value
                  131
Match length
                  40
% identity
                  (AC006068) unknown protein [Arabidopsis thaliana]
NCBI Description
                  263893
Seq. No.
                  6432 6.R1011
Contig ID
5'-most EST
                  LIB3069-038-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  q4115925
BLAST score
                  546
                  7.0e-56
E value
Match length
                  125
                   49
% identity
                  (AF118222) contains similarity to RNA recognition motifs
NCBI Description
                   (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
                  >gi 4539439 emb CAB40027.1 (AL049523) RNA-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                  263894
                   6432 7.R1011
Contig ID
                  dyk7\overline{0}0102049.h1
5'-most EST
Method
                  BLASTX
                  g2129727
NCBI GI
                  180
BLAST score
                  1.0e-20
E value
Match length
                   61
% identity
                  84
                  RNA-binding protein 37 - Arabidopsis thaliana >qi 1174153
NCBI Description
                   (U44134) RNA-binding protein [Arabidopsis thaliana]
Seq. No.
                   263895
                   6436 1.R1011
Contig ID
                  LIB3060-047-Q1-K1-G7
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2828292
                   876
BLAST score
                   3.0e-94
E value
Match length
                   271
                   61
% identity
                  (AL021687) neoxanthin cleavage enzyme-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   263896
Seq. No.
Contig ID
                   6436 2.R1011
                   ceu700423227.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2924325
BLAST score
                  167
                  1.0e-11
E value
                   44
Match length
% identity
```

Seq. No. 263897

NCBI Description (Z93765) hypothetical protein [Malus domestica]



Contig ID 6440 1.R1011 5'-most EST LIB3078-018-Q1-K1-C12 BLASTX Method NCBI GI g131397 BLAST score 193 2.0e-14 E value 115 Match length 36 % identity OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD NCBI Description SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II) >gi 81480_pir__S00008 photosystem II oxygen-evolving complex protein 3 precursor - spinach >gi_755802_emb_CAA29056_ (X05512) 16 kDa protein of the photosynthetic oxygen- evolving protein (OEC) [Spinacia oleracea] >gi 225597 prf__1307179B luminal protein 16kD [Spinacia oleracea] 263898 Seq. No. Contig ID 6441 1.R1011 LIB3150-007-Q1-N1-D9 5'-most EST Method BLASTX q3786017 NCBI GI BLAST score 500 E value 5.0e-50 Match length 232 % identity NCBI Description (AC005499) putative non-green plastid inner envelope membrane protein [Arabidopsis thaliana] 263899 Seq. No. 6441 2.R1011 Contig ID 5'-most EST $cjh7\overline{0}0197272.h1$ 263900 Seq. No. Contig ID 6443_1.R1011 5'-most EST uC-zmflb73116d07b2 Method BLASTX g4093157 NCBI GI BLAST score 518 3.0e-52E value Match length 221 % identity NCBI Description (AF087936) phytochrome-associated protein 2 [Arabidopsis thaliana] Seq. No. 263901 6443 2.R1011 Contig ID 5'-most EST ymt700219872.hl

263902 Seq. No. 6443 3.R1011 Contig ID 5'-most EST $xsy7\overline{0}0213212.h1$

Seq. No. 263903 Contig ID 6443 4.R1011 5'-most EST LIB3136-023-Q1-K1-F9 Method BLASTX



```
NCBI GI
                  q4093157
BLAST score
                  161
E value
                   6.0e-11
Match length
                  120
                   46
% identity
NCBI Description
                  (AF087936) phytochrome-associated protein 2 [Arabidopsis
                  thaliana]
Seq. No.
                  263904
                  6444 1.R1011
Contig ID
5'-most EST
                  xjt700096347.h1
Method
                  BLASTX
                  g3925233
NCBI GI
BLAST score
                  949
                  1.0e-106
E value
                  239
Match length
                  81
% identity
NCBI Description (AF037034) putative peroxidase P7X [Zea mays]
Seq. No.
                  263905
                  6448 1.R1011
Contig ID
                  yyf700348365.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2246378
BLAST score
                   625
E value
                   6.0e-65
Match length
                  135
% identity
                  87
NCBI Description (286094) plastid protein [Arabidopsis thaliana]
                  263906
Seq. No.
                  6448 2.R1011
Contig ID
5'-most EST
                  LIB3181-008-P1-M1-B3
Method
                  BLASTX
NCBI GI
                  q2459425
BLAST score
                   651
E value
                   6.0e - 68
Match length
                  129
                   94
% identity
NCBI Description (AC002332) plastid protein [Arabidopsis thaliana]
                  263907
Seq. No.
                   6448 3.R1011
Contig ID
5'-most EST
                  LIB3137-023-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                  q2246378
BLAST score
                  469
E value
                  7.0e-47
Match length
                  121
% identity
                  80
NCBI Description (Z86094) plastid protein [Arabidopsis thaliana]
                  263908
Seq. No.
                  6448_4.R1011
Contig ID
```

No. 263909

LIB3059-002-Q1-K2-H12

5'-most EST

Seq. No.

BLAST score

E value

768 4.0e-81



```
6450 1.R1011
Contig ID
                  LIB3078-019-Q1-K1-D1
5'-most EST
Seq. No.
                  263910
                  6450 2.R1011
Contig ID
                  LIB3078-032-Q1-K1-C3
5'-most EST
                  BLASTN
Method
                  g3821780
NCBI GI
                  35
BLAST score
                  5.0e-10
E value
                  35
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  263911
Seq. No.
                   6451 1.R1011
Contig ID
                  LIB36-003-Q1-E1-H11
5'-most EST
                  BLASTX
Method
                   q3914465
NCBI GI
BLAST score
                   403
                   6.0e-39
E value
Match length
                   118
                   70
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                   >gi_2981207 (AF052076) photosystem I complex PsaH subunit
                   precursor [Zea mays]
                   263912
Seq. No.
                   6453 1.R1011
Contig ID
                   ntr700074711.h1
5'-most EST
Method
                   BLASTX
                   g4510346
NCBI GI
                   764
BLAST score
                   5.0e-93
E value
                   256
Match length
                   67
 % identity
NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]
                   263913
Seq. No.
                   6453 2.R1011
 Contig ID
                   LIB3069-055-Q1-K1-C12
 5'-most EST
                   BLASTX
Method
                   g4510346
NCBI GI
                   628
 BLAST score
                   3.0e-65
 E value
 Match length
                   195
 % identity
NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                   263914
                   6454 1.R1011
 Contig ID
                   uC-zmflb73064f11b1
 5'-most EST
                   BLASTX
 Method
 NCBI GI
                   q557472
```



```
600
Match length
% identity
                  34
NCBI Description (U15178) arabinosidase [Bacteroides ovatus]
                  263915
Seq. No.
                  6454 2.R1011
Contig ID
                  uC-zmflB73042d03b1
5'-most EST
                  263916
Seq. No.
                  6454 3.R1011
Contig ID
                  LIB3078-003-Q1-K1-G3
5'-most EST
                  263917
Seq. No.
                  6457 1.R1011
Contig ID
                  LIB3061-049-Q1-K1-G1
5'-most EST
                  263918
Seq. No.
                  6459 1.R1011
Contig ID
                  LIB36-021-Q1-E1-F5
5'-most EST
Seq. No.
                  263919
                   6462 1.R1011
Contig ID
                  LIB3078-017-Q1-K1-H5
5'-most EST
                  BLASTX
Method
                   q2190543
NCBI GI
                   254
BLAST score
E value
                   1.0e-21
Match length
                   72
                   74
% identity
                  (AC001229) EST gb_N37484 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
                   263920
Seq. No.
                   6462 2.R1011
 Contig ID
                   LIB3088-023-Q1-K1-F8
 5'-most EST
                   BLASTX
Method
                   q2190543
 NCBI GI
                   416
 BLAST score
                   3.0e-40
 E value
                   249
 Match length
                   43
 % identity
 NCBI Description (AC001229) EST gb_N37484 comes from this gene. [Arabidopsis
                   thaliana]
                   263921
 Seq. No.
                   6462 3.R1011
 Contig ID
                   ntr700075094.h1
 5'-most EST
                   263922
 Seq. No.
                   6463 1.R1011
 Contig ID
 5'-most EST
                   LIB3078-017-Q1-K1-H7
```

 Seq. No.
 263923

 Contig ID
 6464_1.R1011

 5'-most EST
 uC-zmflmo17128b01b1

 Method
 BLASTX

 NCBI GI
 g2583128



BLAST score 1386 E value 1.0e-154 Match length 419 % identity 64

NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No. 263924

Contig ID 6464_2.R1011 5'-most EST pwr700448922.h1

Seq. No. 263925

Contig ID 6465_1.R1011

5'-most EST uC-zmflmo17294g05b1

Method BLASTX
NCBI GI g400879
BLAST score 475
E value 2.0e-47
Match length 145
% identity 65

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR

(PSI-N) >gi_479690_pir__S35159 photosystem I chain psaN - barley >gi 19095 emb CAA47056 (X66428) photosystem I

subunit N [Hordeum vulgare]

Seq. No. 263926

Contig ID 6465 2.R1011

5'-most EST LIB36-017-Q1-E1-D1

Method BLASTX
NCBI GI g400879
BLAST score 419
E value 5.0e-41
Match length 146
% identity 59

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR

(PSI-N) >gi 479690 pir S35159 photosystem I chain psaN -

barley >gi_19095_emb_CAA47056_ (X66428) photosystem I

subunit N [Hordeum vulgare]

Seq. No. 263927

Contig ID 6465_3.R1011

5'-most EST LIB83-014-Q1-E1-C2

Method BLASTX
NCBI GI g3914466
BLAST score 379
E value 2.0e-36
Match length 86
% identity 81

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR

(PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN

subunit precursor [Zea mays]

Seq. No. 263928

Contig ID 6465 4.R1011

5'-most EST LIB84-030-Q1-E1-D3

Method BLASTN
NCBI GI g2981213
BLAST score 196



```
1.0e-106
E value
                  240
Match length
                  100
% identity
                  Zea mays photosystem I complex PsaN subunit precursor
NCBI Description
                   (psaN) mRNA, nuclear gene encoding chloroplast protein,
                  partial cds
                  263929
Seq. No.
                  6468 1.R1011
Contig ID
                  wyr700237165.h1
5'-most EST
Method
                  BLASTX
                  g4506235
NCBI GI
                   204
BLAST score
                   2.0e-15
E value
                   158
Match length
                   34
% identity
                  proteasome (prosome, macropain) 26S subunit, non-ATPase, 9
NCBI Description
                   >gi_3914475_sp_000233_PSD9_HUMAN 26S PROTEASOME REGULATORY
                   SUBUNIT P27 > gi 2055256 dbj BAA19790 (AB003177) proteasome
                   subunit p27 [Homo sapiens]
Seq. No.
                   263930
                   6468 2.R1011
Contig ID
                   ceu700425692.hl
5'-most EST
                   263931
Seq. No.
                   6469 1.R1011
Contig ID
                   uC-zmflmo17027d08a1
5'-most EST
                   BLASTX
Method
                   g4079798
NCBI GI
                   843
BLAST score
                   3.0e-90
E value
                   258
Match length
                   66
 % identity
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
                   263932
 Seq. No.
                   6469 2.R1011
 Contig ID
                   LIB3060-008-Q1-K1-E12
 5'-most EST
                   BLASTX
 Method
                   q4079798
 NCBI GI
                   293
 BLAST score
                   3.0e-26
 E value
                   132
 Match length
 % identity
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
 NCBI Description
                   sativa]
                    263933
 Seq. No.
 Contig ID
                    6469 3.R1011
                    LIB36-005-Q1-E1-A8
 5'-most EST
```

5'-most EST LIB36-005-Q1-E1 Method BLASTX NCBI GI g1398999 BLAST score 174 E value 3.0e-12 Match length 38

% identity 89 (D49713) 23 kDa polypeptide of photosystem II [Oryza NCBI Description satival Seq. No. 263934 6469 5.R1011 Contig ID 5'-most EST LIB3078-017-Q1-K1-F10 Method BLASTN NCBI GI q4079797 BLAST score 57 2.0e-23 E value Match length 89 91 % identity Oryza sativa 23 kDa polypeptide of photosystem II mRNA, NCBI Description complete cds Seq. No. 263935 6469 6.R1011 Contig ID LIB3078-022-Q1-K1-F12 5'-most EST Method BLASTX NCBI GI q4079798 BLAST score 219 E value 8.0e-18 Match length 57 % identity 77 NCBI Description (AF052203) 23 kDa polypeptide of photosystem II [Oryza 263936 Seq. No. 6470 1.R1011 Contig ID 5'-most EST xsy700214853.hl Method BLASTX NCBI GI g517500 BLAST score 965 E value 1.0e-105 Match length 216 % identity 93 NCBI Description (M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >qi 444338 prf 1906386A photosystem II

OE17 protein [Pisum sativum]

263937 Seq. No. 6470 2.R1011 Contig ID

5'-most EST LIB3115-025-P1-K1-D11

Method BLASTX a517500 NCBI GI BLAST score 575 E value 3.0e-59 Match length 133 % identity 87

(M87435) precursor of the oxygen evolving complex 17 kDa NCBI Description

protein [Zea mays] >gi 444338 prf 1906386A photosystem II

OE17 protein [Pisum sativum]

263938 Seq. No. Contig ID 6470 3.R1011

5'-most EST LIB3078-008-Q1-K1-G8



Method BLASTX NCBI GI q517500 BLAST score 280 E value 6.0e-25 Match length 111 % identity 59

(M87435) precursor of the oxygen evolving complex 17 kDa NCBI Description

protein [Zea mays] >gi 444338 prf 1906386A photosystem II

OE17 protein [Pisum sativum]

263939 Seq. No.

6473 1.R1011 Contig ID 5'-most EST fwa700100671.hl

263940 Seq. No.

6473 3.R1011 Contig ID

5'-most EST LIB3137-023-Q1-K1-G12

Method BLASTX NCBI GI a99583 BLAST score 150 2.0e-09 E value Match length 150 33 % identity

NCBI Description seed-specific protein - prince's feather

> >gi 423770 pir A47185 storage protein isoform AmA1, 35K prince's feather >gi 15999 emb CAA77664 (Z11577) seed

specific protein of balanced nutritional quality

[Amaranthus hypochondriacus]

263941 Seq. No.

6473 5.R1011 Contig ID

5'-most EST LIB3137-040-Q1-K1-F3

263942 Seq. No.

Contig ID 6473 6.R1011

5'-most EST uC-zmrob73019d09b1

Seq. No. 263943

Contig ID 6475 1.R1011

5'-most EST LIB3078-017-Q1-K1-G4

263944 Seq. No.

Contig ID 6476 1.R1011

5'-most EST LIB3158-006-Q1-K1-F1

263945 Seq. No.

Contig ID 6476 2.R1011

5'-most EST LIB3115-032-P1-K1-A11

Method BLASTN g3821780 NCBI GI BLAST score 36 E value 2.0e-10 Match length 48 % identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 263946



```
6476 3.R1011
Contia ID
                  pmx700091835.h1
5'-most EST
```

263947 Seq. No. 6476 4.R1011 Contig ID $wty7\overline{0}0167637.h1$ 5'-most EST

263948 Seq. No.

6476 6.R1011 Contig ID

uC-zmflmo17268a07b1 5'-most EST

263949 Seq. No. 6476 7.R1011 Contig ID

LIB3062-010-Q1-K1-E2 5'-most EST

263950 Seq. No.

6476 8.R1011 Contig ID wty700170316.hl 5'-most EST

263951 Seq. No.

6477 1.R1011 Contig ID cyk700048553.f15'-most EST

263952 Seq. No.

6484 1.R1011 Contig ID

LIB3078-014-Q1-K1-G2 5'-most EST

BLASTX Method g3183079 NCBI GI 523 BLAST score 2.0e-80 E value 184 Match length % identity 81

MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR NCBI Description

>gi_1375075_dbj_BAA12870_ (D85763) glyoxysomal malate

dehydrogenase [Oryza sativa]

263953 Seq. No.

6486 1.R1011 Contig ID

 $uC-z\overline{m}flb73143b02b1$ 5'-most EST

BLASTX Method g551047 NCBI GI 690 BLAST score 2.0e-72 E value 170 Match length 75 % identity

NCBI Description (X79277) type II LHCI [Lolium temulentum]

263954 Seq. No.

6486 2.R1011 Contig ID

LIB3078-003-Q1-K1-D3 5'-most EST

BLASTX Method q551047 NCBI GI 908 BLAST score E value 5.0e-98 Match length 187 % identity

NCBI Description (X79277) type II LHCI [Lolium temulentum]

```
263955
Seq. No.
                  6486 3.R1011
Contig ID
                  LIB36-017-Q1-E1-E11
5'-most EST
                  BLASTX
Method
                  g551047
NCBI GI
                  704
BLAST score
                  2.0e-74
E value
                  170
Match length
                  76
% identity
NCBI Description (X79277) type II LHCI [Lolium temulentum]
                  263956
Seq. No.
                   6486 4.R1011
Contig ID
                  LIB3068-010-Q1-K1-C1
5'-most EST
                  BLASTX
Method
                  g2306981
NCBI GI
                   435
BLAST score
                   5.0e-43
E value
                   101
Match length
                   78
% identity
NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]
                   263957
Seq. No.
                   6486 11.R1011
Contig ID
                   ceu700423024.hl
5'-most EST
                   263958
Seq. No.
                   6488 1.R1011
Contig ID
                   uwh700207132.h1
5'-most EST
                   BLASTX
Method
                   g1825727
NCBI GI
                   458
BLAST score
                   4.0e-45
E value
                   156
Match length
                   56
 % identity
                   (U88308) C32E8.5 gene product [Caenorhabditis elegans]
NCBI Description
                   263959
 Seq. No.
                   6489 2.R1011
 Contig ID
                   LIB3060-002-Q1-K2-D7
 5'-most EST
                   263960
 Seq. No.
                   6491 1.R1011
 Contig ID
                   LIB3115-021-P1-K1-D3
 5'-most EST
                   263961
 Seq. No.
                   6492 1.R1011
 Contig ID
                   LIB3062-001-Q1-K2-B10
 5'-most EST
                   263962
 Seq. No.
                   6492 2.R1011
 Contig ID
                   uC-zmflmo17277g06b1
 5'-most EST
                   263963
 Seq. No.
                   6494 1.R1011
 Contig ID
                   LIB3067-035-Q1-K1-A1
 5'-most EST
```



```
BLASTX
Method
                  g3080420
NCBI GI
                  949
BLAST score
                  1.0e-104
E value
                  344
Match length
                  59
% identity
NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis
                  thaliana]
                  263964
Seq. No.
                  6494 2.R1011
Contig ID
                  ymt700223693.h1
5'-most EST
                  BLASTX
Method
                  g3080420
NCBI GI
                  280
BLAST score
                  5.0e-25
E value
                  114
Match length
                  55
% identity
NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis
                  thaliana]
                  263965
Seq. No.
                  6495 1.R1011
Contig ID
                  LIB3137-057-Q1-K1-A11
5'-most EST
                  BLASTX
Method
                  g1174850
NCBI GI
                  756
BLAST score
                  3.0e-80
E value
                  149
Match length
                  92
% identity
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN
                  LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)
                  263966
Seq. No.
Contig ID
                  6495 2.R1011
                  LIB3137-040-Q1-K1-C1
5'-most EST
                  BLASTX
Method
                   g1174850
NCBI GI
                  548
BLAST score
E value
                   5.0e-56
Match length
                   110
 % identity
                   89
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN
                   LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)
                   263967
 Seq. No.
                   6495 3.R1011
 Contig ID
                   LIB3059-012-Q1-K1-H5
 5'-most EST
                   BLASTX
Method
 NCBI GI
                   q1174850
                   496
 BLAST score
                   7.0e-50
 E value
 Match length
                   122
                   80
 % identity
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN
```

LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)



```
263968
Seq. No.
                  6496 1.R1011
Contig ID
                  uC-zmflb73068b09b1
5'-most EST
                  263969
Seq. No.
                   6497 1.R1011
Contig ID
                  dyk700106556.hl
5'-most EST
                  BLASTX
Method
                   q3184288
NCBI GI
BLAST score
                   217
E value
                   2.0e-17
                   62
Match length
                   61
% identity
                  (AC004136) unknown protein [Arabidopsis thaliana]
NCBI Description
                   263970
Seq. No.
                   6497 2.R1011
Contig ID
                   uwc700151322.h1
5'-most EST
                   263971
Seq. No.
                   6504 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73126c03b1
                   263972
Seq. No.
                   6508 1.R1011
Contig ID
                   wyr700236560.hl
5'-most EST
                   BLASTX
Method
                   g1419370
NCBI GI
                   695
BLAST score
                   5.0e-73
E value
                   136
Match length
% identity
                   100
                   (X97726) actin depolymerizing factor [Zea mays]
NCBI Description
                   263973
Seq. No.
                   6508 2.R1011
Contig ID
                   nwy7\overline{0}0446019.h1
5'-most EST
                   BLASTX
Method
                   q1419370
NCBI GI
                   703
BLAST score
                   4.0e-74
E value
                   139
Match length
                   99
% identity
NCBI Description (X97726) actin depolymerizing factor [Zea mays]
                   263974
Seq. No.
                   6508 6.R1011
Contig ID
                   uC-zmroteosinte059e11b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1419370
BLAST score
                   606
                   8.0e-63
E value
                   138
Match length
 % identity
                   (X97726) actin depolymerizing factor [Zea mays]
NCBI Description
```

36628

263975

Seq. No.

NCBI Description



```
6508 7.R1011
Contig ID
                   tfd700575242.h1
5'-most EST
                   BLASTX
Method
                   q1419370
NCBI GI
                   278
BLAST score
                   9.0e-25
E value
                   57
Match length
                   95
% identity
NCBI Description (X97726) actin depolymerizing factor [Zea mays]
                   263976
Seq. No.
                   6508 8.R1011
Contig ID
                   xsy700212045.h1
5'-most EST
                   BLASTX
Method
                   g1419370
NCBI GI
                   267
BLAST score
                   2.0e-23
E value
                   73
Match length
                   75
% identity
                  (X97726) actin depolymerizing factor [Zea mays]
NCBI Description
                   263977
Seq. No.
                   6510 1.R1011
Contig ID
                   uC-zmflb73038d10b1
5'-most EST
                   BLASTX
Method
                   g4587549
NCBI GI
                   242
BLAST score
                   3.0e-20
E value
                   68
Match length
                   63
% identity
                    (AC006577) Similar to gb U55861 RNA binding protein
NCBI Description
                   nucleolysin (TIAR) from \overline{\text{M}}\text{us} musculus and contains several
                   PF_00076 RNA recognition motif domains. ESTs gb_T21032 and
                    gb_T44127 come from this gene. [Arabidopsis t
                    263978
Seq. No.
                    6510 2.R1011
Contig ID
                    xsy700208567.hl
5'-most EST
                    BLASTN
Method
NCBI GI
                    g3821780
                    36
BLAST score
                    1.0e-10
E value
                    36
Match length
                    100
% identity
                   Xenopus laevis cDNA clone 27A6-1
NCBI Description
                    263979
Seq. No.
                    6510 3.R1011
 Contiq ID
                    xsy700217170.hl
 5'-most EST
                    BLASTX
Method
                    q4587549
NCBI GI
 BLAST score
                    149
                    2.0e-09
 E value
                    36
 Match length
                    72
 % identity
                    (AC006577) Similar to gb_U55861 RNA binding protein
```

36629

nucleolysin (TIAR) from $\overline{\text{M}}\text{us}$ musculus and contains several



PF_00076 RNA recognition motif domains. ESTs gb_T21032 and gb_T44127 come from this gene. [Arabidopsis t

 Seq. No.
 263980

 Contig ID
 6511_1.R1011

 5'-most EST
 dhd700197918.h1

 Method
 BLASTX

Method BLASTX
NCBI GI g2655293
BLAST score 905
E value 1.0e-97
Match length 201
% identity 87

NCBI Description (AF032975) germin-like protein 5 [Oryza sativa]

Seq. No. 263981

Contig ID 6513_1.R1011 5'-most EST fwa700097586.h1

Method BLASTX
NCBI GI g133028
BLAST score 596
E value 2.0e-61
Match length 191
% identity 62

NCBI Description 50S RIBOSOMAL PROTEIN L9, CHLOROPLAST PRECURSOR (CL9)

>gi_71257_pir__R5MUL9 ribosomal protein L9 precursor,
chloroplast - Arabidopsis thaliana >gi_16499_emb_CAA77480_

(Z11129) plastid ribosomal protein CL9 [Arabidopsis thaliana] >gi_16501_emb_CAA77594 (Z11509) Chloroplast

ribosomal protein CL9 [Arabidopsis thaliana]

Seq. No. 263982 Contig ID 6513 2.R1011

5'-most EST uC-zmflmo17179e11b1

Method BLASTX
NCBI GI g602758
BLAST score 651
E value 1.0e-67
Match length 198
% identity 67

NCBI Description (L38581) clp-like energy-dependent protease [Lycopersicon

esculentum]

Seq. No. 263983

Contig ID 6514 1.R1011

5'-most EST LIB83-002-Q1-E1-C3

Seq. No. 263984

Contig ID 6514 2.R1011

5'-most EST LIB3137-020-Q1-K1-D4

Method BLASTX
NCBI GI g3885886
BLAST score 994
E value 1.0e-108
Match length 213
% identity 88

NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]



263985 Seq. No. Contig ID 6514 3.R1011 LIB189-008-Q1-E1-H2 5'-most EST Method BLASTX NCBI GI q3885886 BLAST score 199 2.0e-15 E value Match length 39 90 % identity NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa] 263986 Seq. No. Contig ID 6514 4.R1011 5'-most EST LIB3062-047-Q1-K1-C1 263987 Seq. No. Contig ID 6514 5.R1011 5'-most EST LIB3060-002-Q1-K2-F4 Method BLASTX q3885886 NCBI GI 975 BLAST score 1.0e-106 E value 214 Match length 84 % identity NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa] 263988 Seq. No. 6514 7.R1011 Contig ID 5'-most EST LIB36-022-Q1-E1-F1 Method BLASTX NCBI GI q3885886 BLAST score 371 1.0e-35 E value Match length 96 % identity 82 NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa] 263989 Seq. No. Contig ID 6516 1.R1011 5'-most EST clt700043477.f1 BLASTX Method g3510256 NCBI GI 349 BLAST score 1.0e-32 E value 112 Match length % identity NCBI Description (AC005310) unknown protein [Arabidopsis thaliana] 263990 Seq. No.

 Seq. No.
 263990

 Contig ID
 6517_1.R1011

 5'-most EST
 uwc700151090.h1

 Method
 BLASTX

 NCBI GI
 g4314401

 BLAST score
 800

 E value
 2.0e-85

Match length 231 % identity 61

E value

2.0e-13



```
(AC006232) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                  thaliana]
                  263991
Seq. No.
Contig ID
                  6519 1.R1011
                  LIB3078-017-Q1-K1-A2
5'-most EST
Method
                  BLASTX
                  q2244756
NCBI GI
BLAST score
                  598
                  1.0e-61
E value
                  244
Match length
                  51
% identity
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  263992
                  6521_1.R1011
Contig ID
5'-most EST
                  wyr700238294.h1
                  BLASTX
Method
NCBI GI
                  g1890573
BLAST score
                  953
E value
                  1.0e-103
                  259
Match length
% identity
                  66
NCBI Description (X93173) xyloglucan endotransglycosylase (XET) [Hordeum
                  vulgare]
Seq. No.
                  263993
Contig ID
                   6521 2.R1011
5'-most EST
                  wyr700235304.h1
Method
                  BLASTX
                  q1890573
NCBI GI
                  876
BLAST score
                   3.0e-94
E value
                  236
Match length
                   65
% identity
NCBI Description (X93173) xyloglucan endotransglycosylase (XET) [Hordeum
                  vulgare]
Seq. No.
                   263994
                   6521 3.R1011
Contig ID
5'-most EST
                  LIB3068-018-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                   g1890573
BLAST score
                  198
E value
                   6.0e-24
Match length
                  118
% identity
                   49
NCBI Description (X93173) xyloglucan endotransglycosylase (XET) [Hordeum
                  vulgare]
                   263995
Seq. No.
Contig ID
                   6521 4.R1011
5'-most EST
                  wyr700236432.h1
Method
                  BLASTX
NCBI GI
                  q1890573
BLAST score
                  183
```

Match length



```
67
Match length
% identity
                  58
                  (X93173) xyloglucan endotransglycosylase (XET) [Hordeum
NCBI Description
                  vulgare]
                  263996
Seq. No.
                  6521 5.R1011
Contig ID
5'-most EST
                  LIB3068-018-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  g1890573
                  389
BLAST score
E value
                  2.0e-37
                  123
Match length
                  56
% identity
NCBI Description (X93173) xyloglucan endotransglycosylase (XET) [Hordeum
                  vulgare]
                  263997
Seq. No.
Contig ID
                  6521 6.R1011
5'-most EST
                  wyr700243321.h1
Method
                  BLASTX
NCBI GI
                  g1890573
BLAST score
                  481
E value
                  2.0e-48
Match length
                  133
% identity
                  63
NCBI Description (X93173) xyloglucan endotransglycosylase (XET) [Hordeum
                  vulgare]
                  263998
Seq. No.
Contig ID
                  6521 7.R1011
5'-most EST
                  LIB3137-002-Q1-K1-G3
                  263999
Seq. No.
Contig ID
                  6524 1.R1011
5'-most EST
                  ceu700431742.h1
                  264000
Seq. No.
                  .6525 1.R1011
Contig ID
5'-most EST
                  pmx700086072.h1
Method
                  BLASTX
NCBI GI
                  g3377820
BLAST score
                  456
E value
                  5.0e-45
Match length
                  123
                  73
% identity
NCBI Description (AF076275) contains similarity to coatomer zeta chains
                  [Arabidopsis thaliana]
                  264001
Seq. No.
Contig ID
                  6525 4.R1011
5'-most EST
                  nwy700445441.h1
Method
                  BLASTX
NCBI GI
                  q3377820
BLAST score
                  200
E value
                  1.0e-15
```

Contig ID

5'-most EST



```
80
% identity
                   (AF076275) contains similarity to coatomer zeta chains
NCBI Description
                   [Arabidopsis thaliana]
                   264002
Seq. No.
                   6527_1.R1011
Contig ID
                   uC-z\overline{m}flmo17220e08b1
5'-most EST
                   BLASTX
Method
                   q2129636
NCBI GI
                   755
BLAST score
E value
                   6.0e-80
Match length
                   339
                   44
% identity
                   lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase
NCBI Description
                   [Arabidopsis thaliana]
                   264003
Seq. No.
                   6529 1.R1011
Contig ID
                   LIB3115-028-P1-K1-B2
5'-most EST
                   BLASTX
Method
                   q3885896
NCBI GI
BLAST score
                   462
                   9.0e-46
E value
                   99
Match length
                   87
% identity
NCBI Description (AF093636) plastocyanin precursor [Oryza sativa]
                   264004
Seq. No.
                   6529 2.R1011
Contig ID
                   LIB36-020-Q1-E1-B9
5'-most EST
                   BLASTX
Method
                   g3885896
NCBI GI
                   465
BLAST score
                   2.0e-46
E value
                   99
Match length
                   88
% identity
NCBI Description (AF093636) plastocyanin precursor [Oryza sativa]
                   264005
Seq. No.
                   6530 1.R1011
Contig ID
                   LIB3150-041-Q1-N1-A8
5'-most EST
                   BLASTX
Method
                   g3329429
NCBI GI
                   179
BLAST score
                   9.0e-13
E value
                   82
Match length
                    40
 % identity
                   (AF049613) huntingtin interacting protein HYPK [Homo
NCBI Description
                    sapiens]
Seq. No.
                    264006
                    6530 3.R1011
 Contig ID
                    LIB3137-032-Q1-K1-E11
 5'-most EST
 Seq. No.
                    264007
```

36634

6531_2.R1011 pmx700084835.h1



Method BLASTX
NCBI GI g2129755
BLAST score 513
E value 5.0e-52
Match length 131
% identity 71

NCBI Description tryptophan synthase (EC 4.2.1.20) alpha chain - Arabidopsis

thaliana >gi_619753 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] >gi_1585768_prf__2201482A Trp

synthase:SUBUNIT=alpha [Arabidopsis thaliana]

Seq. No. 264008 Contig ID 6531 3.R1011

5'-most EST fwa700101002.h1

Method BLASTX
NCBI GI g2129755
BLAST score 874
E value 5.0e-94
Match length 273
% identity 63

NCBI Description tryptophan synthase (EC 4.2.1.20) alpha chain - Arabidopsis

thaliana >gi_619753 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] >gi_1585768_prf__2201482A Trp

synthase: SUBUNIT=alpha [Arabidopsis thaliana]

Seq. No. 264009 Contig ID 6532 1.R1011

5'-most EST LIB3078-016-Q1-K1-H1

Seq. No. 264010 Contig ID 6535_1.R1011

5'-most EST uC-zmflb73119e02b1

Seq. No. 264011 Contig ID 6537 1.R1011

5'-most EST LIB3078-016-Q1-K1-H3

Method BLASTX
NCBI GI g4510417
BLAST score 263
E value 8.0e-23
Match length 87
% identity 62

NCBI Description (AC006929) putative BEL1 homeotic protein [Arabidopsis

thaliana]

Seq. No. 264012

Contig ID 6538_1.R1011

5'-most EST LIB189-024-Q1-E1-D10

Seq. No. 264013

Contig ID 6540 1.R1011

5'-most EST uC-zmroteosinte023c06b2

Seq. No. 264014

Contig ID 6540_2.R1011

5'-most EST uC-zmrob73071a06b1

Contig ID

5'-most EST



264015 Seq. No. Contig ID 6546 1.R1011 5'-most EST wyr700241534.hl Method BLASTX NCBI GI g3522929 BLAST score 522 3.0e-82 E value Match length 224 % identity 72 NCBI Description (AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi 3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] 264016 Seg. No. 6546 2.R1011 Contig ID dyk700102452.h1 5'-most EST BLASTX Method NCBI GI g2129578 BLAST score 392 E value 1.0e-37 Match length 93 % identity dTDP-qlucose 4-6-dehydratases homolog - Arabidopsis NCBI Description thaliana >gi 928932 emb CAA89205 (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi 1585435 prf 2124427B diamide resistance gene [Arabidopsis thaliana] 264017 Seq. No. 6546 3.R1011 Contig ID LIB84-026-Q1-E1-G10 5'-most EST Method BLASTX NCBI GI q2129578 BLAST score 996 1.0e-108 E value Match length 212 % identity NCBI Description dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi 928932 emb CAA89205 (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435_prf__2124427B diamide resistance gene [Arabidopsis thaliana] Seq. No. 264018 Contig ID 6547 1.R1011 $fwa7\overline{0}0099378.h1$ 5'-most EST Method BLASTX NCBI GI q4586056 BLAST score 417 E value 2.0e-40 260 Match length % identity 36 NCBI Description (AC007020) unknown protein [Arabidopsis thaliana] 264019 Seq. No.

36636

6548 1.R1011

LIB3115-002-Q1-K1-A10



```
BLASTX
Method
NCBI GI
                  q1835731
BLAST score
                 4.44
E value
                  8.0e-44
                  11.3
Match length
                  73
% identity
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  264020
Seq. No.
                  6548 2.R1011
Contig ID
5'-most EST
                  LIB83-006-Q1-E1-B6
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  465
                  3.0e-46
E value
                  116
Match length
% identity
                  76
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  264021
Seq. No.
Contig ID
                  6548 3.R1011
5'-most EST
                  LIB3116-008-Q1-K1-E12
Method
                  BLASTX
NCBI GI
                  g131400
                  179
BLAST score
                  5.0e-13
E value
Match length
                  60
                  58
% identity
NCBI Description PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                  >gi 81471 pir_ S00409 photosystem II 10K protein precursor
                  - spinach >gi 170127 (J03887) 10kd polypeptide precursor
                  [Spinacia oleracea]
                  264022
Seq. No.
Contig ID
                  6549 1.R1011
5'-most EST
                  LIB3078-016-Q1-K1-G2
                  264023
Seq. No.
Contig ID
                  6549 2.R1011
5'-most EST
                  LIB3078-057-Q1-K1-D3
                  264024
Seq. No.
                  6549 3.R1011
Contig ID
5'-most EST
                  LIB83-005-Q1-E1-F6
                  264025
Seq. No.
                  6550 1.R1011
Contig ID
5'-most EST
                  uC-zmroB73028h01b1
Method
                  BLASTX
                  q3402692
NCBI GI
BLAST score
                  666
E value
                  1.0e-69
Match length
                  187
                  70
% identity
                  (AC004697) putative
NCBI Description
                  CDP-diacylglycerol--glycerol-3-phosphate
                  3-phosphatidyltransferase [Arabidopsis thaliana]
```



Seq. No. 264026 Contig ID 6551_1.R1011 5'-most EST LIB3067-030-Q1-K1-D5

Method BLASTX
NCBI GI g2494697
BLAST score 284
E value 8.0e-25
Match length 202
% identity 37

NCBI Description PROBABLE GTP CYCLOHYDROLASE I (GTP-CH-I)

>gi 3876608 emb CAA96650 (Z72509) similar to GTP

cyclohydrolase I [Caenorhabditis elegans]

Seq. No. 264027

Contig ID 6551_2.R1011

5'-most EST LIB3079-005-Q1-K1-H11

Method BLASTX
NCBI GI g1669664
BLAST score 226
E value 1.0e-18
Match length 118
% identity 42

NCBI Description (Z49706) GTP cyclohydrolase I [Dictyostelium discoideum]

Seq. No. 264028 Contig ID 6551_3.R1011

5'-most EST uC-zmflb73131a12a1

Seq. No. 264029

Contig ID 6552 1.R1011 5'-most EST fwa700098282.h1

Method BLASTX
NCBI GI g3789954
BLAST score 1199
E value 1.0e-132
Match length 238
% identity 94

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]

Seq. No. 264030 Contig ID 6552_3.R1011

5'-most EST LIB3137-038-Q1-K1-C2

Method BLASTX
NCBI GI g3789954
BLAST score 827
E value 9.0e-89
Match length 196
% identity 83

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]

Seq. No. 264031
Contig ID 6553_1.R1011

5'-most EST uC-zmflmo17275a09a1

Method BLASTX



```
g3024762
NCBI GI
BLAST score
                  453
                  1.0e-44
E value
                  212
Match length
                  45
% identity
NCBI Description TRNA PSEUDOURIDINE SYNTHASE B (TRNA PSEUDOURIDINE 55
                  SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE)
                  (URACIL HYDROLYASE) >gi_2624315_emb_CAA15588_ (AL008967)
                  truB [Mycobacterium tuberculosis]
Seq. No.
                  264032
Contig ID
                  6556 1.R1011
5'-most EST
                  uC-zmrob73078f11b1
Method
                  BLASTX
NCBI GI
                  q4538967
BLAST score
                  522
                  8.0e-53
E value
Match length
                  209
% identity
                  51
NCBI Description (AL049488) major intrinsic protein (MIP)-like [Arabidopsis
                  thaliana]
                  264033
Seq. No.
                  6556 2.R1011
Contig ID
5'-most EST
                  uC-zmroteosinte043e02b2
Method
                  BLASTX
                  g1346736
NCBI GI
BLAST score
                  177
E value
                  1.0e-12
Match length
                  51
% identity
                  55
NCBI Description POLLEN-SPECIFIC MEMBRANE INTEGRAL PROTEIN >qi 665948
                  (U20490) putative membrane integral protein [Nicotiana
                  alata]
                  264034
Seq. No.
Contig ID
                  6556_3.R1011
5'-most EST
                  LIB3068-021-Q1-K1-F10
Method
                  BLASTX
NCBI GI
                  q1076748
BLAST score
                  144
E value
                   6.0e-09
Match length
                  60
% identity
NCBI Description major intrinsic protein - rice >gi 440869 dbj BAA04257_
                  (D17443) major intrinsic protein [Oryza sativa]
                  264035
Seq. No.
                  6556 4.R1011
Contig ID
                  wyr700238176.h1
5'-most EST
                  264036
Seq. No.
```

Seq. No. 264036 Contig ID 6556_5.R1011 5'-most EST xsy700209783.h1

Seq. No. 264037 Contig ID 6558_1.R1011



```
ntr700076440.hl
   5'-most EST
                     BLASTX
- Method
                     g1421730
  NCBI GI
  BLAST score
                     2667
                     0.0e+00
  E value
  Match length
                     513
   % identity
                     100
  NCBI Description (U43082) RF2 [Zea mays]
  Seq. No.
                     264038
  Contig ID
                     6558 2.R1011
   5'-most EST
                     LIB3067-033-Q1-K1-G3
                     BLASTX
  Method
  NCBI GI
                     q1421730
  BLAST score
                     822
  E value
                     2.0e-95
  Match length
                     192
   % identity
                     96
  NCBI Description (U43082) RF2 [Zea mays]
   Seq. No.
                     264039
                     6560 1.R1011
  Contig ID
                     pmx700083627.h1
   5'-most EST
                     BLASTX
  Method
  NCBI GI
                     q3169883
                     781
  BLAST score
  E value
                     5.0e-83
                     279
  Match length
                     56
   % identity
                     (AF033194) dehydroquinate dehydratase/shikimate:NADP
  NCBI Description
                     oxidoreductase [Lycopersicon esculentum] >gi 3169888
                      (AF034411) dehydroquinate dehydratase/shikimate:NADP
                     oxidoreductase [Lycopersicon esculentum]
                     264040
   Seq. No.
                     6564 1.R1011
   Contig ID
   5'-most EST
                     LIB3156-014-Q1-K1-D5
  Method
                     BLASTX
                     g2062168
  NCBI GI
  BLAST score
                     191
  E value
                      3.0e-14
  Match length
                     58
   % identity
                     60
   NCBI Description (AC001645) hypothetical protein [Arabidopsis thaliana]
                      264041
   Seq. No.
   Contig ID
                      6564 2.R1011
   5'-most EST
                     uer700576802.h1
   Method
                     BLASTX
   NCBI GI
                     g2062168
   BLAST score
                     154
                     4.0e-10
   E value
                     48
  Match length
   % identity
   NCBI Description (AC001645) hypothetical protein [Arabidopsis thaliana]
```

36640

264042

Seq. No.



```
6565 1.R1011
Contig ID
5'-most EST
                  ntr700074672.h1
Method
                  BLASTX
NCBI GI
                  g2496164
BLAST score
                  165
                  7.0e-11
E value
                  89
Match length
                  38
% identity
NCBI Description HYPOTHETICAL PROTEIN MJ1232 >gi_2128738_pir__G64453
                  hypothetical protein MJ1232 - Methanococcus jannaschii
                  >gi 1591864 (U67564) conserved hypothetical protein
                  [Methanococcus jannaschii]
                  264043
Seq. No.
                  6569 1.R1011
Contig ID
5'-most EST
                  wyr700235839.h1
                  264044
Seq. No.
                  6572 1.R1011
Contig ID
                  LIB3078-055-Q1-K1-D8
5'-most EST
Seq. No.
                  264045
                  6573 1.R1011
Contig ID
                  LIB3137-020-Q1-K1-C7
5'-most EST
Method
                  BLASTX
                  q550436
NCBI GI
BLAST score
                  1371
                  0.0e+00
E value
Match length
                  595
% identity
                  91
NCBI Description (X81827) cytochrome P450 [Zea mays]
                  264046
Seq. No.
                  6574_1.R1011
Contig ID
5'-most EST
                  LIB3151-019-Q1-K1-H12
Seq. No.
                  264047
                  6575 1.R1011
Contig ID
5'-most EST
                  LIB3066-008-01-K1-D3
Method
                  BLASTX
NCBI GI
                  g1174867
BLAST score
                  298
E value
                  1.0e-26
Match length
                  72
% identity
NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING
                  PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2
                  KD PROTEIN) >gi 633687 emb CAA55862 (X79275)
                  ubiquinol--cytochrome c reductase [Solanum tuberosum]
                  >gi 1094912 prf 2107179A cytochrome c
```

Seq. No. 264048 6575 2.R1011 Contig ID 5'-most EST LIB3066-051-Q1-K1-B5

BLASTX Method NCBI GI g1174867

oxidase:SUBUNIT=8.2kD [Solanum tuberosum]



BLAST score 9.0e-27 E value Match length 72 % identity

NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING

PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2

KD PROTEIN) >gi_633687_emb_CAA55862_ (X79275)

ubiquinol--cytochrome c reductase [Solanum tuberosum]

>gi_1094912_prf__2107179A cytochrome c oxidase:SUBUNIT=8.2kD [Solanum tuberosum]

264049 Seq. No.

6575 3.R1011 Contig ID 5'-most EST fdz701165881.h1

Method BLASTX NCBI GI q3176686 BLAST score 168 E value 4.0e-13 Match length 80 % identity 53

(AC003671) Similar to high affinity potassium transporter, NCBI Description

HAK1 protein gb U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

264050 Seq. No. Contig ID 6575 5.R1011

LIB3059-029-Q1-K1-G11 5'-most EST

Method BLASTX g1174867 NCBI GI BLAST score 298 7.0e-27 E value Match length 72

74 % identity

NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING

PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2

KD PROTEIN) >gi_633687_emb_CAA55862_ (X79275)

ubiquinol--cytochrome c reductase [Solanum tuberosum] >gi 1094912 prf 2107179A cytochrome c oxidase:SUBUNIT=8.2kD [Solanum tuberosum]

Seq. No. 264051

6577 1.R1011 Contig ID

LIB3078-016-Q1-K1-D3 5'-most EST

Method BLASTX NCBI GI q4467134 BLAST score 275 4.0e-24 E value Match length 183 % identity

NCBI Description (AL035540) protein kinase like protein [Arabidopsis

thaliana]

Seq. No. 264052

Contig ID 6580 1.R1011

5'-most EST LIB3066-052-Q1-K1-F11

Method BLASTX g2497281 NCBI GI



710 BLAST score 1.0e-81 E value 242 Match length 64 % identity TRANSLATION INITIATION FACTOR IF-2 NCBI Description >gi_1651769_dbj_BAA16696_ (D90900) initiation factor IF-2 [Synechocystis sp.] 264053 Seq. No. 6582 1.R1011 Contig ID hrx700704045.hl 5'-most EST BLASTX Method a2431769 NCBI GI 318 BLAST score 5.0e-29 E value 109 Match length 63 % identity (U62752) acidic ribosomal protein Pla [Zea mays] NCBI Description 264054 Seq. No. 6582 2.R1011 Contig ID uC-zmrob73059f10a1 5'-most EST BLASTN Method q2431768 NCBI GI 255 BLAST score 1.0e-141 E value 259 Match length 100 % identity NCBI Description Zea mays acidic ribosomal protein Pla (rppla) mRNA, complete cds 264055 Seq. No. 6582_3.R1011 Contig ID LIB3115-016-P1-K1-H3 5'-most EST BLASTX Method g2431769 NCBI GI 327 BLAST score 3.0e - 30E value 109 Match length % identity NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays] Seq. No. 264056 6582 4.R1011 Contig ID wyr700243938.hl 5'-most EST BLASTX Method g2431769 NCBI GI 323 BLAST score 6.0e-30 E value 109 Match length

% identity

NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]

264057 Seq. No. 6582 6.R1011 Contig ID fdz701163276.h1 5'-most EST BLASTN Method

64



```
g1209700
NCBI GI
                  62
BLAST score
                  2.0e-26
E value
                  169
Match length
                  92
% identity
NCBI Description Zea mays ribosomal protein L12 mRNA, complete cds
                  264058
Seq. No.
                  6587 1.R1011
Contig ID
                  LIB84-006-Q1-E1-B1
5'-most EST
Method
                  BLASTX
                  g3885892
NCBI GI
                  777
BLAST score
                  9.0e-83
E value
                  156
Match length
                  94
% identity
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
                  264059
Seq. No.
                  6587 2.R1011
Contig ID
                  LIB189-012-Q1-E1-E9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g548604
                  560
BLAST score
                   2.0e-57
E value
                  110
Match length
                   91
% identity
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
                   (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
                  >gi_1076728_pir__S51813 photosystem-I PSI-F chain precursor
                   - barley >gi_469560 (U08135) photosystem-I PSI subunit
                   precursor [Hordeum vulgare]
                   264060
Seq. No.
                   6587 3.R1011
Contid ID
                  LIB3156-010-Q1-K1-A5
         TST
 5'-mo.
                  BLASTX
Method
                   g548604
NCBI GI
                   265
BLAST score
                   6.0e-23
 E value
                   56
Match length
                   89
 % identity
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
                   (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-7)
                   >gi_1076728_pir__S51813 photosystem-I PSI-F - precursor
                   - barley >gi 469560 (U08135) photosystem-
                   precursor [Hordeum vulgare]
                   264061
 Seq.
                   6587 4.R1011
 Contig _
 5'-most EST
                   xsy700212406.hl
```

Seq. No. 264062

6587 6.R1011 Contig ID fwa700099529.hl 5'-most EST

264063 Seq. No.



```
6587 7.R1011
Contig ID
5'-most EST
                  xsy700210015.hl
                  264064
Seq. No.
                  6588 1.R1011
Contig ID
5'-most EST
                  LIB3078-016-Q1-K1-B5
                  264065
Seq. No.
                  6589 1.R1011
Contig ID
                  LIB3279-003-P1-K1-H5
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3414809
                  449
BLAST score
                  5.0e-44
E value
                  373
Match length
% identity
NCBI Description (AF061529) rjs [Mus musculus]
                  264066
Seq. No.
                  6591 1.R1011
Contig ID
5'-most EST
                  LIB3078-016-Q1-K1-A6
                  264067
Seq. No.
                  6594 1.R1011
Contig ID
                  LIB3116-016-P1-K1-H10
5'-most EST
Seq. No.
                  264068
                  6594 2.R1011
Contig ID
                  LIB3060-009-Q1-K1-F5
5'-most EST
                  264069
Seq. No.
Contig ID
                  6595 1.R1011
                  LIB148-014-Q1-E1-E2
5'-most EST
Method
                  BLASTX
                  g1762947
NCBI GI
                  304
BLAST score
                  4.0e-27
E value
                  93
Match length
                  62
% identity
                  (U66270) ORF; able to induce HR-like lesions [Nicotiana
NCBI Description
                  tabacum]
                   264070
Seq. No.
                   6596 1.R1011
Contig ID
                  uwc700152652.h1
5'-most EST
                  BLASTX
Method
                  q464707
NCBI GI
                   646
BLAST score
                   2.0e-67
E value
Match length
                   152
% identity
                  78
                  40S RIBOSOMAL PROTEIN S18 >gi 480908_pir__S37496 ribosomal
NCBI Description
```

36645

S18 ribosomal protein [Arabidopsis thaliana]

>gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
[Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)

>qi 434345 emb CAA82274 (Z28702) S18 ribosomal protein

protein S18.A - Arabidopsis thaliana



[Arabidopsis thaliana] >gi 434906 emb CAA82275 (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi 2505871 emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb T21121, gb_Z17755, gb_R64776 and gb R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) \$18.A ribosomal protein [Arabidopsis thaliana]

264071 Seq. No. 6596 2.R1011 Contig ID LIB3159-013-Q1-K1-G10 5'-most EST BLASTX Method q464707 NCBI GI 600 BLAST score E value 5.0e-62 152 Match length 72 % identity NCBI Description

40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana ->gi 405613 emb CAA80684 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb R30430 come from this gene. [Arabidopsis thaliana] $>gi_4538910_{emb_CAB39647.1_ (AL049482)} S18.A ribosomal$ protein [Arabidopsis thaliana]

264072 Seq. No. 6601 1.R1011 Contig ID LIB3078-016-Q1-K1-A1 5'-most EST BLASTX Method g400896 NCBI GI 469 BLAST score 1.0e-46

E value 226 Match length % identity

PHOSPHATIDYLSERINE SYNTHASE I (SERINE-EXCHANGE ENZYME I) NCBI Description >gi 109417 pir A41680 integral membrane protein pssA -

Chinese hamster >gi 220281 dbj BAA01084 (D10234)

phosphatidylserine synthase [Cricetulus sp.]

264073 Seq. No.

Contig ID 6601 2.R1011 uC-zmflm017084f09b1 5'-most EST

BLASTN Method NCBI GI q3821780 BLAST score 35

5.0e-10 E value Match length 35



100 % identity NCBI Description Xenopus laevis cDNA clone 27A6-1 264074 Seq. No. 6601 3.R1011 Contig ID LIB3067-010-Q1-K1-C9 5'-most EST 264075 Seq. No. 6601 4.R1011 Contig ID 5'-most EST uC-zmflmo17292e06a1 264076 Seq. No. 6603 1.R1011 Contig ID uwc700150165.hl 5'-most EST BLASTX Method g3980417 NCBI GI 1039 BLAST score 1.0e-145 E value 356 Match length % identity 25 (AC004561) pumilio-like protein [Arabidopsis thaliana] NCBI Description 264077 Seq. No. 6603 2.R1011 Contig ID uC-zmroteosinte040a08b1 5'-most EST BLASTX Method q3980417 NCBI GI BLAST score 711 6.0e-75 E value 169 Match length 41 % identity NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana] 264078 Seq. No. 6610 1.R1011 Contig ID LIB3115-016-P1-K1-C6 5'-most EST BLASTX Method NCBI GI q131192 BLAST score 466 E value 3.0e-46128 Match length % identity PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR NCBI Description (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >qi 100606 pir S20937 photosystem I chain V precursor - barley >qi 19091 emb CAA42727 (X60158) photosystem I polypeptide PSI-G precursor [Hordeum vulgare] Seq. No. 264079 Contig ID 6610 2.R1011 $LIB3\overline{6}-016-Q2-E2-G3$ 5'-most EST Method BLASTX

NCBI GI q131192 BLAST score 462 6.0e-46E value

Match length 97 89 % identity



NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR

(PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi 100606 pir__S20937

photosystem I chain V precursor - barley

>qi 19091 emb CAA42727 (X60158) photosystem I polypeptide

PSI-G precursor [Hordeum vulgare]

264080 Seq. No.

6611 1.R1011 Contig ID

LIB3060-012-Q1-K1-D1 5'-most EST

BLASTX Method g548603 NCBI GI 732 BLAST score 2.0e-77 E value 159 Match length 89 % identity

PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR NCBI Description

(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)

>gi_478404_pir__JQ2247 photosystem I chain D precursor barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]

264081 Seq. No.

6611 2.R1011 Contig ID

uC-zmflB73045e05b1 5'-most EST

BLASTX Method g548603 NCBI GI 375 BLAST score 7.0e-36 E value 128 Match length 62 % identity

PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR NCBI Description

(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)

>gi 478404 pir JQ2247 photosystem I chain D precursor barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No. 264082 6611 3.R1011 Contig ID

LIB36-015-Q1-E1-B12 5'-most EST

BLASTX Method q417544 NCBI GI

BLAST score 481 3.0e-48E value Match length 97 92 % identity

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR

(PHOTOSYSTEM I 20 KD PROTEIN) (PSI-D) (PS I SUBUNIT 5) >qi 320209 pir A60695 photosystem I chain II precursor cucumber >gi 625966_pir__JQ2132 photosystem I complex 20K protein precursor - cucumber >gi 227772 prf 1710320A

photosystem I 20kD protein [Cucumis sativus]

264083 Seq. No.

6613 1.R1011 Contig ID LIB83-015-Q1-E1-B3 5'-most EST

264084 Seq. No.

6613 2.R1011 Contig ID

LIB3078-048-Q1-K1-F2 5'-most EST

E value

NCBI Description



```
264085
Seq. No.
                   6613 3.R1011
Contig ID
                  LIB36-022-Q1-E1-A9
5'-most EST
                  264086
Seq. No.
                   6613 4.R1011
Contig ID
                  fwa700098534.hl
5'-most EST
                   264087
Seq. No.
                   6613 5.R1011
Contig ID
                  wyr700241590.h1
5'-most EST
                   264088
Seq. No.
                   6614 1.R1011
Contig ID
                  uC-zmflmo17222d03b1
5'-most EST
Method
                  BLASTX
                   g1653508
NCBI GI
                   233
BLAST score
```

9.0e-19

Match length 128 % identity 41 (D90914) hypothetical protein [Synechocystis sp.]

264089 Seq. No. 6619 1.R1011 Contig ID LIB3078-015-Q1-K1-G8 5'-most EST BLASTX Method

g115009 NCBI GI BLAST score 177 E value 1.0e-12 Match length 121 33 % identity

8-AMINO-7-OXONONANOATE SYNTHASE (7-KETO-8-AMINO-PELARGONIC NCBI Description ACID SYNTHETASE) (7-KAP SYNTHETASE) (L-ALANINE--PIMELYL COA

LIGASE) >gi 98180 pir JQ0512 8-amino-7-oxononanoate synthase (EC 2.3.1.47) - Bacillus sphaericus >gi 142595 (M29291) 7-keto-8-aminopelargonic acid synthetase (bioF)

[Bacillus sphaericus]

264090 Seq. No. Contig ID 6621 1.R1011 ymt700221238.h1 5'-most EST Method BLASTX q3860277 NCBI GI BLAST score 873

6.0e-94 E value Match length 215 78 % identity

(AC005824) putative ribosomal protein L10 [Arabidopsis NCBI Description thaliana] >gi 4314394 gb AAD15604 (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 264091 Contig ID 6622 1.R1011

fC-zmst1700334018a1 5'-most EST

BLASTX Method



```
q4539330
NCBI GI
                  694
BLAST score
                  5.0e-73
E value
                  174
Match length
                  74
% identity
                  (AL035679) putative receptor-like protein kinase (fragment)
NCBI Description
                  [Arabidopsis thaliana]
                  264092
Seq. No.
                  6622 2.R1011
Contig ID
                  ceu700428189.h1
5'-most EST
                  BLASTX
Method
                  q1173187
NCBI GI
                  719
BLAST score
                  5.0e-76
E value
                  142
Match length
                  96
% identity
                  40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673
NCBI Description
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                  strawberry >gi 643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
                  264093
Seq. No.
                  6622 3.R1011
Contig ID
                  xyt700345538.hl
5'-most EST
                  BLASTX
Method
                  g1173187
NCBI GI
BLAST score
                   673
                  1.0e-70
E value
Match length
                  133
                   96
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041_pir__S56673
                   ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                   strawberry >qi 643074 (U19940) putative 40S ribosomal
                   protein s12 [Fragaria x ananassa]
                   264094
Seq. No.
                   6622 5.R1011
Contig ID
                   ceu700432627.h1
5'-most EST
                   BLASTX
Method
                   q1173187
NCBI GI
BLAST score
                   719
                   5.0e-76
E value
                   142
Match length
                   96
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041 pir S56673
                   ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                   strawberry >gi 643074 (U19940) putative 40S ribosomal
                   protein s12 [Fragaria x ananassa]
Seq. No.
                   264095
Contig ID
                   6622 7.R1011
```

5'-most EST uC-zmroteosinte093a12b2

Method BLASTX
NCBI GI g1173187
BLAST score 332
E value 9.0e-31



65 Match length 100 % identity 40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 NCBI Description ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa] 264096 Seq. No. 6623 1.R1011 Contig ID rvt700550624.h15'-most EST Method BLASTX NCBI GI q4263696 157 BLAST score 9.0e-16 E value 116 Match length 40 % identity (AC006223) hypothetical protein [Arabidopsis thaliana] NCBI Description 264097 Seq. No. 6624 1.R1011 Contig ID xmt700263676.hl 5'-most EST 264098 Seq. No. 6624 2.R1011 Contig ID LIB3078-040-Q1-K1-D5 5'-most EST 264099 Seq. No. 6625 1.R1011 Contig ID dyk700106694.h15'-most EST BLASTX Method g3334133 NCBI GI BLAST score 734 2.0e-77 E value 397 Match length 42 % identity CYTOCHROME P450 89A2 (CYPLXXXIX) (ATa 6-1) >gi 1432145 NCBI Description (U61231) cytochrome P450 [Arabidopsis thaliana] 264100 Seq. No. 6627 1.R1011 Contig ID LIB189-029-Q1-E1-C11 5'-most EST BLASTX Method g1041815 NCBI GI 237 BLAST score 1.0e-19 E value 67 Match length 58 % identity NCBI Description (U16721) lipid transfer protein [Oryza sativa] 264101 Seq. No. Contig ID 6630 1.R1011

LIB3060-046-Q1-K1-C10 5'-most EST

BLASTX Method NCBI GI q1200205 BLAST score 699 2.0e-73 E value Match length 158

Seq. No.

Contig ID

264107

6634 4.R1011



```
% identity
NCBI Description (X95753) DAG [Antirrhinum majus]
                  264102
Seq. No.
                  6630 3.R1011
Contig ID
                  LIB3115-028-P1-K1-F10
5'-most EST
                  BLASTX
Method
                  g1200205
NCBI GI
BLAST score
                  256
                  2.0e-42
E value
                  102
Match length
                  86
% identity
NCBI Description (X95753) DAG [Antirrhinum majus]
                  264103
Seq. No.
                  6632 1.R1011
Contig ID
                  LIB3078-001-Q1-K1-F1
5'-most EST
                  BLASTX
Method
                  q548605
NCBI GI
                  463
BLAST score
                  5.0e-46
E value
Match length
                  134
                  75
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                   - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
                  264104
Seq. No.
Contig ID
                  6634 1.R1011
5'-most EST
                  uC-zmflmo17285e12b1
                  BLASTX
Method
                  q3258570
NCBI GI
BLAST score
                   592
                   6.0e-61
E value
                   258
Match length
                   47
% identity
                  (U89959) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   264105
Seq. No.
                   6634_2.R1011
Contig ID
                   uC-zmflmo17184d07b1
5'-most EST
Method
                   BLASTX
                   a4455254
NCBI GI
BLAST score
                   197
                   5.0e-15
E value
                   56
Match length
                   59
% identity
                  (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
                   264106
Seq. No.
Contig ID
                   6634 3.R1011
                   LIB36-021-Q1-E1-A12
5'-most EST
```



5'-most EST uC-zmflmo17099f09b1 264108 Seq. No. 6634 6.R1011 Contig ID uC-zmrob73006b10b1 5'-most EST 264109 Seq. No. Contig ID 6635 1.R1011 5'-most EST LIB3078-052-Q1-K1-G9 Method BLASTX NCBI GI g1084336 BLAST score 508 E value 2.0e-51 Match length 109 80 % identity NCBI Description chlorophyll a/b-binding protein type II - Arabidopsis thaliana >gi 541565 (U03395) PSI type II chlorophyll a/b-binding protein [Arabidopsis thaliana] 264110 Seq. No. 6636 1.R1011 Contig ID ymt700219290.hl 5'-most EST Seq. No. 264111 Contig ID 6636 3.R1011 clt700043543.fl 5'-most EST 264112 Seq. No. Contig ID 6637 1.R1011 5'-most EST uC-zmflb73282c09a1 Method BLASTX NCBI GI q2239085 BLAST score 143 E value 9.0e-09 Match length 69 % identity 36 NCBI Description (284384) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] 264113 Seq. No. Contig ID 6638 1.R1011 5'-most EST wyr700241180.hl 264114 Seq. No. Contig ID 6640 1.R1011 5'-most EST LIB3078-015-Q1-K1-C7 264115 Seq. No. 6640 2.R1011 Contig ID 5'-most EST LIB3156-013-Q1-K1-F2 264116 Seq. No.

 Seq. No.
 264116

 Contig ID
 6641_1.R1011

 5'-most EST
 xyt700343379.h1

 Method
 BLASTX

 NCBI GI
 g1495768

1088

BLAST score

BLAST score

286



```
1.0e-119
E value
                  412
Match length
                  54
% identity
                  (Z68506) chloroplast inner envelope protein, 110 kD
NCBI Description
                   (IEP110) [Pisum sativum]
                  264117
Seq. No.
                   6642 1.R1011
Contig ID
                  LIB3078-015-Q1-K1-C9
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2760323
                   698
BLAST score
                  2.0e-73
E value
                   277
Match length
% identity
                   51
NCBI Description (AC002130) F1N21.8 [Arabidopsis thaliana]
                   264118
Seq. No.
                   6642 3.R1011
Contig ID
5'-most EST
                   fdz7\overline{0}1164945.h1
Seq. No.
                   264119
                   6643 1.R1011
Contig ID
                   LIB3116-033-P1-K1-F1
5'-most EST
                   BLASTX
Method
                   q1881585
NCBI GI
BLAST score
                   284
                   7.0e-25
E value
                   126
Match length
                   50
% identity
NCBI Description
                  (U72489) remorin [Solanum tuberosum]
                   264120
Seq. No.
                   6643 2.R1011
Contig ID
                   LIB3150-017-Q1-N1-E8
5'-most EST
                   BLASTX
Method
                   g1881585
NCBI GI
                   273
BLAST score
                   7.0e-24
E value
                   92
Match length
                   66
% identity
NCBI Description (U72489) remorin [Solanum tuberosum]
                   264121
Seq. No.
                   6643 3.R1011
Contig ID
5'-most EST
                   LIB3159-017-Q1-K1-G7
                   264122
Seq. No.
                   6643 4.R1011
Contig ID
                   fwa700100644.h1
5'-most EST
                   264123
Seq. No.
                   6644 1.R1011
Contig ID
5'-most EST
                   hvj700621536.hl
Method
                   BLASTX
                   g2467274
NCBI GI
```



```
E value
                   4.0e-25
Match length
                  114
                   54
% identity
                  (Z99759) rna binding protein [Schizosaccharomyces pombe]
NCBI Description
                  264124
Seq. No.
                   6644 3.R1011
Contig ID
5'-most EST
                  uC-z\overline{m}flb73199a06b1
                  264125
Seq. No.
Contig ID
                  6649 1.R1011
5'-most EST
                  LIB3078-023-Q1-K1-H8
                  264126
Seq. No.
                   6650 1.R1011
Contig ID
                  xsy700210201.hl
5'-most EST
Method
                  BLASTX
                   g2920654
NCBI GI
                   864
BLAST score
                   5.0e-93
E value
Match length
                  181
                   86
% identity
                  (AF047697) putative high-pI laccase [Oryza sativa]
NCBI Description
                   264127
Seq. No.
                   6655 1.R1011
Contig ID
                  uC-zmflmo17289b04b1
5'-most EST
                   264128
Seq. No.
                   6655 2.R1011
Contig ID
                  LIB84-009-Q1-E1-G5
5'-most EST
Seq. No.
                   264129
Contig ID
                   6659 1.R1011
                   LIB3066-008-Q1-K1-G10
5'-most EST
Method
                   BLASTX
                   q3859560
NCBI GI
BLAST score
                   304
                   4.0e-27
E value
                   212
Match length
                   38
% identity
                   (AF098668) acyl-protein thioesterase [Homo sapiens]
NCBI Description
                   >gi 4581413 emb CAB40158.1 (AL031295) dJ886K2.4
                   (acyl-protein thioesterase) [Homo sapiens]
                   264130
Seq. No.
                   6659 3.R1011
Contig ID
                   nwy700446170.h1
5'-most EST
                   BLASTX
Method
                   g3859560
NCBI GI
BLAST score
                   169
```

E value 1.0e-11 64 Match length 47

% identity (AF098668) acyl-protein thioesterase [Homo sapiens] NCBI Description >gi 4581413 emb CAB40158.1 (AL031295) dJ886K2.4

(acyl-protein thioesterase) [Homo sapiens]

Match length

% identity

128

88



```
264131
Seq. No.
                  6659 9.R1011
Contig ID
                  ceu700424393.hl
5'-most EST
                  264132
Seq. No.
                  6660 1.R1011
Contig ID
                  xjt700095319.h1
5'-most EST
                  BLASTX
Method
                  g3036801
NCBI GI
                  163
BLAST score
                  2.0e-10
E value
                  199
Match length
                  35
% identity
                  (AL022373) putative ascorbate peroxidase [Arabidopsis
NCBI Description
                  thaliana] >gi_3805863_emb CAA21483 (AL031986) putative
                  ascorbate peroxidase [Arabidopsis Thaliana]
                  264133
Seq. No.
                   6660 2.R1011
Contig ID
                  gct701173040.h2
5'-most EST
                  264134
Seq. No.
                   6662 1.R1011
Contig ID
                   fC-zmf1700612075d1
5'-most EST
                   BLASTX
Method
                   g1708025
NCBI GI
BLAST score
                   1488
                   1.0e-166
E value
                   342
Match length
                   81
% identity
                   GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+]
NCBI Description
                   >gi 840731 emb CAA56125 (X79677) glycerol-3-phosphate
                   dehydrogenase (NAD+) [Cuphea lanceolata]
                   264135
Seq. No.
                   6662 2.R1011
Contig ID
                   uC-zmroteosinte115g07b1
5'-most EST
                   BLASTX
Method
                   g840908
NCBI GI
                   331
BLAST score
                   1.0e-30
E value
Match length
                   61
% identity
                  (Z22873) beta glucanase [Triticum aestivum]
NCBI Description
                   264136
Seq. No.
                   6662 3.R1011
Contig ID
                   wyr700242830.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g840908
BLAST score
                   613
                   6.0e-64
E value
```

36656

NCBI Description (Z22873) beta glucanase [Triticum aestivum]



264137 Seq. No. 6662 6.R1011 Contig ID wyr700239926.h1 5'-most EST BLASTX Method g1708025 NCBI GI 165 BLAST score 1.0e-12 E value 54 Match length 78 % identity GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+] NCBI Description >gi_840731_emb_CAA56125_ (X79677) glycerol-3-phosphate dehydrogenase (NAD+) [Cuphea lanceolata] 264138 Seq. No. 6663 1.R1011 Contig ID fwa700101743.h1 5'-most EST BLASTX Method g1652164 NCBI GI 593 BLAST score 6.0e-61 E value Match length 231 % identity 54 (D90903) hypothetical protein [Synechocystis sp.] NCBI Description 264139 Seq. No. 6665 1.R1011 Contig ID LIB3078-015-Q1-K1-C10 5'-most EST 264140 Seq. No. 6667 1.R1011 Contig ID uC-zmflb73269f10a15'-most EST BLASTX Method q4417296 NCBI GI 272 BLAST score 1.0e-25 E value Match length 80 71 % identity (AC007019) unknown protein [Arabidopsis thaliana] NCBI Description >qi 4587592 gb AAD25820.1 AC007232_10 (AC007232) unknown protein [Arabidopsis thaliana] 264141 Seq. No. 6668 1.R1011 Contig ID LIB3059-034-Q1-K1-G12 5'-most EST BLASTX Method NCBI GI q3298437 915 BLAST score 8.0e-99 E value 223 Match length % identity (AB010877) chloroplast ribosomal protein L3 [Nicotiana NCBI Description

tabacum]

Seq. No. 264142 6669 1.R1011 Contig ID

5'-most EST LIB3078-014-Q1-K1-H11



```
Seq. No.
                  264143
                   6672 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17259g04b1
                  BLASTX
Method
NCBI GI
                  g3549678
BLAST score
                   1307
                  1.0e-144
E value
                   520
Match length
                   62
% identity
NCBI Description
                  (AL031394) putative aspartate--tRNA ligase [Arabidopsis
                   thalianal
                   264144
Seq. No.
                   6672 2.R1011
Contig ID
                  hvi700619328.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3549678
BLAST score
                   186
                   1.0e-13
E value
                   114
Match length
% identity
                   68
NCBI Description
                  (AL031394) putative aspartate--tRNA ligase [Arabidopsis
                   thalianal
                   264145
Seq. No.
                   6672 4.R1011
Contig ID
5'-most EST
                  LIB3150-077-P1-N1-G8
Method
                   BLASTX
NCBI GI
                   g2739219
BLAST score
                   254
E value
                   1.0e-21
Match length
                   53
% identity
                   98
NCBI Description (AJ001161) rpS28 [Hordeum vulgare]
                   264146
Seq. No.
                   6672 5.R1011
Contig ID
                   LIB3279-012-P1-K1-G4
5'-most EST
                   BLASTX
Method
                   g2739219
NCBI GI
BLAST score
                   245
                   1.0e-20
E value
Match length
                   51
                   98
% identity
NCBI Description
                  (AJ001161) rpS28 [Hordeum vulgare]
                   264147
Seq. No.
                   6672 6.R1011
Contig ID
                   LIB189-018-Q1-E1-G12
5'-most EST
                   BLASTX
Method
                   g2739219
NCBI GI
BLAST score
                   245
                   1.0e-20
E value
Match length
                   51
```

98

NCBI Description (AJ001161) rpS28 [Hordeum vulgare]

% identity



264148 Seq. No. 6672 7.R1011 Contig ID cjh700193656.h1 5'-most EST 264149 Seq. No. 6672 11.R1011 Contig ID LIB3067-002-Q1-K1-H2 5'-most EST BLASTX Method q2739219 NCBI GI BLAST score 231 5.0e-19 E value 51 Match length 94 % identity NCBI Description (AJ001161) rpS28 [Hordeum vulgare] Seq. No. 264150 6675 1.R1011 Contig ID uwc700155868.h1 5'-most EST BLASTX Method g3915008 NCBI GI BLAST score 767 2.0e-81 E value 182 Match length 80 % identity SUPEROXIDE DISMUTASE, CHLOROPLAST [CU-ZN] PRECURSOR NCBI Description >gi 1805502 dbj BAA12745 (D85239) superoxide dismutase precusor [Oryza sativa] 264151 Seq. No. 6677 1.R1011 Contig ID 5'-most EST LIB189-021-Q1-E1-E7 264152 Seq. No. Contig ID 6677 3.R1011 5'-most EST mwy700438744.h1 264153 Seq. No. 6679 1.R1011 Contig ID uC-zmflmo17287d07b1 5'-most EST Method BLASTX NCBI GI q131388 BLAST score 1340 E value 1.0e-148 Match length 316 87 % identity NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260 photosystem II oxygen-evolving complex protein 1 - common

wheat x Sanduri wheat >gi 21844 emb CAA40670 (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum

aestivum]

Seq. No. 264154 Contig ID 6679 2.R1011 5'-most EST xjt700093832.hl Method BLASTX



NCBI GI g482311 BLAST score 504 E value 9.0e-51 Match length 181 % identity 91

NCBI Description photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi 739292 prf 2002393A oxygen-evolving

complex protein 1 [Oryza sativa]

Seq. No. 264155

Contig ID 6679 3.R1011

5'-most EST LIB36-022-Q1-E1-B7
Method BLASTX

NCBI GI g131388 BLAST score 363 E value 1.0e-43 Match length 161 % identity 65

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir__S16260

photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum

aestivum]

Seq. No. 264156 Contig ID 6679_6.R1011

5'-most EST LIB3078-050-Q1-K1-F12

Method BLASTX
NCBI GI g482311
BLAST score 255
E value 5.0e-22
Match length 73
% identity 70

NCBI Description photosystem II oxygen-evolving complex protein 1 - rice

(strain Nihonbare) >gi 739292 prf 2002393A oxygen-evolving

complex protein 1 [Oryza sativa]

Seq. No. 264157 Contig ID 6679 7.R1011

5'-most EST LIB3078-015-Q1-K1-A11

Method BLASTX
NCBI GI g100454
BLAST score 201
E value 9.0e-16
Match length 44
% identity 86

NCBI Description photosystem II oxygen-evolving complex protein 1 - potato

>qi 809113 emb CAA35601 (X17578) 33kDa precursor protein

of oxygen-evolving complex [Solanum tuberosum]

Seq. No. 264158 Contig ID 6681_1.R1011

5'-most EST uC-zmflmo17099g06b1

Method BLASTX NCBI GI g3881189



BLAST score 609
E value 5.0e-63
Match length 184
% identity 58
NCBI Description (Z99281

(Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4

Seq. No. 264159 Contig ID 6683_1.R1011

5'-most EST LIB3078-019-Q1-K1-F11

Method BLASTX
NCBI GI g3402282
BLAST score 160
E value 2.0e-10
Match length 145
% identity 36

NCBI Description (AJ000997) proline-rich protein [Solanum tuberosum]

Seq. No. 264160 Contig ID 6683_2.R1011

5'-most EST LIB3078-052-Q1-K1-C2

Method BLASTX
NCBI GI g3402282
BLAST score 162
E value 1.0e-10
Match length 138
% identity 35

NCBI Description (AJ000997) proline-rich protein [Solanum tuberosum]

 Seq. No.
 264161

 Contig ID
 6685_1.R1011

 5'-most EST
 gct701178783.h2

Method BLASTX
NCBI GI g3560183
BLAST score 334
E value 5.0e-31
Match length 130
% identity 52

NCBI Description (AL031517) conserved hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 264163 Contig ID 6688_1.R1011

5'-most EST LIB3078-014-Q1-K1-F6

Seq. No. 264164 Contig ID 6690_1.R1011

5'-most EST LIB3078-014-Q1-K1-G1

Method BLASTX NCBI GI g464986 BLAST score 768



E value 1.0e-81 147 Match length 95 % identity

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana

>gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana]

>qi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein

ligase UBC9 [Arabidopsis thaliana]

Seq. No. 264165 6690 2.R1011 Contig ID tzu700204465.h1 5'-most EST Method BLASTX NCBI GI g464986 BLAST score 347 1.0e-32

E value Match length 68 93 % identity

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN

LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC

6.3.2.19) UBC9 - Arabidopsis thaliana

>gi 297884 emb CAA78714 (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi 600391 emb CAA51201 (X72626) ubiquitin conjugating

enzyme E2 [Arabidopsis thaliana]

>gi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein

ligase UBC9 [Arabidopsis thaliana]

Seq. No. 264166 Contig ID 6690 4.R1011

5'-most EST LIB3156-008-Q1-K1-E1

Method BLASTX NCBI GI q464986 BLAST score 364 E value 2.0e-34 Match length 115 % identity

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)

>gi_421857_pir__S32674 ubiquitin--protein ligase (EC

6.3.2.19) UBC9 - Arabidopsis thaliana

>gi 297884 emb CAA78714 (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana]

>gi 600391 emb CAA51201 (X72626) ubiquitin conjugating

enzyme E2 [Arabidopsis thaliana]

>gi_4455355_emb_CAB36765.1 (AL035524) ubiquitin-protein

ligase UBC9 [Arabidopsis thaliana]

NCBI Description



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264167
Seq. No.
                  6690 5.R1011
Contig ID
5'-most EST
                  tfd700572568.h1
                  BLASTX
Method
                  q464986
NCBI GI
BLAST score
                  327
                  2.0e-30
E value
                  63
Match length
                  94
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                  >qi 421857 pir S32674 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC9 - Arabidopsis thaliana
                  >gi 297884 emb CAA78714 (Z14990) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                  ubiquitin conjugating enzyme [Arabidopsis thaliana]
                  >gi 600391 emb CAA51201 (X72626) ubiquitin conjugating
                  enzyme E2 [Arabidopsis thaliana]
                  >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein
                  ligase UBC9 [Arabidopsis thaliana]
                  264168
Seq. No.
                  6693 1.R1011
Contig ID
                  LIB83-004-Q1-E2-F4
5'-most EST
                  BLASTX
Method
                  q4239879
NCBI GI
                  485
BLAST score
                  1.0e-48
E value
                  162
Match length
                  56
% identity
                   (AB016780) Glutamine:fructose-6-phosphate amidotransferase
NCBI Description
                  2 [Mus musculus]
                  264169
Seq. No.
Contig ID
                  6696 1.R1011
                  LIB3078-014-Q1-K1-G5
5'-most EST
Method
                  BLASTX
                  q1173027
NCBI GI
                   434
BLAST score
E value
                   9.0e-43
                  113
Match length
                  74
% identity
                  60S RIBOSOMAL PROTEIN L31 >qi 915313 (U23784) ribosomal
NCBI Description
                  protein L31 [Nicotiana glutinosa]
Seq. No.
                   264170
                   6696 2.R1011
Contig ID
                   LIB3116-014-Q1-K1-H1
5'-most EST
                   BLASTX
Method
                   g1173027
NCBI GI
BLAST score
                   417
                   1.0e-40
E value
Match length
                   113
% identity
                   72
```

protein L31 [Nicotiana glutinosa]

60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal



264171 Seq. No. 6696 3.R1011 Contig ID zuv700352629.h1 5'-most EST BLASTN Method g473999 NCBI GI BLAST score 45 4.0e-16 E value 105 Match length 86 % identity NCBI Description Rice mRNA, partial homologous to ribosomal protein L31 gene 264172 Seq. No. 6697 1.R1011 Contig ID LIB3078-014-Q1-K1-G6 5'-most EST 264173 Seq. No. 6699 1.R1011 Contig ID xjt700095752.h1 5'-most EST BLASTX Method g4006872 NCBI GI 626 BLAST score 4.0e-65 E value 193 Match length 63 % identity (Z99707) methionyl aminopeptidase-like protein [Arabidopsis NCBI Description thaliana] 264174 Seq. No. 6701 1.R1011 Contig ID 5'-most EST LIB3078-014-Q1-K1-D8 Method BLASTX NCBI GI g1770301 341 BLAST score 1.0e-31 E value Match length 194 % identity (X95074) Translin [Gallus gallus] NCBI Description 264175 Seq. No. Contig ID 6702 1.R1011 5'-most EST LIB3078-014-Q1-K1-E1 Method BLASTN NCBI GI g4140643 BLAST score 42 2.0e-14E value Match length 58 93 % identity Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, NCBI Description complete sequence 264176 Seq. No. 6705 1.R1011 Contig ID ymt700220408.hl

5'-most EST

BLASTX Method g1710424 NCBI GI 388 BLAST score 2.0e-37 E value



105 Match length 70 % identity 50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21) NCBI Description >gi 2129718_pir S71282 ribosomal protein L21 - Arabidopsis thaliana >gi 1149573 emb CAA89887 (Z49787) chloroplast ribosomal large subunit protein L21 [Arabidopsis thaliana] 264177 Seq. No. 6710 1.R1011 Contig ID pwr700450071.h2 5'-most EST BLASTX Method q4127456 NCBI GI 866 BLAST score 5.0e-93 E value 243 Match length 72 % identity (AJ010818) Cpn21 protein [Arabidopsis thaliana] NCBI Description 264178 Seq. No. 6710 2.R1011 Contig ID uC-zmflmo170114h12b15'-most EST BLASTX Method q4127456 NCBI GI 315 BLAST score E value 7.0e-29 130 Match length 65 % identity NCBI Description (AJ010818) Cpn21 protein [Arabidopsis thaliana] 264179 Seq. No. 6712 1.R1011 Contig ID LIB3078-014-01-K1-F10 5'-most EST 264180 Seq. No. Contig ID 6712 2.R1011 LIB3079-053-Q1-K1-C11 5'-most EST Seq. No. 264181 6713 1.R1011 Contig ID 5'-most EST pmx700087412.h1 BLASTX Method NCBI GI q1350625 BLAST score 632 6.0e-66 E value Match length 149 % identity 81 CHLOROPLAST 50S RIBOSOMAL PROTEIN L1 PRECURSOR NCBI Description >gi 577089 emb CAA58020_ (X82776) chloroplast ribosomal

protein L1 [Pisum sativum]

Seq. No. 264182 Contig ID 6714_1.R1011

5'-most EST uC-zmflMo17009h10b1

 Seq. No.
 264183

 Contig ID
 6715_1.R1011

5'-most EST LIB3181-003-P1-M1-G4



BLASTX Method NCBI GI g2618704 801 BLAST score 3.0e-92 E value 235 Match length % identity (AC002510) putative thioredoxin reductase [Arabidopsis NCBI Description thaliana] 264184 Seq. No. 6719 1.R1011 Contig ID

LIB3067-040-Q1-K1-D4 5'-most EST

264185 Seq. No. 6719 2.R1011 Contig ID

LIB3088-010-Q1-K1-F6 5'-most EST

264186 Seq. No. Contig ID 6719 3.R1011 uC-zmflmo17286f04b1 5'-most EST

BLASTX Method g2239091 NCBI GI BLAST score 294 3.0e - 31E value 212 Match length 40 % identity

(Z84571) anthranilate N-hydroxycinnamoyl/benzoyltransferase NCBI Description

[Dianthus caryophyllus]

264187 Seq. No. 6719 4.R1011 Contig ID

LIB3069-057-Q1-K1-G3 5'-most EST

264188 Seq. No. Contig ID 6722 1.R1011

LIB3059-016-Q1-K1-H11 5'-most EST

BLASTX Method g3717987 NCBI GI BLAST score 262 E value 2.0e-22 110 Match length 53 % identity

(AJ005899) G subunit of Vacuolar-type H+-ATPase [Nicotiana NCBI Description

tabacum]

264189 Seq. No. Contig ID 6722 2.R1011 5'-most EST wty700171528.h1

Method BLASTX NCBI GI g3717987 BLAST score 225 E value 3.0e-18 Match length 58 % identity 76

(AJ005899) G subunit of Vacuolar-type H+-ATPase [Nicotiana NCBI Description

tabacum



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264190
Seq. No.
                  6722 3.R1011
Contig ID
                  ymt700224738.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3717946
BLAST score
                  226
                  1.0e-18
E value
Match length
                  101
                   50
% identity
                  (AJ005901) vag1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   264191
                   6722 5.R1011
Contig ID
                  wty700166530.hl
5'-most EST
                   264192
Seq. No.
                   6724 1.R1011
Contig ID
                   vux700156983.h1
5'-most EST
Method
                   BLASTX
                   g2781363
NCBI GI
BLAST score
                   552
                   2.0e-56
E value
Match length
                   150
% identity
                   71
                  (AC003113) F2401.19 [Arabidopsis thaliana]
NCBI Description
                   264193
Seq. No.
Contig ID
                   6724 2.R1011
                   LIB3062-042-Q1-K1-E3
5'-most EST
                   BLASTX
Method
                   g2781363
NCBI GI
                   164
BLAST score
                   2.0e-18
E value
                   63
Match length
                   78
% identity
                  (AC003113) F2401.19 [Arabidopsis thaliana]
NCBI Description
                   264194
Seq. No.
                   6725 1.R1011
Contig ID
                   LIB3137-018-Q1-K1-G9
5'-most EST
                   BLASTX
Method
                   g3355480
NCBI GI
BLAST score
                   372
                   5.0e-35
E value
                   310
Match length
                   30
% identity
                  (AC004218) Medicago nodulin N21-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   264195
Seq. No.
                   6729 1.R1011
Contig ID
```

 Seq. No.
 264195

 Contig ID
 6729_1.R1011

 5'-most EST
 uC-zmflb73061f01b1

 Method
 BLASTX

 NCBI GI
 g1620898

 BLAST score
 236

 E value
 1.0e-19

Match length 60



% identity (D87957) protein involved in sexual development [Homo NCBI Description sapiens] 264196 Seq. No. 6729 2.R1011 Contig ID LIB3279-060-P1-K1-E1 5'-most EST Method BLASTX g1620898 NCBI GI BLAST score 550 4.0e-56 E value Match length 152 % identity 71 (D87957) protein involved in sexual development [Homo NCBI Description sapiens] 264197 Seq. No. Contig ID 6730 1.R1011 kem700612222.h1 5'-most EST BLASTX Method NCBI GI q4007792 BLAST score 722 6.0e-76E value Match length 429 37 % identity (AL034463) Xenopus 14s cohesin smc1 subunit homolog NCBI Description [Schizosaccharomyces pombe] 264198 Seq. No. 6731 1.R1011 Contig ID cat700016756.rl 5'-most EST 264199 Seq. No. 6731 3.R1011 Contig ID uC-zmflmo17313a11b1 5'-most EST 264200 Seq. No. 6734_1.R1011 Contig ID LIB3078-014-Q1-K1-A8 5'-most EST 264201 Seq. No. 6736 1.R1011 Contig ID bdu700382887.hl 5'-most EST 264202 Seq. No. 6736_2.R1011 Contig ID 5'-most EST $hbs7\overline{0}1181678.h1$

264203 Seq. No.

6738 1.R1011 Contig ID $mwy7\overline{0}0441039.h1$ 5'-most EST

Seq. No. 264204 6739 1.R1011 Contig ID

LIB3157-015-Q1-K1-C11 5'-most EST

264205 Seq. No.



6740 1.R1011 Contig ID 5'-most EST LIB3078-031-Q1-K1-H10 264206 Seq. No. 6741 1.R1011 Contig ID dyk700105853.h1 5'-most EST BLASTX Method q4104457 NCBI GI BLAST score 706 E value 3.0e-74153 Match length 82 % identity (AF036172) 2-oxoglutarate/malate translocator [Zea mays] NCBI Description 264207 Seq. No. 6742 1.R1011 Contig ID 5'-most EST xsy700212072.h1 Seq. No. 264208 Contig ID 6744 1.R1011 uC-zmroB73014a07b1 5'-most EST BLASTX Method g1255951 NCBI GI BLAST score 558 3.0e-95 E value 236 Match length 70 % identity NCBI Description (X96932) PS60 [Nicotiana tabacum] Seq. No. 264209 6745 1.R1011 Contig ID 5'-most EST wyr700242518.hl BLASTX Method q4049341 NCBI GI BLAST score 274 1.0e-23 E value Match length 253 32 % identity NCBI Description (AL034567) putative protein [Arabidopsis thaliana] Seq. No. 264210 Contig ID 6745 2.R1011 LIB3078-007-Q1-K1-F10 5'-most EST Method BLASTX NCBI GI q4049341 BLAST score 146 9.0e-09 E value Match length 131 33 % identity NCBI Description (AL034567) putative protein [Arabidopsis thaliana] Seq. No. 264211

Contig ID 204211 6746_1.R1011

5'-most EST LIB3078-014-Q1-K1-C11

Method BLASTX NCBI GI g2245108 BLAST score 538



E value 2.0e-54 Match length 229 48 % identity

NCBI Description (Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No. 264212 Contig ID 6746 2.R1011

5'-most EST uC-zmroteosinte040b11b1

Method BLASTX NCBI GI g2245108 BLAST score 287 E value 1.0e-25 Match length 121

46 % identity

NCBI Description (Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No. 264213 6748 1.R1011 Contig ID 5'-most EST ymt700220425.hl

BLASTX Method NCBI GI q3328221 BLAST score 1018 1.0e-111 E value Match length 260 77 % identity

(AF076920) thioredoxin peroxidase [Secale cereale] NCBI Description

Seq. No. 264214

Contig ID 6749 1.R1011 5'-most EST wyr700243968.h1

Method BLASTX NCBI GI q1655653 197 BLAST score E value 1.0e-14 149 Match length

% identity 34

NCBI Description (Z81368) hypothetical protein Rv2406c [Mycobacterium

tuberculosis]

264215 Seq. No.

6749 2.R1011 Contig ID

5'-most EST uC-zmflmo17030b04b1

Method BLASTX NCBI GI g1655653 147 BLAST score 5.0e-09 E value 94 Match length 38 % identity

(Z81368) hypothetical protein Rv2406c [Mycobacterium NCBI Description

tuberculosis]

264216 Seq. No. Contig ID 6749 4.R1011

LIB3137-029-01-K1-A2 5'-most EST

Seq. No. 264217 6749 5.R1011 Contig ID



uC-zmflmo17258e07b1 5'-most EST BLASTN Method NCBI GI q3821780 BLAST score 36 E value 1.0e-10 46 Match length 66 % identity NCBI Description Xenopus laevis cDNA clone 27A6-1 264218 Seq. No. 6749 6.R1011 Contig ID uC-zmroteosinte044d04b2 5'-most EST 264219 Seq. No. 6751 1.R1011 Contig ID 5'-most EST LIB3069-039-Q1-K1-E1 Method BLASTX NCBI GI g473949 BLAST score 412 6.0e-40 E value Match length 232 % identity 40 NCBI Description (D29958) KIAA0116 [Homo sapiens] 26422€ Seq. No. Contig ID 6751 2.R1011 5'-most EST LIB3078-013-Q1-K1-H5 264221 Seq. No. 6751 3.R1011 Contig ID 5'-most EST xjt700093615.h1 264222 Seq. No. Contig ID 6754 1.R1011 LIB3078-013-Q1-K1-H8 5'-most EST Seq. No. 264223 Contig ID 6757 1.R1011 LIB3060-048-Q1-K1-A4 5'-most EST Method BLASTX NCBI GI g1402877 BLAST score 576 5.0e-59 E value Match length 186 64 % identity (X98130) unknown [Arabidopsis thaliana] NCBI Description >gi 1495257 emb CAA66117 (X97485) orf03 [Arabidopsis thaliana] 264224 Seq. No. Contig ID 6759 1.R1011

5'-most EST LIB3060-013-Q1-K1-F5

Method BLASTX NCBI GI g1171642 BLAST score 592 2.0e-61 E value Match length 170



% identity 66

NCBI Description PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK

>gi_481206_pir__ \$38326 protein kinase - Arabidopsis
thaliana >gi_166809 (L07248) protein kinase [Arabidopsis

thaliana]

 Seq. No.
 264225

 Contig ID
 6760_1.R1011

 5'-most EST
 fwa700099230.h1

Method BLASTX
NCBI GI g131225
BLAST score 803
E value 1.0e-85
Match length 212
% identity 75

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT

V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein

precursor - barley >gi_167087 (M61146) photosystem I

hydrophobic protein [Hordeum vulgare]

5'-most EST LIB3062-039-Q1-K1-E6

Method BLASTX
NCBI GI g131225
BLAST score 533
E value 2.0e-54
Match length 125
% identity 86

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT

V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein

precursor - barley >gi_167087 (M61146) photosystem I

hydrophobic protein [Hordeum vulgare]

Seq. No. 264227

Contig ID 6760_3.R1011

5'-most EST LIB3060-028-Q1-K1-E12

Method BLASTX
NCBI GI g131225
BLAST score 287
E value 1.0e-25
Match length 89
% identity 74

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT

V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K_protein

precursor - barley >gi_167087 (M61146) photosystem I

hydrophobic protein [Hordeum vulgare]

Seq. No. 264228 Contig ID 6760_4.R1011

5'-most EST LIB84-002-Q1-E1-F5

Method BLASTX
NCBI GI g131225
BLAST score 310
E value 2.0e-28
Match length 78

Match length 78 % identity 74



NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir_A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No. 264229

Contig ID 6764_1.R1011

5'-most EST LIB3059-059-Q1-K1-E7

Method BLASTX
NCBI GI g2582381
BLAST score 444
E value 1.0e-43
Match length 169
% identity 56

NCBI Description (AF021220) cation-chloride co-transporter [Nicotiana

tabacum]

Seq. No. 264230

Contig ID 6765_1.R1011 5'-most EST xsy700214542.h1

Seq. No. 264231

Contig ID 6770 1.R1011

5'-most EST uC-zmrob73033d09b1

Method BLASTX
NCBI GI g2213615
BLAST score 523
E value 5.0e-53
Match length 195

% identity 51

NCBI Description (AC000103) F21J9.9 [Arabidopsis thaliana]

 Seq. No.
 264232

 Contig ID
 6771_1.R1011

 5'-most EST
 gct701174519.h1

Seq. No. 264233 Contig ID 6772 1.R1011

5'-most EST LIB3078-013-Q1-K1-G5

Method BLASTX
NCBI GI g2736147
BLAST score 394
E value 4.0e-38
Match length 93
% identity 73

NCBI Description (AF021804) fatty acid hydroxylase Fahlp [Arabidopsis

thaliana] >gi_3132481 (AC003096) fatty acid hydroxylase,

FAH1 [Arabidopsis thaliana]

Seq. No. 264234

Contig ID 6774 1.R1011

5'-most EST LIB189-032-Q1-E1-D4

Seq. No. 264235 Contig ID 6776 1.R1011

5'-most EST LIB3078-013-Q1-K1-G9



264236 Seq. No.

Contig ID 6780 1.R1011 5'-most EST xyt700343445.h1

Seq. No. 264237

6780 2.R1011 Contig ID

5'-most EST LIB189-028-01-E1-H7

Method BLASTX a3021713 NCBI GI 306 BLAST score 1.0e-27 E value 145 Match length 46 % identity

(AB012605) MRL [Oryza sativa] NCBI Description

264238 Seq. No.

Contig ID 6780 3.R1011

5'-most EST LIB3118-012-Q1-K1-B11

264239 Seq. No.

6780 4.R1011 Contig ID

5'-most EST LIB3078-016-Q1-K1-F12

Seq. No. 264240

Contig ID 6780 7.R1011 5'-most EST uer700581988.h1

264241 Seq. No.

Contig ID 6782 1.R1011 5'-most EST ypc700802144.h1

Method BLASTX NCBI GI q136640 BLAST score 806 E value 5.0e-86 Match length 152 % identity 97

UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN NCBI Description

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 170785 (M62720)

ubiquitin carrier protein [Triticum aestivum]

264242 Seq. No.

6782 2.R1011 Contig ID $dyk7\overline{0}0103371.h1$ 5'-most EST

Method BLASTX NCBI GI g136640 BLAST score 807 E value 3.0e-86 Match length 152 98 % identity

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 170785 (M62720)

ubiquitin carrier protein [Triticum aestivum]

Seq. No. 264243

6782 3.R1011 Contig ID $qmh7\overline{0}0025906.f1$ 5'-most EST

Method BLASTX



NCBI GI g4538975 BLAST score 318 E value 1.0e-28 Match length 157 % identity 50

NCBI Description (AL049487) putative protein [Arabidopsis thaliana]

Seq. No. 264244

Contig ID 6782 4.R1011 5'-most EST uwc700155418.h1

Method BLASTX
NCBI GI g136640
BLAST score 350
E value 5.0e-33
Match length 70
% identity 97

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 170785 (M62720)

ubiquitin carrier protein [Triticum aestivum]

Seq. No. 264245 Contig ID 6782 5.R1011

5'-most EST LIB3136-014-Q1-K2-F2

Method BLASTX
NCBI GI g136640
BLAST score 536
E value 1.0e-54
Match length 102
% identity 97

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 170785 (M62720)

ubiquitin carrier protein [Triticum aestivum]

Seq. No. 264246

Contig ID 6782 6.R1011

5'-most EST LIB3156-004-Q1-K1-D1

Method BLASTX
NCBI GI g729252
BLAST score 522
E value 5.0e-53
Match length 134
% identity 72

NCBI Description CYTOCHROME B5 >gi 167140 (M87514) cytochrome b-5 [Brassica

oleracea] >gi 384338 prf 1905426A cytochrome b5 [Brassica

oleracea]

Seq. No. 264247 Contig ID 6782 7.R1011

5'-most EST uC-zmflb73017d07b1

Method BLASTX
NCBI GI g136640
BLAST score 402
E value 4.0e-39
Match length 79
% identity 92

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_170785 (M62720)



ubiquitin carrier protein [Triticum aestivum]

Seq. No. 264248 Contig ID 6782 8.R1011 5'-most EST wty700164537.hl Method BLASTX NCBI GI q729252 531 BLAST score 5.0e-54E value 134 Match length 73 % identity CYTOCHROME B5 >gi 167140 (M87514) cytochrome b-5 [Brassica NCBI Description oleracea] >gi 384338 prf 1905426A cytochrome b5 [Brassica oleracea] 264249 Seq. No. 6782 15.R1011 Contig ID 5'-most EST tfd700570122.h1 BLASTX Method q136640 NCBI GI 402 BLAST score 2.0e-39 E value Match length 74 99 % identity UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN NCBI Description LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_170785 (M62720) ubiquitin carrier protein [Triticum aestivum] 264250 Seq. No. 6782 18.R1011 Contig ID $wty7\overline{0}0167059.h1$ 5'-most EST BLASTN Method NCBI GI g4096785 BLAST score 50 E value 5.0e-19 Match length 50 % identity 100 NCBI Description Zea mays NADP-malic enzyme root isoform mRNA, complete cds Seq. No. 264251 6782 19.R1011 Contig ID 5'-most EST nbm700470832.h1 Seq. No. 264252 6782 20.R1011 Contig ID uC-zmflmo17217c08b1 5'-most EST Method BLASTX NCBI GI q4538975 BLAST score 262 E value 1.0e-22 58 Match length % identity 84 (AL049487) putative protein [Arabidopsis thaliana] NCBI Description 264253 Seq. No.

6782 21.R1011

LIB3\overline{1}37-015-Q1-K1-A8

Contig ID

5'-most EST



Method BLASTX g4538975 NCBI GI BLAST score 262 9.0e-23 E value Match length 94 60 % identity (AL049487) putative protein [Arabidopsis thaliana] NCBI Description 264254 Sea. No. 6782 23.R1011 Contig ID $dyk7\overline{0}0103415.h1$ 5'-most EST BLASTX Method q729252 NCBI GI BLAST score 257 2.0e-22 E value Match length 63 % identity 71 CYTOCHROME B5 >qi 167140 (M87514) cytochrome b-5 [Brassica NCBI Description oleracea] >gi_384338_prf__1905426A cytochrome b5 [Brassica oleracea] 264255 Seq. No. Contig ID 6783 1.R1011 LIB3062-042-Q1-K1-C2 5'-most EST Seq. No. 264256 6788 2.R1011 Contig ID 5'-most EST nbm700473474.h1264257 Seq. No. 6791 1.R1011 Contig ID LIB3150-091-P1-N1-E9 5'-most EST BLASTX Method g4539545 NCBI GI 1130 BLAST score 1.0e-124 E value 246 Match length % identity 87 NCBI Description (Y16644) PRCI [Nicotiana tabacum] 264258 Seq. No. 6791 2.R1011 Contig ID LIB3068-034-Q1-K1-H7 5'-most EST BLASTX Method q4539545 NCBI GI 274 BLAST score E value 3.0e-24 Match length 66 % identity 82 NCBI Description (Y16644) PRCI [Nicotiana tabacum] Seq. No. 264259

Contig ID 6795_1.R1011 5'-most EST ntr700073918.h1

Method BLASTX
NCBI GI g1729927
BLAST score 1045

BLAST score

% identity

NCBI Description

E value Match length 1.0e-109

thaliana]

316



```
E value
                  1.0e-114
                  474
Match length
% identity
                  46
                  QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE
NCBI Description
                  TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi_940182
                  (U30888) tRNA-Guanine Transglycosylase [Homo sapiens]
                  264260
Seq. No.
                  6795 2.R1011
Contig ID
                  fC-zmst700619965a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1729927
BLAST score
                  142
                  4.0e-17
E value
Match length
                  68
                  66
% identity
                  QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE
NCBI Description
                  TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi 940182
                   (U30888) tRNA-Guanine Transglycosylase [Homo sapiens]
                  264261
Seq. No.
                  6799 1.R1011
Contig ID
                  LIB3150-094-P1-N1-D2
5'-most EST
Method
                  BLASTX
NCBI GI
                   q400986
BLAST score
                   676
                  8.0e-71
E value
Match length
                  179
% identity
                  74
                  50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15)
NCBI Description
                   >gi_81947_pir__S18001 ribosomal protein L15 precursor,
                   chloroplast - garden pea (fragment) >gi_20867_emb_CAA77595_
                   (Z11510) Plastid ribosomal protein CL15 [Pisum sativum]
                   264262
Seq. No.
                   6802 1.R1011
Contig ID
5'-most EST
                  LIB3079-013-Q1-K1-A8
Method
                   BLASTX
NCBI GI
                   a3063446
BLAST score
                   658
                   7.0e-69
E value
Match length
                   206
% identity
                   66
                  (AC003981) F22013.8 [Arabidopsis thaliana]
NCBI Description
                   264263
Seq. No.
                   6804_2.R1011
Contig ID
                   yyf7\overline{0}0347853.h1
5'-most EST
Method
                   BLASTX
                   q2275202
NCBI GI
                   985
```

36678

(ACO02337) acyl-CoA synthetase isolog [Arabidopsis



264264 Seq. No. 6804 3.R1011 Contig ID LIB83-015-Q1-E1-F1 5'-most EST Method BLASTX q2275202 NCBI GI 1030 BLAST score 1.0e-112 E value 324 Match length 58 % identity (ACO02337) acyl-CoA synthetase isolog [Arabidopsis NCBI Description thaliana] 264265 Seq. No. 6805 1.R1011 Contig ID LIB3060-013-Q1-K1-C9 5'-most EST 264266 Seq. No. Contiq ID 6805 2.R1011 LIB143-064-Q1-E1-H11 5'-most EST 264267 Seq. No. 6805 4.R1011 Contig ID nbm700464945.h15'-most EST 264268 Seq. No. 6807 1.R1011 Contig ID LIB3062-025-Q1-K1-H9 5'-most EST Method BLASTX q4336747 NCBI GI 552 BLAST score 9.0e-57 E value Match length 150 % identity 71 NCBI Description (AF104924) unconventional myosin heavy chain [Zea mays] 264269 Seq. No. Contig ID 6808_1.R1011 5'-most EST uC-zmflb73362g02a2 BLASTX Method q2865175 NCBI GI BLAST score 631 2.0e-65 E value 170 Match length % identity NCBI Description (AB010945) AtRer1A [Arabidopsis thaliana] Seq. No. 264270 Contig ID 6810 1.R1011 5'-most EST LIB3078-037-Q1-K1-F3 BLASTX Method NCBI GI q1617206 BLAST score 263

E value 1.0e-22 79 Match length

66 % identity

NCBI Description (Z72489) CP12 [Pisum sativum]



Seq. No. 264271 6810 2.R1011 Contig ID 5'-most EST LIB3115-038-P1-K2-F4 Method BLASTX NCBI GI q1617206 BLAST score 268 E value 2.0e-23 Match length 79 67 % identity (Z72489) CP12 [Pisum sativum] NCBI Description Seq. No. 264272 Contig ID 6812 1.R1011 LIB3078-013-Q1-K1-B3

5'-most EST Method BLASTX NCBI GI q3386621 BLAST score 613 E value 1.0e-63 Match length 167 % identity 69

(AC004665) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 264273 6813 1.R1011 Contig ID

5'-most EST LIB3136-018-Q1-K1-B2

Method BLASTX g4490313 NCBI GI

BLAST score 620 E value 2.0e-64 Match length 212 60 % identity

(AL035678) putative protein [Arabidopsis thaliana] NCBI Description

264274 Seq. No. Contig ID 6817 1.R1011 5'-most EST uC-zmflb73217g03b2

Seq. No. 264275 6817 2.R1011 Contig ID

5'-most EST nbm700466101.h1

264276 Seq. No.

6817 3.R1011 Contig ID 5'-most EST wty700168346.hl

264277 Seq. No.

6817_4.R1011 Contig ID

5'-most EST uC-zmflb73409h07a1

264278 Seq. No. Contig ID

6818 1.R1011

5'-most EST uC-zmflb73265f12b4

Method BLASTX NCBI GI q3789952 BLAST score 1087 E value 1.0e-119 Match length 244



% identity (AF094775) chlorophyll a/b-binding protein presursor [Oryza NCBI Description sativa] 264279 Seq. No. 6818 2.R1011 Contig ID 5'-most EST LIB3078-009-Q1-K1-B9 Method BLASTX NCBI GI q100196 BLAST score 410 7.0e-40E value 91 Match length % identity 80 chlorophyll a/b-binding protein (cab-11) - tomato NCBI Description 264280 Seq. No. Contig ID 6818 3.R1011 5'-most EST xjt700096782.h1 Method BLASTX NCBI GI q3789952 BLAST score 508 1.0e-51 E value Match length 127 % identity 80 (AF094775) chlorophyll a/b-binding protein presursor [Oryza NCBI Description sativa] Seq. No. 264281 Contig ID 6818 4.R1011 clt700042015.f1 5'-most EST BLASTX Method g3789952 NCBI GI BLAST score 620 1.0e-64 E value 162 Match length 75 % identity (AF094775) chlorophyll a/b-binding protein presursor [Oryza NCBI Description sativa] 264282 Seq. No. 6818 5.R1011 Contig ID LIB3060-052-Q1-K1-D8 5'-most EST Method BLASTX q3789952 NCBI GI BLAST score 456 2.0e-45 E value 132 Match length % identity (AF094775) chlorophyll a/b-binding protein presursor [Oryza NCBI Description sativa] 264283 Seq. No. Contig ID 6818 7.R1011 LIB3078-011-Q1-K1-C9 5'-most EST

5'-most EST LIB3078-0 Method BLASTX NCBI GI q3789952

BLAST score 252



```
2.0e-21
E value
Match length
                   63
% identity
                   76
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                   sativa]
                   264284
Seq. No.
                   6818 10.R1011
Contig ID
                   fwa700097279.h1
5'-most EST
                   BLASTX
Method
                   g100196
NCBI GI
BLAST score
                   683
                   6.0e-72
E value
                   184
Match length
% identity
                   71
                   chlorophyll a/b-binding protein (cab-11) - tomato
NCBI Description
Seq. No.
                   264285
                   6821 1.R1011
Contig ID
                   LIB36-022-Q1-E1-B9
5'-most EST
                   264286
Seq. No.
Contig ID
                   6823 1.R1011
                   LIB3060-019-Q1-K1-F3
5'-most EST
Method
                   BLASTX
                   g2664210
NCBI GI
                   1078
BLAST score
-E value
                   1.0e-118
Match length
                   268
                   78
% identity
                   (AJ222644) asparaginyl-tRNA synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   264287
Seq. No.
                   6824 1.R1011
Contig ID
                   uC-z\overline{m}roteosinte073e01b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3287693
                   1585
BLAST score
                   1.0e-177
E value
Match length
                   340
                   86
% identity
                   (AC003979) Similar to LIM17 gene product gb 1653769 from
NCBI Description
                   the genome of Synechocystis sp. gb_D90916. [Arabidopsis
                   thaliana]
Seq. No.
                   264288
                   6828_1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17015e10b1
Method
                   BLASTX
```

Method BLASTX
NCBI GI g4455274
BLAST score 1220
E value 1.0e-134
Match length 499
% identity 63

NCBI Description (AL035527) spliceosome associated protein-like [Arabidopsis

thaliana]



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264289
Seq. No.
                  6830 1.R1011
Contig ID
5'-most EST
                  yyf700347842.h1
                  BLASTX
Method
                  q2462911
NCBI GI
BLAST score
                  1224
                  1.0e-135
E value
Match length
                  254
                  87
% identity
                  (Z83832) UDP-glucose:sterol glucosyltransferase [Avena
NCBI Description
                  sativa]
                  264290
Seq. No.
Contig ID
                   6833 1.R1011
                   uC-zmflmo17289h03b1
5'-most EST
Seq. No.
                   264291
                   6834 1.R1011
Contig ID
                   LIB3078-013-Q1-K1-A6
5'-most EST
                   264292
Seq. No.
Contig ID
                   6836 1.R1011
                   tfd700571737.h1
5'-most EST
                   264293
Seq. No.
                   6837 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73222g10b1
Method
                   BLASTX
                   g2109457
NCBI GI
                   602
BLAST score
                   2.0e-62
E value
                   166
Match length
% identity
                   69
NCBI Description (AF001501) chitinase [Oryza sativa]
                   264294
Seq. No.
Contig ID
                   6837 2.R1011
                   uC-zmflb73179a10b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3258456
BLAST score
                   612
                   2.0e-63
E value
                   206
Match length
                   60
% identity
NCBI Description (AB015655) chitinase [Cucurbita sp.]
                   264295
Seq. No.
                   6837_3.R1011
Contig ID
                   uC-zmflmo17301c12b1
5'-most EST
Method
                   BLASTX
                   q2109457
NCBI GI
BLAST score
                   668
                   7.0e-70
E value
                   256
Match length
% identity
```

36683

NCBI Description (AF001501) chitinase [Oryza sativa]



```
264296
Seq. No.
Contig ID
                  6837 4.R1011
5'-most EST
                  LIB3060-034-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  q3370780
BLAST score
                  1020
                  1.0e-111
E value
Match length
                  226
% identity
                  81
                  (AB016497) chitinase [Oryza sativa]
NCBI Description
                  264297
Seq. No.
Contig ID
                  6838 1.R1011
5'-most EST
                  LIB3067-057-Q1-K1-B4
Method
                  BLASTX
NCBI GI
                  g2492512
BLAST score
                  290
E value
                  5.0e-27
Match length
                  219
% identity
                  41
                  CELL DIVISION PROTEIN FTSH HOMOLOG 3
NCBI Description
                  >gi_1652556_dbj_BAA17477_ (D90906) cell division protein
                  FtsH [Synechocystis sp.]
                  264298
Seq. No.
Contig ID
                   6844 1.R1011
5'-most EST
                  LIB3150-033-Q1-N1-B8
Method
                  BLASTX
                  g2760843
NCBI GI
                  301
BLAST score
                  3.0e-27
E value
                  121
Match length
% identity
                  52
                  (AC003105) unknown protein [Arabidopsis thaliana]
NCBI Description
                  264299
Seq. No.
                   6849 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17236f02b1
Method
                  BLASTX
NCBI GI
                  g4539348
                  597
BLAST score
                   2.0e-61
E value
Match length
                  249
                   49
% identity
                  (AL035539) putative pollen allergen [Arabidopsis thaliana]
NCBI Description
                  264300
Seq. No.
                   6849 2.R1011
Contig ID
5'-most EST
                  uC-zmflb73013h08b1
                  BLASTX
Method
                  g4539348
NCBI GI
BLAST score
                  193
E value
                  1.0e-14
                  117
Match length
% identity
                  (AL035539) putative pollen allergen [Arabidopsis thaliana]
NCBI Description
```



Seq. No. 264301

Contig ID 6849 3.R1011

5'-most EST LIB3157-008-Q1-K1-A3

Method BLASTX
NCBI GI g4539348
BLAST score 240
E value 3.0e-20
Match length 74

Match length 74 % identity 61

NCBI Description (AL035539) putative pollen allergen [Arabidopsis thaliana]

Seq. No. 264302

Contig ID 6855_1.R1011 5'-most EST qmh700029516.f1

Method BLASTX
NCBI GI g548851
BLAST score 513
E value 6.0e-52
Match length 114
% identity 89

NCBI Description 40S RIBOSOMAL PROTEIN S20 >gi_481226_pir_S38356 ribosomal

protein S20 - rice >gi_391875_dbj_BAAO2157_ (D12632) 40S

subunit ribosomal protein [Oryza sativa]

 Seq. No.
 264303

 Contig ID
 6855_2.R1011

 5'-most EST
 pwr700448603.h1

Method BLASTX
NCBI GI g548851
BLAST score 143
E value 2.0e-09
Match length 27
% identity 93

NCBI Description 40S RIBOSOMAL PROTEIN S20 >gi_481226_pir__S38356 ribosomal

protein S20 - rice >gi_391875_dbj_BAA02157_ (D12632) 40S

subunit ribosomal protein [Oryza sativa]

Seq. No. 264304 Contig ID 6856 1.R1011

5'-most EST LIB3078-012-Q1-K1-A11

Method BLASTX
NCBI GI g4314390
BLAST score 258
E value 5.0e-22
Match length 96
% identity 50

NCBI Description (AC006232) putative calcium binding protein [Arabidopsis

thaliana]

Seq. No. 264305

Contig ID 6857_1.R1011 5'-most EST vux700156488.h1

Method BLASTX
NCBI GI g113165
BLAST score 460
E value 1.0e-45



Match length 134 % identity 76

NCBI Description ACYL CARRIER PROTEIN I PRECURSOR (ACP I)

>gi_625337_pir_ AYBH acyl carrier protein I precursor barley >gi_166967 (M58753) acyl carrier protein I [Hordeum

vulgare] >gi_166973 (M24425) acyl carrier protein I

precursor [Hordeum vulgare]

Seq. No. 264306

Contig ID 6861 1.R1011

5'-most EST LIB3078-012-Q1-K1-B3

Seq. No. 264307

Contig ID 6861_4.R1011 5'-most EST xsy700209696.h1

Seq. No. 264308

Contig ID 6864 1.R1011

5'-most EST LIB3116-002-Q1-K1-A5

Method BLASTX
NCBI GI 94091008
BLAST score 1388
E value 1.0e-157
Match length 352
% identity 81

NCBI Description (AF040700) methionyl-tRNA synthetase [Oryza sativa]

Seq. No. 264309

Contig ID 6864 2.R1011

5'-most EST LIB3150-109-P2-K1-B6

Method BLASTX
NCBI GI g4091008
BLAST score 400
E value 1.0e-38
Match length 84

% identity 89

NCBI Description (AF040700) methionyl-tRNA synthetase [Oryza sativa]

Seq. No. 264310

Contig ID 6864_4.R1011 5'-most EST nwy700447195.h1

Method BLASTX
NCBI GI 94091008
BLAST score 291
E value 2.0e-26
Match length 69
% identity 87

NCBI Description (AF040700) methionyl-tRNA synthetase [Oryza sativa]

Seq. No. 264311

Contig ID 6864_5.R1011

5'-most EST uC-zmflb73210q06b1

Method BLASTX
NCBI GI g4091008
BLAST score 272
E value 4.0e-24
Match length 102

BLAST score

E value

447

6.0e-44



```
% identity
                  (AF040700) methionyl-tRNA synthetase [Oryza sativa]
NCBI Description
Seq. No.
                  264312
                  6864 6.R1011
Contig ID
                  nbm700466061.h1
5'-most EST
                  BLASTX
Method
                  q4091008
NCBI GI
BLAST score
                  486
                  3.0e-49
E value
Match length
                  106
                  88
% identity
                  (AF040700) methionyl-tRNA synthetase [Oryza sativa]
NCBI Description
                  264313
Seq. No.
                   6867 1.R1011
Contig ID
5'-most EST
                  wen700334922.hl
                  BLASTX
Method
NCBI GI
                   q2505872
BLAST score
                   191
                   7.0e-14
E value
Match length
                   184
                   32
% identity
                  (Y12227) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   264314
Seq. No.
Contig ID
                   6868 1.R1011
5'-most EST
                   LIB3060-046-Q1-K1-B9
Method
                   BLASTX
                   q72689
NCBI GI
                   1117
BLAST score
                   1.0e-122
E value
Match length
                   236
                   92
% identity
                   NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain ndhK -
NCBI Description
                   maize chloroplast >gi_12427_emb_CAA35482_ (X17438) PSII-G
                   protein (AA 1 - 248) [Zea mays] >gi_552735 (M12704) PSII-G
                   [Zea mays]
                   264315
Seq. No.
                   6869 1.R1011
Contig ID
                   LIB3078-011-01-K1-G3
5'-most EST
                   BLASTX
Method
                   g1001541
NCBI GI
                   229
BLAST score
                   1.0e-18
E value
                   142
Match length
% identity
                  (D64000) ABC transporter [Synechocystis sp.]
NCBI Description
                   264316
Seq. No.
                   6875_1.R1011
Contig ID
                   uC-zmroteosinte115g11b1
5'-most EST
Method
                   BLASTX
                   g2253411
NCBI GI
```



```
Match length
                   191
% identity
                  (AF007219) PP2A inhibitor [Tetraodon fluviatilis]
NCBI Description
                   264317
Seq. No.
                   6875 2.R1011
Contig ID
                   uC-zmflb73039e03b1
5'-most EST
Method
                   BLASTX
                   q2253411
NCBI GI
BLAST score
                   211
                   1.0e-22
E value
Match length
                   122
% identity
                   43
                   (AF007219) PP2A inhibitor [Tetraodon fluviatilis]
NCBI Description
                   264318
Seq. No.
                   6875 3.R1011
Contig ID
5'-most EST
                   uC-zmflb73270e02a1
                   264319
Seq. No.
                   6877 1.R1011
Contig ID
                   LIB3078-011-Q1-K1-H12
5'-most EST
                   264320
Seq. No.
                   6879 1.R1011
Contig ID
                   uC-zmroB73020a12b1
5'-most EST
                   BLASTX
Method
                   q2921304
NCBI GI
BLAST score
                   1775
                   0.0e+00
E value
                   363
Match length
                   95
% identity
                   (AF033496) herbicide safener binding protein [Zea mays]
NCBI Description
                   264321
Seq. No.
                   6879 2.R1011
Contig ID
                   uC-z\overline{m}flb73180a04a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2921304
                   1595
BLAST score
                   1.0e-178
E value
                   363
Match length
                    87
% identity
                   (AF033496) herbicide safener binding protein [Zea mays]
NCBI Description
                    264322
Seq. No.
                    6879_3.R1011
Contig ID
                    uC-zmroteosinte045c08b2
5'-most EST
                    BLASTX
Method
                    g2921304
NCBI GI
                    444
BLAST score
                    6.0e-44
E value
Match length
                    117
```

Seq. No. 264323

75

% identity

NCBI Description

36688

(AF033496) herbicide safener binding protein [Zea mays]



```
6879 4.R1011
 Contig ID
                    LIB3068-025-Q1-K1-C6
 5'-most EST
                    BLASTX
 Method
                    g2921304
 NCBI GI
                    306
 BLAST score
                    7.0e-28
 E value
                    58
 Match length
                    100
 % identity
                    (AF033496) herbicide safener binding protein [Zea mays]
 NCBI Description
                    264324
 Seq. No.
                    6879 9.R1011
 Contig ID
                    uC-zmromo17031g03a1
 5'-most EST
                    BLASTN
 Method
                    g2921303
 NCBI GI
 BLAST score
                     315
                     1.0e-177
 E value
 Match length
                     335
                     99
 % identity
                    Zea mays herbicide safener binding protein (SBP1) mRNA,
 NCBI Description
                     complete cds
                     264325
 Seq. No.
                     6879 10.R1011
 Contig ID
                     \mathtt{uC-zm} \mathtt{f1b73260f06a1}
 5'-most EST
                     {\tt BLASTN}
 Method
                     g2921303
 NCBI GI
 BLAST score
                     184
                     8.0e-99
 E value
                     529
 Match length
                     95
 % identity
                     Zea mays herbicide safener binding protein (SBP1) mRNA,
 NCBI Description
                     complete cds
                     264326
 Seq. No.
                     6879_14.R1011
 Contig ID
                     yyf700351238.hl
  5'-most EST
 Method
                     BLASTN
                     g2921303
 NCBI GI
                     161
 BLAST score
                     2.0e-85
 E value
 Match length
                     225
                     93
  % identity
                     Zea mays herbicide safener binding protein (SBP1) mRNA,
  NCBI Description
                     complete cds
  Seq. No.
                     264327
  Contig ID
                     6882 1.R1011
  5'-most EST
                     LIB3078-012-Q1-K1-H4
  Method
                     BLASTX
                     q3763916
  NCBI GI
                     483
- BLAST score
  E value
                     3.0e-48
  Match length
                     191
                     52
  % identity
                     (AC004450) unknown protein [Arabidopsis thaliana]
  NCBI Description
```

>gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown

Contig ID

5'-most EST



protein [Arabidopsis thaliana]

```
Seq. No.
                   264328
                   6882 2.R1011
Contig ID
                   uC-zmflb73196f08b1
5'-most EST
                   BLASTX
Method
                   q3763916
NCBI GI
                   726
BLAST score
                   1.0e-76
E value
                   343
Match length
                   45
% identity
                   (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4531439 gb AAD22124.1 AC006224_6 (AC006224) unknown
                   protein [Arabidopsis thaliana]
                   264329
Seq. No.
                   6882 4.R1011
Contig ID
                   xmt700264033.h1
5'-most EST
                   BLASTX
Method
                   g3763916
NCBI GI
                   249
BLAST score
                   1.0e-31
E value
                   258
Match length
                   34
% identity
                   (AC004450) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4531439 gb AAD22124.1 AC006224 6 (AC006224) unknown
                   protein [Arabidopsis thaliana]
                   264330
Seq. No.
                   6883 1.R1011
Contig ID
                   LIB3078-011-Q1-K1-E4
5'-most EST
                   BLASTX
Method
                   g2118425
NCBI GI
                   335
BLAST score
                   3.0e-31
E value
                   73
Match length
                   92
% identity
NCBI Description
                   subtilisin/chymotrypsin inhibitor - maize
                   >gi_475253_emb_CAA55588_ (X78988) proteinase inhibitor [Zea
                   mays] >gi_475922_emb_CAA49593_ (X69972) proteinase inhibitor [Zea mays] >gi_559538_emb_CAA57677_ (X82187)
                   substilin /chymotrypsin-like inhibitor [Zea mays]
                   264331
Seq. No.
                   6883 3.R1011
Contig ID
                   uer700577208.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q475252
BLAST score
                   183
                   1.0e-98
E value
                   257
Match length
                   99
% identity
NCBI Description Z.mays MPI gene
Seq. No.
                    264332
```

6884 1.R1011

LIB3137-023-Q1-K1-H5



```
Method
                  BLASTX
                  g2894534
NCBI GI
BLAST score
                  1374
                  1.0e-152
E value
Match length
                  285
                  92
% identity
                  (AJ224327) aquaporin [Oryza sativa]
NCBI Description
                  264333
Seq. No.
                  6885 1.R1011
Contig ID
                  LIB3060-015-Q1-K1-H1
5'-most EST
                  264334
Seq. No.
                  6887 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17129e02a1
Method
                  BLASTX
                  q3288883
NCBI GI
BLAST score
                  214
                  1.0e-16
E value
                  114
Match length
                   48
% identity
                  (AB015431) SAR DNA binding protein [Oryza sativa]
NCBI Description
                   264335
Seq. No.
                   6887 2.R1011
Contig ID
                   uC-zmrob73006g11b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3288883
BLAST score
                   2172
                   0.0e + 00
E value
                   484
Match length
% identity
                   90
                  (AB015431) SAR DNA binding protein [Oryza sativa]
NCBI Description
                   264336
Seq. No.
                   6887 4.R1011
Contig ID
5'-most EST
                   yyf700352360.hl
                   BLASTX
Method
NCBI GI
                   g3288883
BLAST score
                   343
                   3.0e-32
E value
Match length
                   94
% identity
                   80
                  (AB015431) SAR DNA binding protein [Oryza sativa]
NCBI Description
                   264337
Seq. No.
Contig ID
                   6889 1.R1011
5'-most EST
                   LIB3078-011-Q1-K1-G2
Seq. No.
                   264338
Contig ID
                   6889 2.R1011
```

Seq. No. 264339 Contig ID 6889 3.R1011

5'-most EST

5'-most EST LIB3078-025-Q1-K1-A10

LIB3159-008-Q1-K1-A9



 Seq. No.
 264340

 Contig ID
 6889_4.R1011

 5'-most EST
 pwr700451528.h1

Seq. No. 264341 Contig ID 6889_5.R1011 5'-most EST nwy700447379.h1

Seq. No. 264342 Contig ID 6890_1.R1011

5'-most EST LIB3078-011-Q1-K1-G11

5'-most EST LIB83-009-Q1-E1-A12

Seq. No. 264344 Contig ID 6891_1.R1011 5'-most EST zuv700354470.h1

Method BLASTX
NCBI GI g3063450
BLAST score 490
E value 5.0e-49
Match length 176
% identity 55

NCBI Description (AC003981) F22013.12 [Arabidopsis thaliana]

Seq. No. 264345

Contig ID 6893_1.R1011

5'-most EST LIB3116-004-Q1-K2-C2

Seq. No. 264346 Contig ID 6893_2.R1011 5'-most EST wty700163218.h1

Seq. No. 264347

Contig ID 6894_1.R1011

5'-most EST LIB3078-011-Q1-K1-D1

Seq. No. 264348

Contig ID 6904_1.R1011

5'-most EST LIB3078-011-Q1-K1-D8

Seq. No. 264349

Contig ID 6912_1.R1011

5'-most EST LIB3078-011-Q1-K1-C10

Method BLASTX
NCBI GI g1172861
BLAST score 655
E value 1.0e-68
Match length 139
% identity 92

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR

(RUBISCO LARGE SUBUNIT) >gi_1363613_pir__S58560

ribulose-bisphosphate carboxylase ($\overline{\text{EC}}$ 4.1.1.39) large chain

- maize chloroplast >gi_18036_emb_CAA78027_ (Z11973)

Ribulose bisphosphate carboxylase [Zea mays]



>gi_902230_emb_CAA60294_ (X86563) rubisco large subunit
[Zea mays]

Seq. No. 264350

Contig ID 6912_2.R1011

5'-most EST uC-zmflmo17245c08a1

Method BLASTX
NCBI GI g1172861
BLAST score 369
E value 3.0e-35
Match length 74
% identity 93

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR

(RUBISCO LARGE SUBUNIT) >gi 1363613 pir__S58560

ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain

- maize chloroplast >gi_18036_emb_CAA78027_ (Z11973)

Ribulose bisphosphate carboxylase [Zea mays]

>gi_902230_emb_CAA60294_ (X86563) rubisco large subunit

[Zea mays]

Seq. No. 264351

Contig ID 6912_4.R1011

5'-most EST LIB84-015-Q1-E1-B4

Method BLASTX
NCBI GI g131999
BLAST score 360
E value 2.0e-34
Match length 83
% identity 82

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR

(RUBISCO LARGE SUBUNIT) >gi 68146 pir RKNULT

ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - Neurachne tenuifolia chloroplast >gi_11798_emb_CAA39353_ (X55827) rubisco large subunit [Neurachne tenuifolia]

Seq. No. 264352

Contig ID 6921 1.R1011

5'-most EST LIB3115-036-P1-K2-F9

Method BLASTX
NCBI GI g2764574
BLAST score 508
E value 3.0e-51
Match length 223
% identity 46

NCBI Description (AJ001009) pore protein of 24 kD (OEP24) [Pisum sativum]

Seq. No. 264353 Contig ID 6923_1.R1011

5'-most EST LIB3078-009-Q1-K1-H3

Method BLASTX
NCBI GI g1652084
BLAST score 435
E value 1.0e-42
Match length 237
% identity 39

NCBI Description (D90902) hypothetical protein [Synechocystis sp.]



264354 Seq. No.

Contig ID 6926 1.R1011

LIB3078-009-Q1-K1-H7 5'-most EST

Method BLASTX NCBI GI q3608144 BLAST score 468 8.0e-47 E value Match length 137 % identity 59

(AC005314) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 264355

Contig ID 6927 1.R1011

5'-most EST LIB3078-009-Q1-K1-H8

264356 Seq. No.

Contig ID 6929 1.R1011

5'-most EST LIB84-008-Q1-E1-F12

Method BLASTX q1351357 NCBI GI BLAST score 418 9.0e-41 E value Match length 123 % identity 67

UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KD PROTEIN NCBI Description

(CR14) >qi 633681 emb CAA55863 (X79276)

ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No. 264357 6929 2.R1011 Contig ID ntr700075243.hl 5'-most EST

BLASTX Method g1351357 NCBI GI 330 BLAST score 1.0e-30 E value 107 Match length 60 % identity

NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KD PROTEIN

(CR14) >gi_633681_emb_CAA55863_ (X79276)

ubiquinol--cytochrome c reductase [Solanum tuberosum]

264358 Seq. No.

Contig ID 6929 3.R1011

5'-most EST uC-zmflb73221f02a2

264359 Seq. No. 6929 4.R1011 Contig ID

5'-most EST wyr700238885.h1

264360 Seq. No.

6931 1.R1011 Contig ID xyt700344105.h1 5'-most EST

Method BLASTX q3687251 NCBI GI BLAST score 518 2.0e-52 E value 144 Match length



% identity (AC005169) unknown protein [Arabidopsis thaliana] NCBI Description 264361 Seq. No. 6931 2.R1011 Contig ID 5'-most EST LIB3069-009-Q1-K1-D7 Method BLASTX g3687251 NCBI GI 503 BLAST score 1.0e-50 E value Match length 143 % identity 70 (AC005169) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 264362 Contig ID 6931 4.R1011 xsy700207465.h1 5'-most EST Method BLASTX q3687251 NCBI GI 336 BLAST score 1.0e-31 E value 84 Match length 76 % identity (AC005169) unknown protein [Arabidopsis thaliana] NCBI Description 264363 Seq. No. 6933 1.R1011 Contig ID pmx700084453.h1 5'-most EST BLASTX Method g2736155 NCBI GI 749 BLAST score 1.0e-79E value 179 Match length 78 % identity (AF022082) sulfolipid biosynthesis protein [Arabidopsis NCBI Description thaliana] >gi_3688184_emb_CAA21212_ (AL031804) sulfolipid biosynthesis protein $\overline{SQD1}$ [Arabidopsis thaliana] 264364 Seq. No. 6935 1.R1011 Contig ID LIB3115-026-P1-K1-E8 5'-most EST Method BLASTN q2446997 NCBI GI 279 BLAST score 1.0e-155 E value 333 Match length % identity 95 NCBI Description Zea mays FAD7 gene for fatty acid desaturase, complete cds

Seq. No. 264365

6936 1.R1011 Contig ID 5'-most EST pmx700084673.h1

Method BLASTX NCBI GI g4454466 BLAST score 204 E value 1.0e-15 Match length 57



% identity 65
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 264366 Contig ID 6936_2.R1011 5'-most EST zuv700352688.h1

Method BLASTX
NCBI GI 94454466
BLAST score 174
E value 3.0e-12
Match length 51

% identity 65

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 264367

Contig ID 6936_3.R1011

5'-most EST uC-zmflb73020f06b1

Seq. No. 264368

Contig ID 6937_1.R1011

5'-most EST LIB3060-035-Q1-K1-F12

Seq. No. 264369 Contig ID 6937_2.R1011

5'-most EST LIB3078-027-Q1-K1-C9

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36

Match length 36 % identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 264370

Contig ID 6941_1.R1011

5'-most EST LIB3078-009-Q1-K1-G1

Seq. No. 264371

Contig ID 6947_1.R1011

5'-most EST LIB189-004-Q1-E1-B4

Seq. No. 264372

Contig ID 6954_1.R1011

5'-most EST uC-zmflb73294g05b1

Seq. No. 264373

Contig ID 6954_2.R1011

5'-most EST LIB143-058-Q1-E1-A6

Seq. No. 264374

Contig ID 6954 3.R1011

5'-most EST LIB3115-010-Q1-K1-E2

Seq. No. 264375

Contig ID 6955_1.R1011 5'-most EST dyk700104723.h1

Method BLASTX



```
NCBI GI
                  q4006818
                  1114
BLAST score
                  1.0e-122
E value
                  343
Match length
                  63
% identity
                   (AC005970) putative translation initiation factor eIF-2B,
NCBI Description
                  alpha subunit [Arabidopsis thaliana]
                  264376
Seq. No.
                  6959 1.R1011
Contig ID
                  uC-zmflb73131a03b2
5'-most EST
                  264377
Seq. No.
                   6965 1.R1011
Contig ID
                   qw1700618506.h1
5'-most EST
Method
                  BLASTX
                  q940288
NCBI GI
BLAST score
                   385
                   1.0e-36
E value
                   162
Match length
                   49
% identity
                  (L43510) protein localized in the nucleoli of pea nuclei;
NCBI Description
                   ORF; putative [Pisum sativum]
                   264378
Seq. No.
                   6965 2.R1011
Contig ID
                   uC-zmrob73035f03a1
5'-most EST
                   264379
Seq. No.
                   6968 1.R1011
Contig ID
                   LIB36-008-Q1-E1-A8
5'-most EST
                   BLASTX
Method
                   g217909
NCBI GI
                   878
BLAST score
                   1.0e-94
E value
Match length
                   214
                   81
% identity
                  (D14044) glycolate oxidase [Cucurbita sp.]
NCBI Description
                   264380
Seq. No.
                   6969 1.R1011
Contig ID
                   LIB3061-026-Q1-K1-A8
5'-most EST
Method
                   BLASTX
NCBI GI
                   g730558
BLAST score
                   444
                   8.0e-44
E value
Match length
                   95
% identity
                   91
                   60S RIBOSOMAL PROTEIN L34 >gi 1076636_pir___S48027 ribosomal
NCBI Description
                   protein L34 - common tobacco >gi 2129964 pir S48028
                   ribosomal protein L34.e, cytosolic - common tobacco
                   >gi 436030 (L27089) 60S ribosomal protein L34 [Nicotiana
```

Seq. No. 264381 Contig ID 6969_2.R1011

[Nicotiana tabacum]

36697

tabacum] >gi_436032 (L27107) 60S ribosomal protein L34



```
5'-most EST
                  LIB3157-017-Q1-K1-E8
Seq. No.
                  264382
                  6969 3.R1011
Contig ID
                  LIB3078-051-Q1-K1-A1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q730558
                  444
BLAST score
                  6.0e-44
E value
Match length
                  95
                  91
% identity
                  60S RIBOSOMAL PROTEIN L34 >gi_1076636_pir__S48027 ribosomal
NCBI Description
                  protein L34 - common tobacco >gi_2129964_pir__S48028
                  ribosomal protein L34.e, cytosolic - common tobacco
                  >gi 436030 (L27089) 60S ribosomal protein L34 [Nicotiana
                  tabacum] >gi_436032 (L27107) 60S ribosomal protein L34
                   [Nicotiana tabacum]
                  264383
Seq. No.
                  6970 1.R1011
Contig ID
                  xsy700207643.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  `g134102
BLAST score
                  1577
                  1.0e-176
E value
Match length
                  401
                   80
% identity
                  RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60
NCBI Description
                   KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA)
                   >gi_72959_pir__HHWTBA ribulose-bisphosphate carboxylase
                   subunit-binding protein alpha chain - wheat (fragment)
                   >qi 1345582 emb CAA30699 (X07851) rubisco subunit
                   binding-protein alpha subunit (543 AA) [Triticum
                   aestivum]
                   264384
Seq. No.
Contig ID
                   6974 1.R1011
5'-most EST
                   LIB3078-009-Q1-K1-A8
                   264385
Seq. No.
                   6976 1.R1011
Contig ID
5'-most EST
                   LIB3078-009-Q1-K1-B1
Method
                   BLASTX
NCBI GI
                   g2623295
BLAST score
                   679
                   4.0e-71
E value
Match length
                   265
% identity
                   53
                  (AC002409) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 264386

Contig ID 6977_2.R1011 5'-most EST ntr700075551.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10



```
Match length
                  36
% identity
                  100
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
Seq. No.
                  264387
                  6977 3.R1011
Contig ID
5'-most EST
                  ymt700222442.h1
Method
                  BLASTX
                  q2499015
NCBI GI
BLAST score
                  183
                  2.0e-13
E value
                  108
Match length
% identity
                  34
                  TRIGGER FACTOR (TF) >gi 1001378_dbj BAA10868 (D64006)
NCBI Description
                  trigger factor [Synechocystis sp.]
```

Seq. No. 264388 Contig ID 6978_1.R1011 5'-most EST LIB189-028-Q1-E1-H1

Seq. No. 264389

Contig ID 6978_2.R1011
5'-most EST LIB3060-051-Q1-K1-A10

 Seq. No.
 264390

 Contig ID
 6979_1.R1011

 5'-most EST
 LIB3062-021-Q1-K1-B3

 Method
 BLASTX

Method BLASTX
NCBI GI g1491615
BLAST score 558
E value 5.0e-57
Match length 267
% identity 41

NCBI Description (X99923) male sterility 2-like protein [Arabidopsis

thaliana]

 Seq. No.
 264391

 Contig ID
 6979_3.R1011

 5'-most EST
 gct701178180.h1

Seq. No. 264392 Contig ID 6980 1.R1011

5'-most EST LIB3078-009-Q1-K1-B6

Method BLASTX
NCBI GI 94490317
BLAST score 623
E value 1.0e-64
Match length 331
% identity 43

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 264393 Contig ID 6983_1.R1011

5'-most EST LIB3115-014-P1-K1-D7

Method BLASTX NCBI GI g1707008 BLAST score 447



E value 2.0e-44 Match length 109 77 % identity (U78721) 30S ribosomal protein S5 isolog [Arabidopsis NCBI Description thaliana] Seq. No. 264394 Contig ID 6985 1.R1011 LIB3059-060-Q1-K1-A7 5'-most EST BLASTX Method NCBI GI g3914535 BLAST score 776 E value 1.0e-82 201 Match length 74 % identity 60S RIBOSOMAL PROTEIN L13A >qi 2791948 emb CAA11283 NCBI Description (AJ223363) ribosomal protein L13a [Lupinus luteus] 264395

Seq. No. 6985 3.R1011 Contig ID uC-zmflb73207q07b1 5'-most EST BLASTX Method g3914535 NCBI GI BLAST score 399 2.0e-38 E value 168 Match length

52

% identity NCBI Description 60S RIBOSOMAL PROTEIN L13A >gi 2791948 emb CAA11283_ (AJ223363) ribosomal protein L13a [Lupinus luteus]

264396 Seq. No. 6985 4.R1011 Contig ID

LIB3078-053-Q1-K1-E1 5'-most EST

Method BLASTX g3914535 NCBI GI 223 BLAST score 4.0e-18 E value 58 Match length 72 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L13A >gi_2791948_emb_CAA11283_ (AJ223363) ribosomal protein L13a [Lupinus luteus]

264397 Seq. No. 6986 1.R1011 Contig ID

LIB3137-041-Q1-K1-E5 5'-most EST

BLASTX Method g4101568 NCBI GI BLAST score 636 3.0e-66 E value Match length 224 % identity

NCBI Description (AF004816) unknown [Triticum aestivum]

264398 Seq. No. 6989 1.R1011 Contig ID

uC-zmflmo17171c02b1 5'-most EST

BLASTX Method



```
g1498597
NCBI GI
BLAST score
                  467
                  2.0e-46
E value
Match length
                  121
                  76
% identity
                  (U66105) phospholipid transfer protein [Zea mays]
NCBI Description
                  264399
Seq. No.
                  6989 2.R1011
Contig ID
                  LIB143-020-Q1-E1-H2
5'-most EST
                  BLASTX
Method
                  g128388
NCBI GI
                  406
BLAST score
                  3.0e-39
E value
                  121
Match length
                  71
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP)
NCBI Description
                   (PHOSPHOLIPID TRANSFER PROTEIN) (PLTP)
                  >gi 82711 pir A31779 phospholipid transfer protein 9C2
                  precursor - maize >gi 168576 (J04176) phospholipid transfer
                  protein precursor [Zea mays]
                  264400
Seq. No.
                   6989 3.R1011
Contig ID
                  uC-zmflb73163b06b2
5'-most EST
                  BLASTN
Method
NCBI GI
                  g1498596
BLAST score
                   152
                   5.0e-80
E value
                   250
Match length
                   97
% identity
                 Zea mays phospholipid transfer protein mRNA, complete cds
NCBI Description
                   264401
Seq. No.
                   6989_4.R1011
Contig ID
5'-most EST
                   uC-zmflb73280e10b2
Method
                   BLASTX
NCBI GI
                   q1498597
BLAST score
                   334
                   7.0e - 31
E value
Match length
                   92
% identity
                   82
                  (U66105) phospholipid transfer protein [Zea mays]
NCBI Description
                   264402
Seq. No.
                   6989 6.R1011
Contig ID
5'-most EST
                   uC-zmflb73201h06b1
Method
                   BLASTX
NCBI GI
                   g1498597
BLAST score
                   451
E value
                   8.0e-45
Match length
                   121
% identity
                   74
                  (U66105) phospholipid transfer protein [Zea mays]
NCBI Description
```

Seq. No. 264403

Contig ID 6989_13.R1011



5'-most EST LIB3136-001-P1-K1-D1 Method BLASTN

Method BLASTN
NCBI GI g168575
BLAST score 59
E value 1.0e-24
Match length 184
% identity 91

NCBI Description Maize phospholipid transfer protein mRNA, complete cds. of

clone 9C2

Seq. No. 264404

Contig ID 6993_1.R1011 5'-most EST pmx700086758.h1

Method BLASTX
NCBI GI g2252836
BLAST score 583
E value 8.0e-60
Match length 258
% identity 50

NCBI Description (AF013293) contains weak similarity to S. cerevisiae BOB1

protein (PIR:S45444) [Arabidopsis thaliana]

 Seq. No.
 264405

 Contig ID
 6994_1.R1011

 5'-most EST
 ntr700073330.h1

Method BLASTX
NCBI GI g2564253
BLAST score 850
E value 4.0e-91
Match length 182
% identity 88

NCBI Description (Z99996) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase

[Hordeum vulgare]

Seq. No. 264406

Contig ID 6994_2.R1011

5'-most EST LIB84-024-Q1-E1-G5

Method BLASTX
NCBI GI g2564253
BLAST score 411
E value 7.0e-40
Match length 81
% identity 90

NCBI Description (Z99996) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase

[Hordeum vulgare]

Seq. No. 264407 Contig ID 6998_1.R1011

5'-most EST LIB3078-002-Q1-K1-C5

Seq. No. 264408 Contig ID 6998 2.R1011

5'-most EST LIB3067-017-Q1-K1-C12

Method BLASTX
NCBI GI g1532167
BLAST score 186
E value 7.0e-14



Match length 65 % identity 51

NCBI Description (U63815) localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to

an area of similarity since the initation codon and stop codon could not be precisely determined [Arabidopsis

thaliana]

Seq. No. 264409

Contig ID 6999_1.R1011

5'-most EST uC-zmflB73002b09b1

Method BLASTX
NCBI GI g3335341
BLAST score 638
E value 3.0e-66
Match length 284
% identity 51

NCBI Description (AC004512) T8F5.10 [Arabidopsis thaliana]

Seq. No. 264410

Contig ID 7001 1.R1011

5'-most EST uC-zmflb73100c10b1

Method BLASTN
NCBI GI g22348
BLAST score 195
E value 1.0e-105

Match length 380 % identity 99

NCBI Description Z.mays mRNA for iojap protein

Seq. No. 264411

Contig ID 7003 1.R1011

5'-most EST LIB3079-001-Q1-K1-A11

5'-most EST uC-zmflb73234c03b2

Method BLASTX
NCBI GI g82080
BLAST score 1078
E value 1.0e-118
Match length 258
% identity 80

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

>gi_226872_prf__1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 264413

Contig ID 7006 1.R1011

5'-most EST uC-zmflb73177a03b1

Seq. No. 264414

Contig ID 7006_2.R1011 5'-most EST pmx700084740.h1

Seq. No. 264415

Contig ID 7008_1.R1011



5'-most EST xyt700342314.h1

Method BLASTX
NCBI GI g4185143
BLAST score 721
E value 5.0e-76
Match length 248
% identity 56

NCBI Description (AC005724) putative signal recognition particle receptor

beta subunit [Arabidopsis thaliana]

Seq. No. 264416 Contig ID 7008_2.R1011

5'-most EST uC-zmroteosinte090g09b2

Method BLASTX
NCBI GI g4185143
BLAST score 355
E value 3.0e-33
Match length 103
% identity 64

NCBI Description (AC005724) putative signal recognition particle receptor

beta subunit [Arabidopsis thaliana]

 Seq. No.
 264417

 Contig ID
 7009_1.R1011

 5'-most EST
 wyr700244194.h1

Seq. No. 264418

Contig ID 7011_1.R1011

5'-most EST uC-zmflb73264c04b1

Seq. No. 264419

Contig ID 7011_2.R1011

5'-most EST LIB3067-038-Q1-K1-F6

Seq. No. 264420

Contig ID 7011_4.R1011

5'-most EST LIB3180-005-P2-M1-B12

Seq. No. 264421

Contig ID 7011_5.R1011

5'-most EST LIB3059-060-Q1-K1-B8

Seq. No. 264422

Contig ID 7014_1.R1011 5'-most EST ntr700072714.h1

Method BLASTX
NCBI GI g2791806
BLAST score 521
E value 1.0e-52
Match length 164
% identity 59

NCBI Description (AF041433) bet3 [Mus musculus]

 Seq. No.
 264423

 Contig ID
 7014_2.R1011

 5'-most EST
 uC-zmflb73197c12b1

Method BLASTX

```
NCBI GI
                  g2791806
                  348
BLAST score
                  8.0e-33
E value
Match length
                  99
                  64
% identity
                  (AF041433) bet3 [Mus musculus]
NCBI Description
                  264424
Seq. No.
                  7015 1.R1011
Contig ID
                  pwr700448668.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3834382
                  201
BLAST score
                  4.0e-15
E value
Match length
                  196
% identity
                  28
                  (AF033109) syntaxin 8 [Rattus norvegicus]
NCBI Description
                  264425
Seq. No.
Contiq ID
                  7015 2.R1011
5'-most EST
                  yyf700351053.h1
Seq. No.
                  264426
Contig ID
                  7015 4.R1011
                  uC-zmflmo17395g04a1
5'-most EST
                  264427
Seq. No.
Contig ID
                  7016 1.R1011
                  LIB3078-008-Q1-K1-C8
5'-most EST
                  BLASTX
Method
                  g3881381
NCBI GI
BLAST score
                   411
E value
                   5.0e-40
                  162
Match length
                   49
% identity
                  (Z68270) Similarity to Yeast Man(0)-alpha-mannosidase
NCBI Description
                   (SW:MNS1 YEAST); cDNA EST EMBL:D71247 comes from this gene;
                   cDNA EST EMBL: D73896 comes from this gene [Caenorhabditis
                   elegans]
                   264428
Seq. No.
                   7019 1.R1011
Contig ID
                   uC-zmflb73263f05b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g130709
BLAST score
                   1671
E value
                   0.0e+00
Match length
                   316
% identity
                   98
                   SERINE/THREONINE PROTEIN PHOSPHATASE PP1
NCBI Description
                   >gi_322875_pir__S29317 phosphoprotein phosphatase (EC
```

3.1.3.16) 1 - maize >gi_168723 (M60215) protein phosphatase-1 [Zea mays] >gi_445586_prf__1909338A protein

phosphatase 1 [Zea mays]

Seq. No. 264429 Contig ID 7019 2.R1011



```
5'-most EST
                   LIB3059-044-Q1-K1-B12
Method
                   BLASTX
NCBI GI
                   q130709
BLAST score
                   806
E value
                   3.0e-86
Match length
                   178
                   89
% identity
                   SERINE/THREONINE PROTEIN PHOSPHATASE PP1
NCBI Description
                   >gi_322875_pir S29317 phosphoprotein phosphatase (EC
                   3.1.3.16) 1 - maize >gi 168723 (M60215) protein
                   phosphatase-1 [Zea mays] >gi_445586_prf__1909338A protein
                   phosphatase 1 [Zea mays]
                   264430
Seq. No.
Contig ID
                   7019 3.R1011
5'-most EST
                   LIB3137-057-Q1-K1-C9
Method
                   BLASTX
NCBI GI
                   q130709
BLAST score
                   485
                   2.0e-93
E value
Match length
                   189
% identity
                   90
                   SERINE/THREONINE PROTEIN PHOSPHATASE PP1
NCBI Description
                   >gi 322875 pir S29317 phosphoprotein phosphatase (EC
                    3.1.3.16) \overline{1} - \overline{\text{maize}} >gi 168723 (M60215) protein
                   phosphatase-1 [Zea mays] >gi_445586_prf__1909338A protein
                   phosphatase 1 [Zea mays]
Seq. No.
                   264431
                   7019 4.R1011
Contig ID
                   LIB143-011-Q1-E1-C5
5'-most EST
                   BLASTN
Method
                   g168722
NCBI GI
·BLAST score
                   76
E value
                   2.0e-34
                   297
Match length
                    90
% identity
NCBI Description Z.mays protein phosphatase-1 (ZmPP1) mRNA, complete cds
                    264432
Seq. No.
                   7022 1.R1011
Contig ID
5'-most EST
                   LIB3078-008-01-K1-D3
                    264433
Seq. No.
Contig ID
                    7025 1.R1011
                   rv17\overline{0}0455610.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                    g3024629
BLAST score
                    320
E value
                    6.0e-29
Match length
                    261
% identity
NCBI Description
```

GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-GAMMA) >gi_423252_pir__S32369 gamma-SNAP protein - bovine
>gi_298669_bbs_127528 gamma soluble NSF attachment protein,

gamma SNAP=N-ethyl-maleimide-sensitive fusion protein attachment protein [cattle, brain, Peptide, 328 aa]



>gi_445846_prf__1910317C NSF attachment protein
(SNAP):ISOTYPE=gamma [Bos taurus]

Seq. No. 264434

Contig ID 7025_2.R1011 5'-most EST qmh700028726.f1

Seq. No. 264435

Contig ID 7025_4.R1011 5'-most EST yne700378421.h1

Seq. No. 264436

Contig ID 7027 1.R1011

5'-most EST LIB3157-019-Q1-K1-D6

Method BLASTX
NCBI GI g132918
BLAST score 260
E value 3.0e-22
Match length 85

% identity 65

NCBI Description 50S RIBOSOMAL PROTEIN L35, CHLOROPLAST PRECURSOR (CL35)

>gi_81486_pir__A36107 ribosomal protein L35 precursor;

chloroplast - spinach >gi_170139 (M60449) ribosomal protein

L35 [Spinacia oleracea]

Seq. No. 264437

Contig ID 7028 1.R1011

5'-most EST LIB3078-008-Q1-K1-E1

Seq. No. 264438

Contig ID 7029 1.R1011 5'-most EST xsy700213420.h1

Method BLASTX
NCBI GI 9729775
BLAST score 521
E value 2.0e-52
Match length 332
% identity 45

NCBI Description HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION

FACTOR 8) (HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR)

>gi_100264_pir__ S25481 heat shock transcription factor 8 Peruvian tomato >gi_19492_emb_CAA47869_ (X67600) heat shock

transcription factor 8 [Lycopersicon peruvianum]

Seq. No. 264439

Contig ID 7029_2.R1011

5'-most EST uC-zmflmo17265a07b1

Seq. No. 264440

Contig ID 7029_3.R1011

5'-most EST uC-zmrob73050a10a1

Seq. No. 264441

Contig ID 7033 1.R1011

5'-most EST LIB3059-036-Q1-K1-B4

Method BLASTX NCBI GI g462195



BLAST score 544
E value 2.0e-55
Match length 115
% identity 90

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)

>gi_100682_pir___S21636 GOS2 protein - rice

>gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]

>gi 3789950 (AF094774) translation initiation factor [Oryza

sativa]

Seq. No. 264442

Contig ID 7034 1.R1011

5'-most EST LIB3078-008-Q1-K1-B2

Seq. No. 264443

Contig ID 7036 1.R1011

5'-most EST LIB3061-040-Q1-K1-B9

Method BLASTX
NCBI GI g4006859
BLAST score 193
E value 7.0e-15
Match length 72

Match length 72 % identity 56

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 264444

Contig ID 7038 1.R1011

5'-most EST LIB3115-038-P1-K2-D4

Seq. No. 264445

Contig ID 7038 2.R1011

5'-most EST uC-zmflb73054f08b1

Seq. No. 264446

Contig ID 7038_3.R1011 5'-most EST xyt700347229.h1

Method BLASTX
NCBI GI g1839188
BLAST score 1486
E value 1.0e-165
Match length 489
% identity 60

NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No. 264447

Contig ID 7038_7.R1011

5'-most EST uC-zmflb73053c04b2

Method BLASTX
NCBI GI g1839188
BLAST score 291
E value 1.0e-38
Match length 130
% identity 63

NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No. 264448 Contig ID 7038_8.R1011

E value

Match length

287



```
uC-zmflmo170114b04b1
5'-most EST
                  264449
Seq. No.
                  7039 2.R1011
Contig ID
                  LIB3078-008-Q1-K1-B7
5'-most EST
                  BLASTX
Method
                  q3236248
NCBI GI
BLAST score
                   265
                   4.0e-23
E value
                   85
Match length
                   67
% identity
                  (AC004684) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   264450
                   7041 1.R1011
Contig ID
5'-most EST
                   LIB3060-026-Q1-K1-F7
Method
                   BLASTX
                   g2160148
NCBI GI
BLAST score
                   678
                   6.0e-71
E value
                   190
Match length
                   69
% identity
                  (AC000375) EST gb_H37044 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
                   264451
Seq. No.
                   7041 2.R1011
Contig ID
                   LIB3060-008-Q1-K1-D8
5'-most EST
                   264452
Seq. No.
                   7043 1.R1011
Contig ID
                   uer7\overline{0}0581552.h1
5'-most EST
                   264453
Seq. No.
                   7046 1.R1011
Contig ID
                   xsy700213042.h1
5'-most EST
Seq. No.
                   264454
                   7048 1.R1011
Contig ID
                   xyt700345531.h1
5'-most EST
                   BLASTX
Method
                   g2688299
NCBI GI
BLAST score
                   575
                   5.0e-59
E value
                   294
Match length
                   43
% identity
NCBI Description (AE001145) prolyl-tRNA synthetase (proS) [Borrelia
                   burgdorferi]
                   264455
Seq. No.
                   7050 1.R1011
Contig ID
                   xyt700346674.h1
5'-most EST
                   BLASTX
Method
                   g4249662
NCBI GI
                   899
BLAST score
                   7.0e-97
```



```
% identity
                   (AF089810) Altered Response to Gravity [Arabidopsis
NCBI Description
                   thaliana]
                   264456
Seq. No.
                   7050 2.R1011
Contig ID
                   LIB3\overline{0}88-041-Q1-K1-G3
5'-most EST
                   BLASTX
Method
                   g2266985
NCBI GI
                   397
BLAST score
                   3.0e - 38
E value
Match length
                   114
% identity
                   65
                   (Y13943) METRS [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   264457
                   7050 3.R1011
Contig ID
                   uC-zmflb73098e09b1
5'-most EST
                   BLASTX
Method
                   q4249662
NCBI GI
                   620
BLAST score
                   4.0e-64
E value
Match length
                   265
                   49
% identity
                   (AF089810) Altered Response to Gravity [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   264458
                   7050 4.R1011
Contig ID
                   LIB3157-012-Q1-K1-E6
5'-most EST
                   264459
Seq. No.
                   7054_1.R1011
Contig ID
                   LIB3078-008-Q1-K1-A2
5'-most EST
                   BLASTX
Method
                   g1655536
NCBI GI
BLAST score
                   343
                   2.0e-32
E value
                   94
Match length
                   70
% identity
                   (Y09095) chloride channel [Arabidopsis thaliana]
NCBI Description
                   >gi_1742957_emb_CAA96059_ (Z71447) CLC-c chloride channel
                   protein [Arabidopsis thaliana]
                   264460
Seq. No.
Contig ID
                   7060 1.R1011
5'-most EST
                   uC-zmroteosinte109a05b3
Method
                   BLASTX
NCBI GI
                   q3421087
BLAST score
                   1106
```

1.0e-121 E value Match length 237 % identity 91

(AF043524) 20S proteasome subunit PAE1 [Arabidopsis NCBI Description

thaliana]

Seq. No. 264461



Contig ID 7060_2.R1011
5'-most EST uC-zmroteosinte049f05b1
Method BLASTX
NCBI GI g3421087

BLAST score 971 E value 1.0e-105 Match length 211 % identity 93

NCBI Description (AF043524) 20S proteasome subunit PAE1 [Arabidopsis

thaliana]

Seq. No. 264462

Contig ID 7060_3.R1011

5'-most EST LIB3079-023-Q1-K1-A2

Method BLASTX
NCBI GI g3421087
BLAST score 334
E value 4.0e-31
Match length 84
% identity 79

NCBI Description (AF043524) 20S proteasome subunit PAE1 [Arabidopsis

thaliana]

Seq. No. 264463

Contig ID 7060_4.R1011 5'-most EST yyf700350837.h1

Method BLASTX
NCBI GI g3421087
BLAST score 484
E value 7.0e-49
Match length 99
% identity 96

NCBI Description (AF043524) 20S proteasome subunit PAE1 [Arabidopsis

thaliana]

Seq. No. 264464

Contig ID 7061_1.R1011 5'-most EST uwc700154573.h1

Method BLASTX
NCBI GI g1297187
BLAST score 216
E value 1.0e-16
Match length 72
% identity 60

NCBI Description (U53501) similar to protein encoded by GenBank Accession

Number U41815, nucleoporin 98 [Arabidopsis thaliana]

Seq. No. 264465 Contig ID 7061 2.R1011

5'-most EST uC-zmflb73195f06b1

Method BLASTX
NCBI GI g1297187
BLAST score 353
E value 7.0e-33
Match length 164
% identity 48

NCBI Description (U53501) similar to protein encoded by GenBank Accession



Number U41815, nucleoporin 98 [Arabidopsis thaliana]

264466 Seq. No. 7061 3.R1011 Contig ID 5'-most EST ypc700802434.h1

264467 Seq. No.

7062 1.R1011 Contig ID zuv700357180.h1 5'-most EST

BLASTX Method NCBI GI g3413704 BLAST score 271 2.0e-23 E value Match length 122 46 % identity

(AC004747) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 264468

7063 1.R1011 Contig ID

5'-most EST LIB3067-057-Q1-K1-C12

BLASTX Method NCBI GI g3157928 BLAST score 1513 1.0e-169 E value 421 Match length % identity 65

NCBI Description (AC002131) Similar to fumarylacetoacetate hydrolase,

gb_L41670 from Emericella nidulans. [Arabidopsis thaliana]

264469 Seq. No.

7063 2.R1011 Contig ID

5'-most EST LIB189-028-Q1-E1-B11

BLASTX Method NCBI GI g4557587 395 BLAST score E value 4.0e-38 Match length 113 % identity

fumarylacetoacetase >gi 119778 sp P16930 FAAA HUMAN NCBI Description FUMARYLACETOACETASE (FUMARYLACETOACETATE HYDROLASE)

(BETA-DIKETONASE) (FAA) >gi_106043_pir__A37926

fumarylacetoacetase (EC 3.7.1.2) - human >gi_182393 (M55150) fumarylacetoacetate hydrolase [Homo sapiens]

Seq. No. 264470

Contig ID 7064 1.R1011

5'-most EST LIB3079-036-Q1-K1-E5

Seq. No. 264471

Contig ID 7064 2.R1011

LIB3279-049-P1-K1-E12 5'-most EST

Method BLASTX NCBI GI g4417286 BLAST score 201 3.0e-15E value

Match length 167 31 % identity



```
(AC007019) putative shikimate kinase [Arabidopsis thaliana]
NCBI Description
                  264472
Seq. No.
                  7067 1.R1011
Contig ID
                  LIB3061-041-Q1-K1-D12
5'-most EST
                  264473
Seq. No.
                  7068 1.R1011
Contig ID
                  uC-zmflmo17060d09b1
5'-most EST
                  BLASTX
Method
                  g3643608
NCBI GI
                   250
BLAST score
                   6.0e-21
E value
                  104
Match length
% identity
                   46
                   (AC005395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   264474
                   7068 2.R1011
Contig ID
                   uC-zmrob73024e12a1
5'-most EST
                   BLASTX
Method
                   g4415908
NCBI GI
                   571
BLAST score
                   3.0e-58
E value
                   231
Match length
                   59
% identity
                  (AC006282) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   264475
                   7071 1.R1011
Contig ID
                   LIB3\overline{159}-011-Q1-K1-D1
5'-most EST
                   BLASTX
Method
                   q4512657
NCBI GI
                   289
BLAST score
                   7.0e-26
E value
                   134
Match length
                   43
% identity
                   (AC006931) putative APG protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4544463_gb_AAD22370.1 AC006580_2 (AC006580) putative
                   APG isolog protein [Arabidopsis thaliana]
                   264476
Seq. No.
                   7076 1.R1011
Contig ID
                   uC-zmflb73200c07b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2129675
BLAST score
                   1417
E value
                   1.0e-157
Match length
                   336
% identity
                   probable chlorophyll synthetase G4 - Arabidopsis thaliana
NCBI Description
                   >qi 972938 (U19382) putative chlorophyll synthetase
                   [Arabidopsis thaliana] >gi 3068709 (AF049236) putative
```

chlorophyll synthetase [Arabidopsis thaliana]

264477 Seq. No. 7077 1.R1011 Contig ID

Match length

% identity

116

64



fwa700100356.h1 5'-most EST BLASTX Method g1657851 NCBI GI 374 BLAST score 2.0e-35 E value Match length 86 39 % identity (U73214) cold acclimation protein WCOR518 [Triticum NCBI Description aestivum] 264478 Seq. No. 7077 2.R1011 Contig ID LIB83-005-Q1-E1-A2 5'-most EST BLASTX Method g1657851 NCBI GI 375 BLAST score 1.0e-35 E value Match length 86 38 % identity (U73214) cold acclimation protein WCOR518 [Triticum NCBI Description aestivum] 264479 Seq. No. 7077 4.R1011 Contig ID uC-zmflb73244e05b25'-most EST BLASTX Method q1657851 NCBI GI BLAST score 367 9.0e-35 E value 86 Match length 38 % identity (U73214) cold acclimation protein WCOR518 [Triticum NCBI Description aestivum] Seq. No. 264480 7082_1.R1011 Contig ID uC-zmflm017025b04b15'-most EST Method BLASTX g1711618 NCBI GI BLAST score 633 4.0e-66 E value Match length 177 68 % identity LOW AFFINITY SULPHATE TRANSPORTER 3 >gi 1085993 pir__S51765 NCBI Description low affinity sulphate transporter - Stylosanthes hamata >gi_607188_emb CAA57831 (X82454) low affinity sulphate transporter [Stylosanthes hamata] Seq. No. 264481 7083 1.R1011 Contig ID 5'-most EST LIB3078-007-Q1-K1-D9 BLASTX Method NCBI GI q4006902 BLAST score 403 E value 4.0e-39



(Z99708) putative protein [Arabidopsis thaliana] NCBI Description 264482 Seq. No. 7087 1.R1011 Contig ID $xmt7\overline{0}0262353.h1$ 5'-most EST 264483 Seq. No. 7094 2.R1011 Contig ID clt700044739.fl 5'-most EST 264484 Seq. No. Contig ID 7095 1.R1011 fwa700098285.h1 5'-most EST 264485 Seq. No. 7101 1.R1011 Contig ID wen700335322.h1 5'-most EST Method BLASTX q1103318 NCBI GI BLAST score 867 3.0e-93 E value Match length 305 % identity 60 (X78818) casein kinase I [Arabidopsis thaliana] NCBI Description >qi 2244791 emb CAB10213.1 (Z97336) casein kinase I [Arabidopsis thaliana] Seq. No. 264486 7106 1.R1011 Contig ID xyt700344375.h1 5'-most EST BLASTX Method g21693 NCBI GI BLAST score 1366 1.0e-151 E value 298 Match length 81 % identity NCBI Description (X66012) cathepsin B [Triticum aestivum] 264487 Seq. No. 7106 2.R1011 Contig ID uC-zmflMo17093h02b1 5'-most EST BLASTX Method g21699 NCBI GI 371 BLAST score

Method BLASIX
NCBI GI g21699
BLAST score 371
E value 3.0e-35
Match length 181
% identity 39

NCBI Description (X66013) cathepsin B [Triticum aestivum]

 Seq. No.
 264488

 Contig ID
 7106_3.R1011

 5'-most EST
 nbm700475604.h1

 Method
 BLASTX

 NCBI GI
 g21693

BLAST score 219 E value 2.0e-31 Match length 67



% identity

(X66012) cathepsin B [Triticum aestivum] NCBI Description

Seq. No. 264489

Contig ID

7113 1.R1011

5'-most EST

LIB3078-017-Q1-K1-E3

Method NCBI GI BLAST score BLASTX g131176 440

E value Match length % identity

3.0e-43138

68 PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR

NCBI Description

(PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)

>gi 72683 pir F1BH4 photosystem I chain IV precursor barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A

10.8kD photosystem I protein [Hordeum vulgare var.

distichum]

Seq. No.

264490

7113 2.R1011 Contig ID 5'-most EST cat700018407.r

Method BLASTX q131176 NCBI GI BLAST score 424 2.0e-41E value Match length 135 % identity 68

NCBI Description

PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR

(PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)

>gi 72683 pir F1BH4 photosystem I chain IV precursor barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A 10.8kD photosystem I protein [Hordeum vulgare var.

distichum]

Seq. No. 264491

Contig ID 7115 1.R1011

LIB36-019-Q1-E1-B4 5'-most EST

264492 Seq. No.

Contig ID 7119 1.R1011 $yyf7\overline{0}0349535.h1$ 5'-most EST

Method BLASTX NCBI GI g111999 BLAST score 151 E value 4.0e-09 Match length 251 % identity

NCBI Description myosin heavy chain, neuronal - rat

Seq. No. 264493

Contig ID 7121 1.R1011

5'-most EST uC-zmflmo17241c10b1

Seq. No. 264494



```
Contig ID
                  7123 1.R1011
5'-most EST
                  LIB36-014-Q1-E1-D1
Method
                  BLASTX
NCBI GI
                  q3417455
BLAST score
                  576
                  3.0e-59
E value
Match length
                  140
% identity
                  83
                  (AB016810) ferredoxin [Zea mays]
NCBI Description
Seq. No.
                  264495
                  7123 2.R1011
Contig ID
5'-most EST
                  clt700044148.r1
                  BLASTX
Method
NCBI GI
                  g119928
BLAST score
                  480
E value
                  6.0e-48
Match length
                  150
% identity
                  66
                  FERREDOXIN I PRECURSOR (FD I) >gi 168469 (M73829)
NCBI Description
                  ferredoxin [Zea mays] >qi 168471 (M73830) ferredoxin [Zea
                  mays] >gi 444685 prf 1907324B ferredoxin:ISOTYPE=I [Zea
                  mays]
                  264496
Seq. No.
                  7123 3.R1011
Contig ID
                  fwa700098414.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q119961
                  489
BLAST score
                  5.0e-49
E value
Match length
                  136
                  77
% identity
NCBI Description FERREDOXIN V PRECURSOR (FD V) >gi 168475 (M73828)
                  ferredoxin [Zea mays] >gi_444684_prf__1907324A
                  ferredoxin:ISOTYPE=V [Zea mays]
Seq. No.
                  264497
Contig ID
                  7124 1.R1011
                  LIB3062-048-Q1-K1-G3
5'-most EST
                  264498
Seq. No.
Contig ID
                  7128 1.R1011
5'-most EST
                  uC-zmflb73143f04b1
                  BLASTX
Method
NCBI GI
                  g2414593
BLAST score
                  341
E value
                  8.0e-32
                  150
Match length
                  44
% identity
                  (Z99258) molybdopterin biosynthesis [Schizosaccharomyces
NCBI Description
```

Seq. No. 264499 Contig ID 7129_1.R1011

5'-most EST LIB3078-006-Q1-K1-D3

pombe]

Method BLASTX



```
NCBI GI
                    g584892
BLAST score
                    213
                    1.0e-16
E value
                    87
Match length
% identity
                    79
                   SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)
NCBI Description
                    >gi_629805_pir__S43516 serine carboxypeptidase I - rice
>gi_409580_dbj_BAA04510_ (D17586) serine carboxypeptidase I
                    [Oryza satīva]
                    264500
Seq. No.
Contig ID
                    7132 1.R1011
                    uC-z\overline{m} \verb|flmo17043d01b1|
5'-most EST
Method
                    BLASTX
NCBI GI
                    q4176424
                    518
BLAST score
                    2.0e-52
E value
Match length
                    167
                    70
% identity
                   (AB022674) ribosomal protein L12 [Oryza sativa]
NCBI Description
Seq. No.
                    264501
                    7133 1.R1011
Contig ID
5'-most EST
                    LIB3078-006-Q1-K1-E10
                    264502
Seq. No.
Contig ID
                    7136 1.R1011
5'-most EST
                    uC-zmflmo17335c08b1
                    264503
Seq. No.
Contig ID
                    7136 2.R1011
5'-most EST
                    uC-zmflb73077g11b2
                    264504
Seq. No.
                    7139 1.R1011
Contig ID
5'-most EST
                    uC-zmflb73210d02a1
                    264505
Seq. No.
Contig ID
                    7139 2.R1011
5'-most EST
                    uC-zmflb73161d01b2
Method
                    BLASTX
NCBI GI
                    g4581149
BLAST score
                    658
E value
                    3.0e-68
Match length
                    478
% identity
                  (AC006919) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    264506
                    7141 1.R1011
Contig ID
5'-most EST
                    uC-zmroteosinte010d10b1
```

 Seq. No.
 264507

 Contig ID
 7143_1.R1011

 5'-most EST
 xmt700262632.h1

 Method
 BLASTX

 NCBI GI
 q4567302



272 BLAST score 6.0e-24 E value 73 Match length 78 % identity (AC005956) unknown protein [Arabidopsis thaliana] NCBI Description 264508 Seq. No. 7146_1.R1011 Contig ID LIB3\overline{1}36-051-Q1-K1-C5 5'-most EST BLASTX Method

q4337175 NCBI GI 318 BLAST score 5.0e-29 E value 130 Match length 48 % identity

NCBI Description

(AC006416) ESTs gb T20589, gb T04648, gb AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb R90004, gb T45020, gb T42457, gb T20921, gb AA042762 and

gb AA720210 come from this gene. [Arabidopsis thaliana]

264509 Seq. No. 7148 1.R1011 Contig ID ymt700223721.h1 5'-most EST

BLASTX Method g4454056 NCBI GI 759 BLAST score 1.0e-80 E value Match length 184 80 % identity

(AJ000930) ClpP [Arabidopsis thaliana] NCBI Description

264510 Seq. No.

7148_2.R1011 Contig ID

uC-zmflmo17303d03b1 5'-most EST

BLASTX Method NCBI GI g4454056 BLAST score 408 6.0e-44E value 116 Match length % identity 72

(AJ000930) ClpP [Arabidopsis thaliana] NCBI Description

264511 Seq. No.

7157 1.R1011 Contig ID xmt700265140.h15'-most EST

BLASTX Method NCBI GI q1651805 BLAST score 262 E value 2.0e-22 Match length 131 % identity

NCBI Description (D90900) hypothetical protein [Synechocystis sp.]

264512 Seq. No. 7159 1.R1011 Contig ID

LIB3078-006-Q1-K1-A2 5'-most EST

Method BLASTX



```
NCBI GI
                  g3386617
                  267
BLAST score
                   3.0e-23
E value
                   60
Match length
                  85
% identity
                   (AC004665) putative cell division protein (ftsY)
NCBI Description
                   [Arabidopsis thaliana]
                   264513
Seq. No.
                  7161 1.R1011
Contig ID
                  LIB3059-053-Q1-K1-F4
5'-most EST
Method
                   BLASTX
                   q1946373
NCBI GI
                   724
BLAST score
                   2.0e-76
E value
Match length
                   182
                   74
% identity
                  (U93215) leader peptidase I isolog [Arabidopsis thaliana]
NCBI Description
                   264514
Seq. No.
                   7163 1.R1011
Contig ID
                   uC-zmflmo17217a04b1
5'-most EST
                   264515
Seq. No.
                   7164 1.R1011
Contig ID
                   pmx700086693.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4263712
                   465
BLAST score
                   3.0e-46
E value
                   122
Match length
                   70
% identity
                  (AC006223) putative ribosomal protein S12 [Arabidopsis
NCBI Description
                   thaliana]
                   264516
Seq. No.
Contig ID
                   7164 2.R1011
                   LIB3062-019-Q1-K1-A4
5'-most EST
                   BLASTX
Method
                   a4263712
NCBI GI
                   476
BLAST score
E value
                   1.0e-47
                   140
Match length
% identity
                   (AC006223) putative ribosomal protein S12 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   264517
Contig ID
                   7164 3.R1011
                   LIB143-046-Q1-E1-G2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4263712
BLAST score
                   467
E value
                   2.0e-46
```

% identity 67
NCBI Description (AC006223) putative ribosomal protein S12 [Arabidopsis

129

Match length

NCBI Description

3' end



thaliana]

```
Seq. No.
                   264518
                   7164 4.R1011
Contig ID
                   LIB3<u>1</u>15-025-P1-K1-B7
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4263712
BLAST score
                   369
                   4.0e-35
E value
Match length
                   115
                   64
% identity
                   (AC006223) putative ribosomal protein S12 [Arabidopsis
NCBI Description
                   thaliana]
                   264519
Seq. No.
Contig ID
                   7164 5.R1011
                   uC-zmflb73158d10b2
5'-most EST
                   BLASTX
Method
                   q4263712
NCBI GI
BLAST score
                   282
                   4.0e-25
E value
Match length
                   93
                   62
% identity
                   (AC006223) putative ribosomal protein S12 [Arabidopsis
NCBI Description
                   thaliana]
                   264520
Seq. No.
Contig ID
                   7164 6.R1011
                   LIB3150-099-P1-N1-A7
5'-most EST
Method
                   BLASTX
                   q4263712
NCBI GI
                   256
BLAST score
                   1.0e-21
E value
                   135
Match length
                   46
% identity
                   (AC006223) putative ribosomal protein S12 [Arabidopsis
NCBI Description
                   thaliana]
                   264521
Seq. No.
                   7164 15.R1011
Contig ID
                   pwr700450320.hl
5'-most EST
                   264522
Seq. No.
                   7167 1.R1011
Contig ID
                   uC-zmflb73230h04b2
5'-most EST
                   264523
Seq. No.
Contig ID
                   7178 1.R1011
                   LIB189-014-Q1-E1-B8
5'-most EST
Method
                   BLASTN
                   q295500
NCBI GI
                   46
BLAST score
E value
                   2.0e-16
                   82
Match length
                   89
% identity
```

Triticum aestivum heat shock protein 16.9C (hsp16.9C) mRNA,



```
264524
Seq. No.
Contig ID
                  7178 2.R1011
5'-most EST
                  LIB3116-017-P1-K1-E11
                  264525
Seq. No.
Contig ID
                  7183 1.R1011
                  uC-zmflmo17100h06b1
5'-most EST
                  BLASTX
Method
                  g3873707
NCBI GI
BLAST score
                  287
                  5.0e-25
E value
Match length
                  244
                  33
% identity
NCBI Description
                  (Z73102) Similarity to B. subtilis DNAJ protein
                   (SW:DNAJ BACSU); cDNA EST yk437a1.5 comes from this gene
                  [Caenorhabditis elegans]
Seq. No.
                  264526
Contig ID
                  7183 2.R1011
5'-most EST
                  LIB3078-056-Q1-K1-H4
Seq. No.
                  264527
Contig ID
                  7185 2.R1011
5'-most EST
                  LIB3150-047-Q1-N1-H12
Seq. No.
                  264528
Contig ID
                  7187 1.R1011
5'-most EST
                  LIB3078-004-Q1-K1-F3
                  264529
Seq. No.
                  7188 1.R1011
Contig ID
5'-most EST
                  LIB3069-038-Q1-K1-E12
                  264530
Seq. No.
                  7189 1.R1011
Contig ID
5'-most EST
                  LIB3116-031-P1-K1-H2
Method
                  BLASTX
                  g2911043
NCBI GI
BLAST score
                  167
E value
                  1.0e-11
                  106
Match length
% identity
                   36
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
                   264531
Seq. No.
Contig ID
                  7194_1.R1011
5'-most EST
                  LIB3180-059-P2-M1-D7
```

Match length 149 % identity 93

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN

LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)



Seq. No. 264532

Contig ID 7194 2.R1011

5'-most EST LIB3180-010-P2-M1-B1

Method BLASTX
NCBI GI g1174850
BLAST score 685
E value 4.0e-72
Match length 149
% identity 87

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN

LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)

Seq. No. 264533

Contig ID 7197 1.R1011

5'-most EST uC-zmflmo17044b06b1

Method BLASTX
NCBI GI g1351365
BLAST score 157
E value 2.0e-10
Match length 50
% identity 56

NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 6.7 KD PROTEIN

(CR6) >gi_2130002_pir__S68969 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) - potato >gi_633683_emb_CAA57768_ (X82325) cytochrome c reductase subunit [Solanum tuberosum]

Seq. No. 264534

Contig ID 7198_1.R1011

5'-most EST LIB3078-004-Q1-K1-D12

Seq. No. 264535 Contig ID 7198 2.R1011

5'-most EST LIB189-032-Q1-E1-A2

Seq. No. 264536

Contig ID 7198_3.R1011 5'-most EST uwc700156310.h1

Seq. No. 264537

Contig ID 7200 1.R1011

5'-most EST LIB3061-037-Q1-K1-A2

Seq. No. 264538

Contig ID 7200 2.R1011

5'-most EST LIB3069-048-Q1-K1-B3

Seq. No. 264539

Contig ID 7200_4.R1011

5'-most EST LIB3060-049-Q1-K1-E1

Seq. No. 264540

Contig ID 7203_1.R1011 5'-most EST ntr700076829.h1

Method BLASTX
NCBI GI g4567263
BLAST score 443
E value 2.0e-43



Match length 202 52 % identity NCBI Description

(AC006841) putative cell division inhibitor [Arabidopsis

thaliana]

264541

Contig ID

Seq. No.

7204 1.R1011

5'-most EST

LIB84-005-Q1-E1-E9

Method BLASTX g733458 NCBI GI BLAST score 1068 E value 1.0e-117 Match length 205 96 % identity

(U23190) chlorophyll a/b-binding apoprotein CP24 precursor NCBI Description

[Zea mays]

Seq. No.

264542

Contig ID

7204 2.R1011

5'-most EST

LIB189-001-Q1-E1-E2

BLASTX Method NCBI GI g733458 BLAST score 436 5.0e-43E value 87 Match length 95 % identity

NCBI Description (U23190) chlorophyll a/b-binding apoprotein CP24 precursor

[Zea mays]

Seq. No.

264543

Contig ID 5'-most EST 7204 3.R1011 ceu700422674.h1

BLASTX Method NCBI GI q733458 BLAST score 221 E value 8.0e-18 66

Match length % identity 74

(U23190) chlorophyll a/b-binding apoprotein CP24 precursor NCBI Description

[Zea mays]

Seq. No.

264544

Contig ID

7210 1.R1011

5'-most EST

LIB3067-028-Q1-K1-B4

Method BLASTX NCBI GI q1082761 BLAST score 307 E value 2.0e-27 Match length 332 % identity 32

brain and reproductive organ-expressed protein - human NCBI Description

> >qi 603445 (L38616) brain and reproductive organ-expressed protein [Homo sapiens] >gi 2353177 (AF015767) brain and reproductive organ-expressed protein [Homo sapiens]

Seq. No.

264545

Contig ID

7215 1.R1011

E value

Match length

4.0e-52 206



```
LIB3062-016-Q1-K1-B12
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1173027
BLAST score
                  440
E value
                  2.0e-43
Match length
                  113
                  76
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal
                  protein L31 [Nicotiana glutinosa]
                  264546
Seq. No.
Contig ID
                  7215 2.R1011
5'-most EST
                  LIB3069-051-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g1173027
BLAST score
                  432
                  2.0e-42
E value
                  113
Match length
                  73
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal
                  protein L31 [Nicotiana glutinosa]
                  264547
Seq. No.
                  7215 3.R1011
Contig ID
5'-most EST
                  LIB83-006-Q1-E1-B3
                  BLASTX
Method
NCBI GI
                  q1173027
BLAST score
                   417
E value
                  1.0e-40
Match length
                  112
                   72
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L31 >gi 915313 (U23784) ribosomal
                  protein L31 [Nicotiana glutinosa]
                   264548
Seq. No.
Contig ID
                   7215 4.R1011
5'-most EST
                  uC-zmflb73022f07b1
Seq. No.
                   264549
Contig ID
                   7217 1.R1011
5'-most EST
                   uC-zmflmo17273a01b1
Method
                  BLASTX
NCBI GI
                   q4324470
BLAST score
                   250
E value
                   6.0e-21
Match length
                   169
% identity
                   35
NCBI Description (AF105010) LAG1Ce-1 [Caenorhabditis elegans]
Seq. No.
                   264550
Contig ID
                   7223 1.R1011
                   LIB3078-003-Q1-K1-H5
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2128748
BLAST score
                   515
```



```
% identity
                  52
                  hypothetical protein MJ1249 - Methanococcus jannaschii
NCBI Description
                  >gi 1591882 (U67565) conserved hypothetical protein
                  [Methanococcus jannaschii]
Seq. No.
                  264551
Contig ID
                  7233 1.R1011
                  LIB143-042-Q1-E1-F4
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1362051
BLAST score
                  307
E value
                  7.0e-28
Match length
                  112
                  57
% identity
                  protein kinase 3 - soybean >gi 310582 (L19361) protein
NCBI Description
                  kinase 3 [Glycine max]
Seq. No.
                  264552
Contig ID
                  7245 1.R1011
                  LIB3079-043-Q1-K2-G3
5'-most EST
                  264553
Seq. No.
Contig ID
                  7247 1.R1011
5'-most EST
                  pmx700086564.h1
                 - BLASTX
Method
NCBI GI
                  g3337361
BLAST score
                  2172
E value
                  0.0e+00
Match length
                  629
% identity
                  64
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
                  264554
Seq. No.
                  7249 2.R1011
Contig ID
                  LIB3078-003-Q1-K1-E10
5'-most EST
                  BLASTN
Method
NCBI GI
                  g3821780
BLAST score
                  36
                  2.0e-10
E value
                  48
Match length
                   67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  264555
                  7251 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73124e10a1
                  BLASTX
Method
NCBI GI
                  g1402902
                  278
BLAST score
E value
                   1.0e-24
```

86 Match length

63

(X98323) peroxidase [Arabidopsis thaliana] NCBI Description

>gi 1419386_emb_CAA67428_ (X98928) peroxidase ATP10a

[Arabidopsis thaliana]

264556 Seq. No.

% identity



```
Contig ID
                   7259 1.R1011
5'-most EST
                   mwy7\overline{0}0442687.h1
                   264557
Seq. No.
                   7260 1.R1011
Contig ID
                   uer700580838.h1
5'-most EST
Method
                   BLASTX
                   g4263509
NCBI GI
                   654
BLAST score
                   2.0e-68
E value
                   175
Match length
% identity
                   70
                   (AC004044) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   264558
Seq. No.
Contig ID
                   7262 1.R1011
5'-most EST
                   LIB3078-003-Q1-K1-C3
Method
                   BLASTX
                   g3878119
NCBI GI
BLAST score
                   312
                   1.0e-28
E value
                   138
Match length
% identity
                   43
                   (Z49068) similar to GTP-binding protein; cDNA EST
NCBI Description
                   EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709
                   comes from this gene; cDNA EST EMBL:D27708 comes from this
                   gene; cDNA EST EMBL: D73788 comes from this gene; cDNA EST
                   yk353
                   264559
Seq. No.
                   7265 1.R1011
Contig ID
5'-most EST
                   LIB3078-003-Q1-K1-C6
                   264560
Seq. No.
                   7266_1.R1011
Contig ID
5'-most EST
                   LIB84-004-Q1-E1-B6
Method
                   BLASTX
                   g3043529
NCBI GI
BLAST score
                   2488
                   0.0e + 00
E value
                   471
Match length
                   100
% identity
                  (AJ002204) polyamine oxidase [Zea mays]
NCBI Description
                   264561
Seq. No.
                   7269 1.R1011
Contig ID
5'-most EST
                   LIB189-016-Q1-E1-D7
Method
                   BLASTX
NCBI GI
                   g1550715
BLAST score
                   165
                   2.0e-11
E value
```

Match length 53 % identity

(Z80225) hypothetical protein Rv2674 [Mycobacterium NCBI Description

tuberculosis]

Seq. No. 264562



7270 1.R1011 Contig ID LIB3078-003-Q1-K1-D11 5'-most EST 264563 Seq. No. 7274 1.R1011 Contig ID afb700381835.h1 5'-most EST BLASTX Method g1076715 NCBI GI 225 BLAST score 6.0e-18 E value Match length 71 56 % identity abscisic acid-induced protein HVA22 - barley >gi_404589 NCBI Description (L19119) A22 [Hordeum vulgare] 264564 Seq. No. Contig ID 7274 2.R1011 5'-most EST LIB3078-051-Q1-K1-A6 Method BLASTX NCBI GI q1076715 BLAST score 272 9.0e-24 E value 88 Match length 55 % identity NCBI Description abscisic acid-induced protein HVA22 - barley >gi_404589 (L19119) A22 [Hordeum vulgare] 264565 Seq. No. Contig ID 7278 1.R1011 tzu700206802.h1 5'-most EST Method BLASTX g2914703 NCBI GI 755 BLAST score E value 3.0e-80 274 Match length % identity 50 NCBI Description (AC003974) unknown protein [Arabidopsis thaliana] Seq. No. 264566 Contig ID 7280 1.R1011 5'-most EST LIB3150-017-01-N1-A11 Method BLASTX NCBI GI q585963 BLAST score 271 E value 1.0e-23 Match length 69 % identity 81 NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

5'-most EST LIB3078-003-Q1-K1-B2

Method BLASTX
NCBI GI g585963
BLAST score 270
E value 1.0e-23
Match length 69



% identity 80

NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

Seq. No. 264568

Contig ID 7280 3.R1011

5'-most EST LIB3150-077-P2-N2-G4

Method BLASTX
NCBI GI g585963
BLAST score 273
E value 7.0e-24
Match length 69

Match length 69 % identity 81

NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

Seq. No. 264569

Contig ID 7280_4.R1011 5'-most EST xsy700217802.h1

Method BLASTX
NCBI GI g585963
BLAST score 268
E value 2.0e-23
Match length 69
% identity 80

NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

Seq. No. 264570

Contig ID 7282 1.R1011

5'-most EST uC-zmflmo17294c02b1

Method BLASTX
NCBI GI g1174448
BLAST score 608
E value 8.0e-63
Match length 200
% identity 57

NCBI Description TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR

(TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative

[Arabidopsis thaliana]

Seq. No. 264571

Contig ID 7282 2.R1011

5'-most EST uC-zmflb73303h09b1

Method BLASTX
NCBI GI g1174448
BLAST score 164
E value 4.0e-23
Match length 95
% identity 61

NCBI Description TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR

(TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi 547391 (L32016) alpha-subunit; putative

[Arabidopsis thaliana]

Seq. No. 264572 Contig ID 7282_4.R1011

5'-most EST uC-zmflmo17334h04a1

Method BLASTX



NCBI GI g1174448 BLAST score 211 E value 9.0e-17 Match length 59 % identity 68

NCBI Description TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT)

(SSR-ALPHA) >gi 547391 (L32016) alpha-subunit; putative

[Arabidopsis thaliana]

Seq. No. 264573

Contig ID 7292 1.R1011

5'-most EST LIB3078-002-Q1-K1-H8

Method BLASTX
NCBI GI 9732311
BLAST score 147
E value 3.0e-09
Match length 49
% identity 53

NCBI Description HYPOTHETICAL 15.7 KD PROTEIN IN PBPD-COMA INTERGENIC REGION

(ORF2) >gi_1075880_pir__B55220 pbpD 3'-region hypothetical protein - Bacillus subtilis >gi_520537 (U11882) unknown [Bacillus subtilis] >gi_1934785_emb_CAB07916_ (Z93933) unknown [Bacillus subtilis] >gi_2635646_emb_CAB15139_ (Z99120) alternate gene name: yugD [Bacillus subtilis]

Seq. No. 264574 Contig ID 7299 1.R1011

5'-most EST uC-zmflb73230d12b2

Method BLASTX
NCBI GI g4506221
BLAST score 890
E value 1.0e-95
Match length 430
% identity 43

NCBI Description proteasome (prosome, macropain) 26S subunit, non-ATPase, 12

>gi 1945611 dbj BAA19749 (AB003103) 26S proteasome subunit

p55 [Homo sapiens]

Seq. No. 264575

Contig ID 7299_2.R1011

5'-most EST uC-zmflmo17123f01a1

Method BLASTX
NCBI GI g4506221
BLAST score 228
E value 8.0e-25
Match length 164
% identity 41

NCBI Description proteasome (prosome, macropain) 26S subunit, non-ATPase, 12

>gi_1945611_dbj_BAA19749_ (AB003103) 26S proteasome subunit

p55 [Homo sapiens]

Seq. No. 264576

Contig ID 7299_3.R1011 5'-most EST fwa700097712.h1

Method BLASTX NCBI GI g4506221



221 BLAST score 6.0e-18 E value 98 Match length % identity 44 proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 NCBI Description >qi 1945611 dbj BAA19749 (AB003103) 26S proteasome subunit p55 [Homo sapiens] 264577 Seq. No. 7299 5.R1011 Contig ID ypc700805106.hl 5'-most EST BLASTX Method NCBI GI g4506221 BLAST score 149 1.0e-09 E value 58 Match length 48 % identity proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 NCBI Description >gi 1945611_dbj_BAA19749_ (AB003103) 26S proteasome subunit p55 [Homo sapiens] 264578 Seq. No. 7300 1.R1011 Contig ID LIB3070-003-Q1-N1-A5 5'-most EST BLASTX Method q4544434 NCBI GI BLAST score 364 2.0e-34 E value Match length 74 96 % identity (AC006955) putative DNA-directed RNA polymerase II NCBI Description [Arabidopsis thaliana] 264579 Seq. No. 7300 2.R1011 Contig ID fwa700100896.h1 5'-most EST BLASTX Method NCBI GI g4544434 BLAST score 275 1.0e-23 E value 55 Match length 95 % identity (AC006955) putative DNA-directed RNA polymerase II NCBI Description [Arabidopsis thaliana] 2,64580 Seq. No. 7300 5.R1011 Contig ID 5'-most EST LIB3060-001-Q1-K2-A11

Seq. No. 264581

Contig ID 7300_8.R1011

5'-most EST uC-zmromo17072b09a1

 Seq. No.
 264582

 Contig ID
 7304_1.R1011

 5'-most EST
 xsy700210581.h1

Method BLASTX



```
g4432840
NCBI GI
BLAST score
                  404
                  6.0e-39
E value
Match length
                  122
% identity
                  (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                  264583
Seq. No.
                  7308 1.R1011
Contig ID
                  LIB3059-019-Q1-K1-E12
5'-most EST
                  BLASTX
Method
                  g3548801
NCBI GI
BLAST score
                  476
                  2.0e-47
E value
                  188
Match length
                  48
% identity
                  (AC005313) putative transmembrane protein [Arabidopsis
NCBI Description
                  thaliana] >gi 4335768 gb AAD17445 (AC006284) putative
                  integral membrane protein [Arabidopsis thaliana]
                  264584
Seq. No.
                  7308 3.R1011
Contig ID
                  LIB3136-042-P1-K1-G11
5'-most EST
Method
                  BLASTX
                  g3548801
NCBI GI
                  192
BLAST score
                   1.0e-14
E value
                   68
Match length
% identity
                   56
                  (AC005313) putative transmembrane protein [Arabidopsis
NCBI Description
                   thaliana] >gi 4335768 gb AAD17445_ (AC006284) putative
                   integral membrane protein [Arabidopsis thaliana]
Seq. No.
                   264585
                   7309 1.R1011
Contig ID
                   LIB3078-002-Q1-K1-H10
5'-most EST
                   BLASTX
Method
                   g586527
NCBI GI
BLAST score
                   193
                   3.0e-14
E value
                   159
Match length
                   33
% identity
                  HYPOTHETICAL 32.6 KD PROTEIN IN VPS15-YMC2 INTERGENIC
NCBI Description
                   REGION >gi_1077500_pir__S48266 hypothetical protein YBR101c
                   - yeast (Saccharomyces cerevisiae) >gi_476057_emb_CAA55604_
                   (X78993) YBR0830 [Saccharomyces cerevisiae]
                   >gi 536384 emb_CAA85056_ (Z35970) ORF YBR101c
                   [Saccharomyces cerevisiae]
```

Seq. No. 264586 Contig ID 7315 1.R1011

LIB3150-031-Q1-N1-A12 5'-most EST

BLASTX Method g3935167 NCBI GI 446 BLAST score 5.0e-44E value 121 Match length

36732



50

[Arabidopsis thaliana]

% identity

NCBI Description

```
% identity
NCBI Description (AC004557) F17L21.10 [Arabidopsis thaliana]
Seq. No.
                  264587
Contig ID
                  7315 2.R1011
                  LIB3059-020-Q1-K1-D6
5'-most EST
                  264588
Seq. No.
Contig ID
                  7317 1.R1011
5'-most EST
                  LIB3159-012-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  q2979543
BLAST score
                  492
E value
                  3.0e-49
Match length
                  162
                   71
% identity
NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]
                  264589
Seq. No.
Contig ID
                  7317_2.R1011
5'-most EST
                  LIB3078-002-Q1-K1-F8
                  BLASTX
Method
NCBI GI
                  q2979543
BLAST score
                  445
                   3.0e-44
E value
Match length
                   135
% identity
NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]
                   264590
Seq. No.
                   7319 1.R1011
Contig ID
                   tfd700574406.h1
5'-most EST
Seq. No.
                   264591
                   7322 1.R1011
Contig ID
                  LIB3079-013-Q1-K1-A9
5'-most EST
Method
                  BLASTX
NCBI GI
                   q4538920
BLAST score
                   373
E value
                   9.0e-36
                   129
Match length
                   63
% identity
NCBI Description (AL049483) nitrogen fixation like protein [Arabidopsis
                   thaliana]
Seq. No.
                   264592
                   7323 1.R1011
Contig ID
                   LIB3078-002-Q1-K1-E11
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3522956
BLAST score
                   330
E value
                   1.0e-30
Match length
                   119
```

36733

(AC004411) putative pectinacetylesterase precursor



264593 Seq. No.

Contig ID 7325 1.R1011

5'-most EST LIB3067-036-01-K1-E10

264594 Seq. No.

7326 1.R1011 Contig ID 5'-most EST ymt700223814.h1

Seq. No. 264595

7338_1.R1011 Contig ID 5'-most EST mwy700442752.h1

BLASTX Method NCBI GI q3281849 BLAST score 560 E value 2.0e-57 Match length 142 74 % identity

(AL031004) methyltransferase - like protein [Arabidopsis NCBI Description

thaliana]

264596 Seq. No.

Contig ID 7339 1.R1011

5'-most EST LIB3078-002-Q1-K1-A6

Method BLASTX NCBI GI q3776575 BLAST score 412 E value 2.0e-40 Match length 120 69 % identity

NCBI Description (AC005388) Similar to Schizosaccharomyces CCAAT-binding

factor F7G19.16 gi_1922964 from Arabidopsis thaliana BAC gb_AC000106. EST gb_H36963 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 264597 Contig ID 7340 1.R1011

uC-zmflb73280c02b2 5'-most EST

Method BLASTX NCBI GI g3152940 BLAST score 322 E value 2.0e-29 Match length 276 % identity 31

NCBI Description (AF065483) sorting nexin 1 [Homo sapiens]

Seq. No. 264598

7340 2.R1011 Contig ID

5'-most EST uC-zmflmo170114f08b1

264599 Seq. No.

Contig ID 7340 3.R1011

5'-most EST uC-zmroteosinte009g10b1

264600 Seq. No.

Contig ID 7340 4.R1011

5'-most EST uC-zmflMo17013b08b1



Seq. No. 264601

Contig ID 7340_5.R1011 5'-most EST qmh700026702.f1

Seq. No. 264602

Contig ID 7340_6.R1011 5'-most EST fdz701167006.h1

Seq. No. 264603

Contig ID 7341_1.R1011

5'-most EST LIB3078-002-Q1-K1-A9

Method BLASTX
NCBI GI g3608139
BLAST score 545
E value 8.0e-56
Match length 180
% identity 57

NCBI Description (AC005314) putative fibrillin [Arabidopsis thaliana]

Seq. No. 264604

Contig ID 7353 1.R1011

5'-most EST LIB3078-001-Q1-K1-B4

Seq. No. 264605

Contig ID 7354_1.R1011

5'-most EST LIB3062-012-Q1-K1-D2

Method BLASTX
NCBI GI g4539262
BLAST score 175
E value 5.0e-12
Match length 111
% identity 37

NCBI Description (AL049495) conserved phosducin-like hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 264606

Contig ID 7358_1.R1011

5'-most EST uC-zmroB73070c12b1

Method BLASTX
NCBI GI g1730843
BLAST score 338
E value 3.0e-31
Match length 185
% identity 28

NCBI Description HYPOTHETICAL 17.1 KD PROTEIN IN SIP3-MRPL30 INTERGENIC

REGION >gi_2131945_pir__S63228 hypothetical protein YNL255c

- yeast (Saccharomyces cerevisiae)

>gi_1255963_emb_CAA65489_ (X96722) ORF N0852 [Saccharomyces cerevisiae] >gi_1302303_emb_CAA96162_ (Z71531) ORF YNL255c

[Saccharomyces cerevisiae]

Seq. No. 264607

Contig ID 7358_2.R1011 5'-most EST afb700381773.h1

Seq. No. 264608

Contig ID 7360 1.R1011



5'-most EST LIB3069-005-Q1-K1-B7

Seq. No. 264609

Contig ID 7363 1.R1011

5'-most EST uC-zmflmo17268e10b1

Method BLASTX
NCBI GI g2244898
BLAST score 383
E value 1.0e-36
Match length 89
% identity 81

NCBI Description (Z97338) strong similarity to protein phosphatase 2A

regulatory chain, 74K [Arabidopsis thaliana]

Seq. No. 264610

Contig ID 7365 1.R1011

5'-most EST LIB3156-008-Q1-K1-E3

Method BLASTX
NCBI GI g3983103
BLAST score 620
E value 1.0e-70
Match length 272
% identity 53

NCBI Description (AF097441) phenylalanine-tRNA synthetase [Homo sapiens]

Seq. No. 264611

Contig ID 7367_1.R1011

5'-most EST uC-zmflmo17365d08a1

Method BLASTX
NCBI GI g3023751
BLAST score 2149
E value 0.0e+00
Match length 498
% identity 50

NCBI Description 70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS

ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383

peptidylprolyl isomerase (EC 5.2.1.8) - wheat

>gi 854626 emb CAA60505 (X86903) peptidylprolyl isomerase

[Triticum aestivum]

Seq. No. 264612 Contig ID 7367 2.R1011

5'-most EST LIB3059-058-Q1-K1-H11

Method BLASTX
NCBI GI g3023751
BLAST score 454
E value 5.0e-45
Match length 121
% identity 75

NCBI Description 70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS

ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi 1076772_pir_ S55383

peptidylprolyl isomerase (EC 5.2.1.8) - wheat

>gi 854626 emb CAA60505 (X86903) peptidylprolyl isomerase

[Triticum aestivum]

Seq. No. 264613

Contig ID 7367 4.R1011



5!-most EST pmx700091519.h1 BLASTX Method g3023751 NCBI GI 435 BLAST score 4.0e-43E value 119 Match length 43 % identity 70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS NCBI Description ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi 854626 emb CAA60505_ (X86903) peptidylprolyl isomerase [Triticum aestivum] 264614 Seq. No. 7371 1.R1011 Contig ID uC-zmflb73157d09b2 5'-most EST Method BLASTX q1729907 NCBI GI 936 BLAST score 1.0e-101 E value 190 Match length 98 % identity TRANSCRIPTION INITIATION FACTOR TFIID-1 (TATA-BOX FACTOR 1) NCBI Description (TATA SEQUENCE-BINDING PROTEIN 1) (TBP-1) >gi_100928_pir__S21140 transcription initiation factor IID.1 - maize >gi_293904 (L13301) TATA-binding protein [Zea mays] 264615 Seq. No. 7372 1.R1011 Contig ID pmx700083590.h1 5'-most EST 264616 Seq. No. Contig ID 7373 1.R1011 xsy700217463.h1 5'-most EST Method BLASTX NCBI GI q2828285 BLAST score 256 1.0e-21 E value Match length 98 51 % identity NCBI Description (AL021687) putative protein [Arabidopsis thaliana] 264617 Seq. No. 7374 1.R1011 Contig ID 5'-most EST LIB3137-004-Q1-K1-A6 Method BLASTX NCBI GI g2130108 BLAST score 917 E value 5.0e-99 Match length 271

% identity

porin VDAC2 - wheat (fragment) >gi 558650 emb_CAA57647 NCBI Description (X82149) Voltage dependent anion channel (VDAC) [Triticum

aestivum]

Seq. No. 264618

% identity



```
7375 1.R1011
Contig ID
                  LIB3069-009-Q1-K1-A9
5'-most EST
Method
                  BLASTX
                  q3618314
NCBI GI
BLAST score
                  726
                  1.0e-76
E value
Match length
                  256
% identity
                  62
                  (AB001885) zinc finger protein [Oryza sativa]
NCBI Description
                  264619
Seq. No.
Contig ID
                  7375 2.R1011
                  uC-zmflmo17240e03b1
5'-most EST
                  BLASTX
Method
                  g3618310
NCBI GI
BLAST score
                  729
                  6.0e-77
E value
Match length
                  259
% identity
                  59
NCBI Description (AB001883) zinc finger protein [Oryza sativa]
                  264620
Seq. No.
Contiq ID
                  7375 3.R1011
                  uC-zmflmo17100b03b1
5'-most EST
Method
                  BLASTX
                  g3618314
NCBI GI
BLAST score
                  539
E value
                  5.0e-55
Match length
                  132
                   77
% identity
                  (AB001885) zinc finger protein [Oryza sativa]
NCBI Description
                   264621
Seq. No.
                   7375 4.R1011
Contig ID
                   LIB3088-050-Q1-K1-E3
5'-most EST
                   264622
Seq. No.
Contig ID
                   7375 5.R1011
                   LIB3159-017-Q1-K1-E7
5'-most EST
                   BLASTX
Method
                   g3618314
NCBI GI
                   519
BLAST score
                   6.0e-53
E value
                   101
Match length
                   93
% identity
NCBI Description (AB001885) zinc finger protein [Oryza sativa]
Seq. No.
                   264623
                   7375 6.R1011
Contig ID
                   LIB3136-017-Q1-K1-E10
5'-most EST
                   BLASTX
Method
                   g3618314
NCBI GI
BLAST score
                   345
                   3.0e - 32
E value
                   160
Match length
```

36738

NCBI Description (AB001885) zinc finger protein [Oryza sativa]

```
264624
Seq. No.
                  7377 1.R1011
Contig ID
                  fwa700098757.hl
5'-most EST
                  BLASTX
Method
                  g1015370
NCBI GI
BLAST score
                  195
                  1.0e-14
E value
                  123
Match length
                  41
% identity
                  (U34742) 24 kDa RNA binding protein [Spinacia oleracea]
NCBI Description
                  264625
Seq. No.
                  7379 1.R1011
Contig ID
5'-most EST
                  LIB3061-044-Q1-K1-D3
                  BLASTX
Method
                  q2961357
NCBI GI
                  470
BLAST score
                  8.0e-47
E value
                  140
Match length
% identity
                   62
                  (AL022140) putative protein [Arabidopsis thaliana]
NCBI Description
                  264626
Seq. No.
                  7380 1.R1011
Contig ID
                  uC-zmflb73276c06b1
5'-most EST
Method
                  BLASTX
                  g3122673
NCBI GI
BLAST score
                  837
                   9.0e-90
E value
Match length
                   200
% identity
                   78
NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                   264627
Seq. No.
Contig ID
                   7380 2.R1011
5'-most EST
                   LIB3069-005-Q1-K1-C3
                   BLASTX
Method
NCBI GI
                   q3122673
BLAST score
                   632
E value
                   1.0e-65
Match length
                   171
                   71
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi_2245027 emb_CAB10447_
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
```

 Seq. No.
 264628

 Contig ID
 7380_3.R1011

 5'-most EST
 wyr700242950.h1

 Method
 BLASTX

 NCBI GI
 g3122673

 BLAST score
 156

 E value
 6.0e-19

Match length 56 % identity 84

NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_



(Z97341) ribosomal protein [Arabidopsis thaliana]

264629 Seq. No. 7380 4.R1011 Contig ID wty700166909.hl 5'-most EST BLASTX Method NCBI GI q3122673 BLAST score 510 1.0e-51E value Match length 153 66 % identity 60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb CAB10447_ NCBI Description (Z97341) ribosomal protein [Arabidopsis thaliana] 264630 Seq. No. 7380 7.R1011 Contig ID uwc700154628.h1 5'-most EST BLASTX Method q3122673 NCBI GI 253 BLAST score 5.0e-22 E value Match length 54 89 % identity 60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb_CAB10447_ NCBI Description (Z97341) ribosomal protein [Arabidopsis thaliana] 264631 Seq. No. Contig ID 7380 9.R1011 LIB3066-008-Q1-K1-D5 5'-most EST Method BLASTX q3122673 NCBI GI 294 BLAST score 1.0e-26 E value 84 Match length 69 % identity 60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ NCBI Description (Z97341) ribosomal protein [Arabidopsis thaliana] 264632 Seq. No. 7383 1.R1011 Contig ID 5'-most EST xsy700207569.hl BLASTX Method g2344854 NCBI GI 213 BLAST score 2.0e-16 E value 251 Match length 29 % identity (Z98756) endopeptidase IV [Mycobacterium leprae] NCBI Description 264633 Seq. No. 7386 1.R1011 Contig ID

5'-most EST

LIB3078-056-Q1-K1-D6

264634 Seq. No. 7387 1.R1011 Contig ID fwa700098072.h1 5'-most EST Method BLASTX

36740



```
NCBI GI
                  g3334659
                  344
BLAST score
                  3.0e-32
E value
Match length
                  203
% identity
                  36
                  (Y10489) putative cytochrome P450 [Glycine max]
NCBI Description
                  264635
Seq. No.
                  7394 1.R1011
Contig ID
5'-most EST
                  uC-zmf1B73045g02b1
Method
                  BLASTX
NCBI GI
                  g2492953
                  792
BLAST score
                  2.0e-84
E value
Match length
                  231
% identity
                  66
                  CHORISMATE SYNTHASE 2 PRECURSOR
NCBI Description
                   (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 2)
                  >gi 542027 pir S40409 chorismate synthase (EC 4.6.1.4) 2
                  precursor - tomato >gi 410484 emb CAA79854 (Z21791)
                   chorismate synthase 2 [Lycopersicon esculentum]
Seq. No.
                  264636
                  7407 1.R1011
Contig ID
                  uwc700150626.h1
5'-most EST
Method
                  BLASTX
                  q556409
NCBI GI
BLAST score
                  326
                  3.0e - 30
E value
                  94
Match length
                  72
% identity
                  (L34551) transcriptional activator protein [Oryza sativa]
NCBI Description
                  264637
Seq. No.
                  7409 1.R1011
Contig ID
5'-most EST
                  xyt700346938.h1
Seq. No.
                  264638
Contig ID
                  7409 2.R1011
5'-most EST
                  LIB84-029-Q1-E1-C11
                  264639
Seq. No.
Contig ID
                  7410 1.R1011
5'-most EST
                  qmh700026616.f1
Method
                  BLASTX
NCBI GI
                  q4038471
BLAST score '
                  401
E value
                  7.0e - 39
Match length
                  86
% identity
NCBI Description
                  (AF111029) 40S ribosomal protein S27 homolog [Zea mays]
Seq. No.
                  264640
```

Contig ID 7410 2.R1011

5'-most EST LIB3067-033-Q1-K1-G7

Method BLASTX NCBI GI g4038471

36741

NCBI GI BLAST score

E value

215 1.0e-34



```
401
BLAST score
                   9.0e-39
E value
                  86
Match length
                   88
% identity
                  (AF111029) 40S ribosomal protein S27 homolog [Zea mays]
NCBI Description
                   264641
Seq. No.
                  7410_3.R1011
Contig ID
                   cat700018305.rl
5'-most EST
                  BLASTX
Method
                   g4038471
NCBI GI
                   319
BLAST score
                   3.0e-29
E value
                   86
Match length
                   74
% identity
                  (AF111029) 40S ribosomal protein S27 homolog [Zea mays]
NCBI Description
                   264642
Seq. No.
                   7410 5.R1011
Contig ID
                   tfd700573249.h1
5'-most EST
                   BLASTX
Method
                   g4038471
NCBI GI
                   435
BLAST score
                   3.0e-43
E value
                  84
Match length
% identity
                   96
                  (AF111029) 40S ribosomal protein S27 homolog [Zea mays]
NCBI Description
                   264643
Seq. No.
                   7410 6.R1011
Contig ID
5'-most EST
                   fdz701158987.h2
Method
                   BLASTX
                   g4038471
NCBI GI
                   289
BLAST score
                   3.0e-26
E value
Match length
                   57
% identity
                   98
                  (AF111029) 40S ribosomal protein S27 homolog [Zea mays]
NCBI Description
                   264644
Seq. No.
                   7416 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17158a03a1
Method
                   BLASTX
NCBI GI
                   g3087888
BLAST score
                   219
                   2.0e-17
E value
Match length-
                   109
% identity
                   45
                  (X94302) hexokinase [Solanum tuberosum]
NCBI Description
                   264645
Seq. No.
                   7419 1.R1011
Contig ID
                   wyr700239579.h1
5'-most EST
                   BLASTX
Method
                   g399900
```



Match length 157 % identity 52 NCBI Description HOM

HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT5 (HD-ZIP PROTEIN 5) (HD-ZIP PROTEIN ATHB-1) >gi 99659 pir S16325 homeotic

protein Athb-1 - Arabidopsis thaliana

>gi_16329_emb_CAA41625_ (X58821) Athb-1 protein

[Arabidopsis thaliana]

Seq. No. 264646 Contig ID 7420_1.R1011

5'-most EST uC-zmflmo17179a06a1

Method BLASTX
NCBI GI g4098244
BLAST score 797
E value 2.0e-90
Match length 204
% identity 81

NCBI Description (U76409) homeobox 1 protein [Lycopersicon esculentum]

Seq. No. 264647 Contig ID 7422 1.R1011

5'-most EST uC-zmflb73064d06b1

Method BLASTX
NCBI GI g2826882
BLAST score 461
E value 1.0e-45
Match length 106
% identity 83

NCBI Description (AJ223634) transcription factor IIA small subunit

[Arabidopsis thaliana]

Seq. No. 264649

Contig ID 7423_1.R1011

5'-most EST LIB3078-050-Q1-K1-B6

Method BLASTX
NCBI GI g2104679
BLAST score 223
E value 7.0e-18
Match length 81
% identity 49

NCBI Description (X97906) transcription factor [Vicia faba]

Seq. No. 264650

*Contig ID 7424_1.R1011 5'-most EST gct701177470.h1

Method BLASTX
NCBI GI g1076660
BLAST score 274
E value 9.0e-24
Match length 67
% identity 78

NCBI Description D13F(MYBST1) protein - potato >gi_786426_bbs_159122 (S74753) MybSt1=Myb-related transcriptional activator



264651

264652

7424 2.R1011

{DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]

Contig ID uwc700151452.h15'-most EST Method BLASTX NCBI GI g2062176 BLAST score 233 E value 3.0e-19 67 Match length 64 % identity

Seq. No.

Seq. No.

(ACO01645) Myb-related transcription activator (MybSt1) NCBI Description

isolog [Arabidopsis thaliana]

7424 3.R1011 Contig ID tzu700205986.h1 5'-most EST BLASTX Method NCBI GI q2062176 BLAST score 196 8.0e-15 E value

156 Match length 38 % identity

(AC001645) Myb-related transcription activator (MybSt1) NCBI Description

isolog [Arabidopsis thaliana]

Seq. No. 264653 7428 1.R1011 Contig ID

LIB3062-011-Q1-K1-B9 5'-most EST

Method BLASTX NCBI GI q2493809 BLAST score 1204 1.0e-133 E value Match length 228 % identity 92

NCBI Description COPROPORPHYRINOGEN III OXIDASE PRECURSOR

(COPROPORPHYRINOGENASE) (COPROGEN OXIDASE)
>gi_1212994 emb_CAA58037_ (X82830) coproporphyrinogen

oxidase [Hordeum vulgare]

Seq. No. 264654 7428 2.R1011 Contig ID

LIB3062-019-Q1-K1-A9 5'-most EST

Method BLASTX NCBI GI q2493810 BLAST score 168 7.0e-12 E value 40 Match length 72 % identity

COPROPORPHYRINOGEN III OXIDASE PRECURSOR NCBI Description

(COPROPORPHYRINOGENASE) (COPROGEN OXIDASE)

>gi 1213067 emb CAA58038 (X82831) coproporphyrinogen

oxidase [Nicotiana tabacum]

Seq. No. 264655

7429 1.R1011 Contig ID

36744



```
5'-most EST
                  LIB3078-007-Q1-K1-F2
Method
                  BLASTX
NCBI GI
                  g2495180
                  1214
BLAST score
                  1.0e-134
E value
Match length
                  311
                  76
% identity
                  PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG)
NCBI Description
                  (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN
                  SYNTHASE) >gi_421882_pir__S35873 hydroxymethylbilane
                  synthase (EC 4.3.1.8) - garden pea >gi_541971_pir__JQ2278
                  hydroxymethylbilane synthase (EC 4.3.1.8) precursor -
                  garden pea chloroplast >gi 313724_emb CAA51820 (X73418)
                  hydroxymethylbilane synthase [Pisum sativum]
                  264656
Seq. No.
                  7431 1.R1011
Contig ID
5'-most EST
                  uwc700154602.h1
Method
                  BLASTX
                  q1170029
NCBI GI
BLAST score
                  655
                  2.0e-68
E value
Match length
                  184
% identity
                  81
                  GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA)
NCBI Description
                  (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)
                  >gi 100581 pir A35789 glutamate-1-semialdehyde
                  2,1-aminomutase (EC 5.4.3.8) - barley >gi_506383 (M31545)
                  glutamate 1-semialdehyde aminotransferase [Hordeum vulgare]
                  264657
Seq. No.
                  7433 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17061f07b1
Method
                  BLASTX
                  q3420233
NCBI GI
BLAST score
                  1081
                  1.0e-118
E value
Match length
                  212
                  99
% identity
                  (AF058763) uroporphyrinogen decarboxylase [Zea mays]
NCBI Description
                  264658
Seq. No.
Contig ID
                  7436 1.R1011
                  fwa700100752.h1
5'-most EST
                  BLASTX
Method
                  q3913641
NCBI GI
BLAST score
                  808
                  2.0e-86
E value
                  219
Match length
                  76
% identity
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
```

(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)

>gi_3041777_dbj_BAA25423_ (AB007194)

fructose-1,6-bisphosphatase [Oryza sativa]

264659 Seq. No. Contig ID 7439 1.R1011



```
5'-most EST
                   xsy700212042.h1
Method
                   BLASTX
NCBI GI
                   q1174745
                   1229
BLAST score
E value
                   1.0e-135
Match length
                   262
% identity
                   89
NCBI Description
                  TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)
                   >qi 1363523 pir S53761 triose-phosphate isomerase (EC
                   5.3.1.1) precursor, chloroplast - rye
                   >gi 609262 emb CAA83533 (Z32521) triosephosphate isomerase
                   [Secale cereale] >gi 1095494 prf 2109226B triosephosphate
                   isomerase [Secale cereale]
Seq. No.
                   264660
Contig ID
                   7439 2.R1011
                   LIB3061-009-Q1-K1-G10
5'-most EST
                   264661
Seq. No.
                   7439 3.R1011
Contig ID
5'-most EST
                   LIB3078-049-Q1-K1-E4
                   BLASTX
Method
NCBI GI
                   g1174745
BLAST score
                   291
                   3.0e-26
E value
                   66
Match length
                   86
% identity
NCBI Description
                  TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)
                   >gi 1363523 pir S53761 triose-phosphate isomerase (EC
                   5.3.1.1) precursor, chloroplast - rye
                   >gi 609262 emb CAA83533 (Z32521) triosephosphate isomerase
                   [Secale cereale] >gi 1095494 prf 2109226B triosephosphate
                   isomerase [Secale cereale]
                   264662
Seq. No.
Contig ID
                   7439 5.R1011
5'-most EST
                   LIB3067-045-Q1-K1-E5
Method
                   BLASTX
NCBI GI
                   q1174745
BLAST score
                   266
E value
                   3.0e-23
Match length
                   56
% identity
                   91
                   TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)
NCBI Description
                   >gi_1363523_pir__S53761 triose-phosphate isomerase (EC
                   5.3.1.1) precursor, chloroplast - rye
                   >gi_609262_emb_CAA83533_ (Z32521) triosephosphate isomerase
                   [Secale cereale] >gi_1095494_prf_ 2109226B triosephosphate
                   isomerase [Secale cereale]
```

 Seq. No.
 264663

 Contig ID
 7441_1.R1011

 5'-most EST
 LIB3136-059-Q1-K1-H1

 Method
 BLASTX

 NCBI GI
 q4587519

NCBI GI g4587519
BLAST score 1000
E value 1.0e-109



```
252
Match length
% identity
                   (AC007060) Strong similarity to F19I3.7 gi_3033380 putative
NCBI Description
                   coatomer epsilon subunit from Arabidopsis Thaliana BAC
                   gb AC004238. ESTs gb Z17908, gb_AA728673, gb_N96555,
                   gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g
Seq. No.
                   264664
                   7441 2.R1011
Contig ID
                   LIB3<u>1</u>50-052-Q1-N1-D11
5'-most EST
                   BLASTX
Method
                   g4587519
NCBI GI
BLAST score
                   280
                   8.0e-50
E value
Match length
                   170
                   61
% identity
                   (AC007060) Strong similarity to F19I3.7 gi_3033380 putative
NCBI Description
                   coatomer epsilon subunit from Arabidopsis thaliana BAC
                   gb AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555,
                   gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g
                   264665
Seq. No.
                   7447 1.R1011
Contig ID
                   xsy700213015.hl
5'-most EST
                   BLASTX
Method
                   g1762945
NCBI GI
BLAST score
                   404
E value
                   5.0e-39
Match length
                   158
                   51
% identity
                   (U66269) ORF; able to induce HR-like lesions [Nicotiana
NCBI Description
                   tabacum]
                   264666
Seq. No.
                   7447 2.R1011
Contig ID
                   uC-z\bar{m}flb73239e03a1
5'-most EST
                   BLASTN
Method
                   g1185553
NCBI GI
                   36
BLAST score
                   1.0e-10
E value
                   56
Match length
                   91
% identity
                   Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)
NCBI Description
                   gene, complete cds
                   264667
Seq. No.
                   7447 3.R1011
Contig ID
5'-most EST
                   cyk700047976.f1
                   BLASTX
Method
NCBI GI
                   q1762945
BLAST score
                   418
                   8.0e-41
E value
```

% identity 50
NCBI Description (U66269) ORF; able to induce HR-like lesions [Nicotiana tabacum]

157

Match length



```
264668
Seq. No.
Contig ID
                  7453 1.R1011
                  xjt700095168.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3850583
                  1125
BLAST score
                  1.0e-123
E value
Match length
                  456
                  56
% identity
                  (AC005278) Contains similarity to transcription initiation
NCBI Description
                  factor IIE, alpha subunit gb_X63468 from Homo sapiens.
                   [Arabidopsis thaliana]
                  264669
Seq. No.
                  7453 3.R1011
Contig ID
                  uC-zmflmo17320e07a1
5'-most EST
                  264670
Seq. No.
Contig ID
                  7453 4.R1011
5'-most EST
                  ceu700422019.hl
                   264671
Seq. No.
                   7455 1.R1011
Contig ID
5'-most EST
                  LIB3078-025-Q1-K1-B8
                   BLASTX
Method
                   q4581162
NCBI GI
BLAST score
                   529
                   1.0e-53
E value
Match length
                   115
% identity
                  (AC006220) putative symbiosis-related protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   264672
                   7455 2.R1011
Contig ID
                   qmh700030114.f1
5'-most EST
                   BLASTX
Method
                   g4581162
NCBI GI
                   525
BLAST score
                   4.0e-53
E value
Match length
                   115
                   87
% identity
                  (AC006220) putative symbiosis-related protein [Arabidopsis
NCBI Description
                   thaliana]
```

 Seq. No.
 264673

 Contig ID
 7455_3.R1011

 5'-most EST
 LIB3279-051-P1-K1-C11

Method BLASTX
NCBI GI g4581162
BLAST score 384
E value 5.0e-37
Match length 84
% identity 89

NCBI Description (AC006220) putative symbiosis-related protein [Arabidopsis thaliana]

E value Match length

% identity

51 51



```
264674
Seq. No.
                  7455 4.R1011
Contig ID
                  uC-zmflmo17057a10b1
5'-most EST
Method
                  BLASTX
                  q4581162
NCBI GI
BLAST score
                  293
                  2.0e-26
E value
Match length
                  66
                  86
% identity
                   (AC006220) putative symbiosis-related protein [Arabidopsis
NCBI Description
                  thaliana]
                  264675
Seq. No.
                  7455 5.R1011
Contig ID
                  LIB3136-022-Q1-K1-H8
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4581162
BLAST score
                   233
                   2.0e-19
E value
Match length
                   55
                   82
% identity
                  (AC006220) putative symbiosis-related protein [Arabidopsis
NCBI Description
                   thaliana]
                   264676
Seq. No.
                   7462 1.R1011
Contig ID
                   LIB3078-057-Q1-K1-B3
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3746568
                   1388
BLAST score
                   1.0e-154
E value
                   326
Match length
                   79
% identity
                  (AF061638) branched-chain alpha-keto acid decarboxylase E1
NCBI Description
                   beta subunit [Arabidopsis thaliana]
                   264677
Seq. No.
                   7463 1.R1011
Contig ID
                   pmx700087641.h1
5'-most EST
                   BLASTX
Method
                   g3881507
NCBI GI
                   457
BLAST score
                   4.0e-45
E value
                   154
Match length
                   53
% identity
                  (Z47357) cDNA EST yk375c3.5 comes from this gene; cDNA EST
NCBI Description
                   yk375c3.3 comes from this gene [Caenorhabditis elegans]
                   264678
Seq. No.
                   7463 2.R1011
Contig ID
 5'-most EST
                   LIB3136-011-Q1-K1-A9
                   BLASTX
Method
NCBI GI
                   q3881507
                   152
BLAST score
                   7.0e-10
```

36749



```
(Z47357) cDNA EST yk375c3.5 comes from this gene; cDNA EST
NCBI Description
                  yk375c3.3 comes from this gene [Caenorhabditis elegans]
                  264679
Seq. No.
                  7463 4.R1011
Contig ID
                  xmt700264772.h1
5'-most EST
                  264680
Seq. No.
                  7464 1.R1011
Contig ID
                  wyr700237317.hl
5'-most EST
                  BLASTX
Method
                  g1652591
NCBI GI
BLAST score
                  181
                   2.0e-22
E value
                   220
Match length
                   32
% identity
                  (D90906) chloroplast import-associated channel IAP75
NCBI Description
                   [Synechocystis sp.]
                   264681
Seq. No.
                   7465 1.R1011
Contig ID
                   uC-zmflb73117b07a1
5'-most EST
                   264682
Seq. No.
                   7466 1.R1011
Contig ID
                   uC-zmflmo17038g05b1
5'-most EST
                   BLASTX
Method
                   q3850063
NCBI GI
BLAST score
                   698
E value
                   3.0e-73
                   419
Match length
                   37
% identity
NCBI Description (AJ223830) ARE1 [Rattus norvegicus]
                   264683
Seq. No.
                   7466 2.R1011
Contig ID
                   uC-zmflb73317a10b1
5'-most EST
                   BLASTX
Method
                   g3850063
NCBI GI
BLAST score
                   646
                   4.0e-67
E value
                   417
Match length
                   34
 % identity
 NCBI Description (AJ223830) ARE1 [Rattus norvegicus]
                   264684
 Seq. No.
                   7474 1.R1011
 Contig ID
                   LIB3078-012-Q1-K1-F1
 5'-most EST
                   BLASTN
 Method
                   g1245938
 NCBI GI
                   35
 BLAST score
                   5.0e-10
 E value
                   35
 Match length
```

36750

NCBI Description rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,

heart atrium, mRNA, 2998 nt]

100

% identity



264685 Seq. No. 7475 1.R1011 Contig ID $kem7\overline{0}0611479.h1$ 5'-most EST 264686 Seq. No. 7482 1.R1011 Contig ID pmx700083875.h15'-most EST Method BLASTX g4205079 NCBI GI 643 BLAST score 6.0e-67 E value 240 Match length % identity 55 (U70425) ankyrin repeat-containing protein 2 [Arabidopsis NCBI Description thaliana] 264687 Seq. No. 7482 3.R1011 Contig ID xsy700209625.h1 5'-most EST BLASTX Method q2262170 NCBI GI 221 BLAST score 3.0e-18 E value Match length 67 64 % identity (AC002329) predicted glycosyl hydrolase [Arabidopsis NCBI Description thaliana] 264688 Seq. No. 7485 2.R1011 Contig ID uC-zmflmo17281g11b1 5'-most EST BLASTX Method g4581856 NCBI GI 1835 BLAST score 0.0e+00E value 459 Match length 79 % identity NCBI Description (AF116825) 1-deoxy-D-xylulose-5-phosphate reductoisomerase [Mentha x piperita] 264689 Seq. No. 7488 1.R1011 Contig ID LIB3078-053-Q1-K1-G6 5'-most EST 264690 Seq. No. 7491_1.R1011 Contig ID LIB3136-059-Q1-K1-F9 5'-most EST BLASTX Method g3776023 NCBI GI 878 BLAST score 1.0e-94 E value

243 Match length

68 % identity

NCBI Description (AJ010473) RNA helicase [Arabidopsis thaliana]

264691 Seq. No. 7493 1.R1011 Contig ID



LIB189-027-Q1-E1-C8 5'-most EST BLASTX Method g417260 NCBI GI 300 BLAST score 7.0e-27 E value 123 Match length 51 % identity NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632 lir1 protein - rice >gi 20263 emb CAA48706 (X68807) light-regulated gene [Oryza sativa] 264692 Seq. No. Contig ID 7493 2.R1011 5'-most EST uC-zmflb73260f07b2 BLASTX Method NCBI GI q4490727 BLAST score 208 E value 9.0e-16 Match length 279 % identity 28 NCBI Description (AL035709) putative protein [Arabidopsis thaliana] 264693 Seq. No. 7493 3.R1011 Contig ID 5'-most EST uer700577702.h1 Seq. No. 264694 7493 4.R1011 Contig ID 5'-most EST LIB3279-013-P1-K1-A9 Seq. No. 264695 7493_5.R1011 Contig ID 5'-most EST LIB189-012-Q1-E1-D2 Method BLASTX NCBI GI q417260 BLAST score 150 E value 9.0e-15 68 Match length % identity 68 NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632 lir1 protein - rice >gi 20263 emb CAA48706 (X68807) light-regulated gene [Oryza sativa] Seq. No. 264696 Contig ID 7493 6.R1011 5'-most EST LIB3062-003-Q1-K1-E1 Seq. No. 264697 Contig ID 7493 7.R1011 5'-most EST LIB3115-024-P1-K1-A8 264698 Seq. No. Contig ID 7494 1.R1011 5'-most EST uC-zmflmo17017e05b1

36752

BLASTX

544

g4102839

Method NCBI GI

BLAST score



E value 6.0e-99
Match length 247
% identity 70

NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No. 264699 Contig ID 7496_1.R1011

5'-most EST uC-zmroteosinte008b05b1

Method BLASTX
NCBI GI g417103
BLAST score 679
E value 2.0e-71
Match length 136
% identity 100

NCBI Description HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
(U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460)
histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone
H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2

[Medicago sativa] >gi_488577 (U09465) histone H3.2

[Medicago sativa] >gi_510911_emb_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum]

>gi_2558944 (AF024716) histone 3 [Gossypium hirsutum]

>gi_2330344 (AF024710) histone 5 (G033yFidam hirsdtdam)
>gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]
>gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 264700 Contig ID 7497 1.R1011

5'-most EST LIB3078-056-Q1-K1-G4

Method BLASTX
NCBI GI g2062167
BLAST score 323
E value 1.0e-29
Match length 152
% identity 39

NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis

thaliana]

Seq. No. 264701

Contig ID 7500_1.R1011

5'-most EST LIB3068-034-Q1-K1-C10

Method BLASTX
NCBI GI g3421413
BLAST score 2238
E value 0.0e+00
Match length 515
% identity 84

NCBI Description (AF081922) protein phosphatase 2A 55 kDa B regulatory

subunit [Oryza sativa] >gi_3421415 (AF081923) protein



phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

264702 Seq. No. 7500 2.R1011 Contig ID wyr700236304.hl 5'-most EST Method BLASTX NCBI GI g3421413 BLAST score 300 7.0e-27 E value Match length 68 % identity 88 (AF081922) protein phosphatase 2A 55 kDa B regulatory NCBI Description subunit [Oryza sativa] >gi 3421415 (AF081923) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa] 264703 Seq. No. Contig ID 7501 1.R1011 5'-most EST uC-zmflb73041e09b1 Method BLASTX q3550485 NCBI GI BLAST score 494 2.0e-49 E value 166 Match length % identity NCBI Description (AJ224325) cp33Hv [Hordeum vulgare] 264704 Seq. No. Contig ID 7507 1.R1011 5'-most EST uC-zmrob73079h08b1 Method BLASTX NCBI GI g4539301 BLAST score 418 4.0e-57 E value Match length 160 69 % identity NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis thalianal 264705 Seq. No. 7508 1.R1011 Contig ID 5'-most EST ceu700429550.h1 Seq. No. 264706 Contig ID 7513 1.R1011 LIB3062-042-Q1-K1-B6 5'-most EST Seq. No. 264707 Contig ID 7519 1.R1011 5'-most EST pmx700081874.h1 264708 Seq. No. Contig ID 7519 2.R1011 5'-most EST LIB3062-017-Q1-K1-B12

36754

264709

7519 3.R1011

wen700336626.h1

Seq. No. Contig ID

5'-most EST



```
Seq. No.
                  264710
Contig ID
                  7520 1.R1011
5'-most EST
                  uwc700151903.hl
                  264711
Seq. No.
                  7521 1.R1011
Contig ID
                  LIB3136-027-P1-K1-H6
5'-most EST
Method
                  BLASTX
NCBI GI
                  q730558
BLAST score
                  451
                  1.0e-44
E value
Match length
                  95
                  91
% identity
NCBI Description
```

60S RIBOSOMAL PROTEIN L34 >gi 1076636 pir S48027 ribosomal protein L34 - common tobacco >gi 2129964 pir S48028 ribosomal protein L34.e, cytosolic - common tobacco >gi 436030 (L27089) 60S ribosomal protein L34 [Nicotiana tabacum] >qi 436032 (L27107) 60S ribosomal protein L34 [Nicotiana tabacum]

264712 Seq. No. 7521_2.R1011 Contig ID 5'-most EST LIB3059-049-Q1-K1-C8 Method BLASTX NCBI GI q730558 BLAST score 450 E value 1.0e-44Match length 95 % identity 91

NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi_1076636_pir__S48027 ribosomal protein L34 - common tobacco >gi_2129964 pir_ S48028 ribosomal protein L34.e, cytosolic - common tobacco >gi 436030 (L27089) 60S ribosomal protein L34 [Nicotiana tabacum] >gi 436032 (L27107) 60S ribosomal protein L34 [Nicotiana tabacum]

Seq. No. 264713 Contig ID 7521 4.R1011 5'-most EST xdb700338708.h1

Seq. No. 264714 Contig ID 7523 1.R1011 5'-most EST ypc700804929.h1 BLASTX Method NCBI GI g232172 2159 BLAST score

E value 0.0e+00Match length 475 % identity

NCBI Description GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT

PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE

PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE

ADENYL TRANSFERASE) >gi_481816_pir__S39504

glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) wheat >gi_21687 emb CAA46879 (X66080) ADP-glucose

pyrophosphorylase [Triticum aestivum]



```
264715
Seq. No.
                  7523 2.R1011
Contig ID
                  uC-zmflmo17310f12b1
5'-most EST
                  BLASTX
Method
                  g2130035
NCBI GI
                  443
BLAST score
                  1.0e-43
E value
                  101
Match length
                  84
% identity
                  glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) small
NCBI Description
                  chain A - barley >gi_1143500_emb_CAA88449_ (Z48562)
                  ADP-glucose pyrophosphorylase small subunit [Hordeum
                  vulgare]
                  264716
Seq. No.
                  7523 3.R1011
Contig ID
                  LIB3059-010-Q1-K1-F10
5'-most EST
                  BLASTX
Method
                  g121289
NCBI GI
                   366
BLAST score
                   5.0e-35
E value
                   80
Match length
                   90
% identity
                   GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT
NCBI Description
                   PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE
                   PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE
                   ADENYL TRANSFERASE) >gi_82468_pir__JU0444
                   glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) -
                   rice >gi_169761 (M31616) ADPglucose pyrophosphorylase
                   [Oryza sativa]
                   264717
Seq. No.
                   7523 4.R1011
Contig ID
                   afb700381390.h1
5'-most EST
                   BLASTX
Method
                   q633678
NCBI GI
                   152
BLAST score
                   1.0e-09
E value
                   44
Match length
                   73
 % identity
NCBI Description (X83500) ADP-glucose pyrophosphorylase [Spinacia oleracea]
                   264718
 Seq. No.
                   7523 5.R1011
 Contig ID
                   uC-zmflmo170114b09b1
 5'-most EST
                   BLASTX
 Method
                   g121289
 NCBI GI
                   756
 BLAST score
                   1.0e-138
 E value
                   275
 Match length
 % identity
                   GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT
 NCBI Description
                   PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE
                   PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE
```

glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) -

ADENYL TRANSFERASE) >gi_82468_pir__JU0444



rice >gi 169761 (M31616) ADPglucose pyrophosphorylase [Oryza sativa]

264719 Seq. No. 7523 7.R1011 Contig ID yyf700349227.h1 5'-most EST BLASTX Method NCBI GI g1707940 BLAST score 337 E value 2.0e-31 68 Match length

96 % identity

NCBI Description GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT

PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE

PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE

ADENYL TRANSFERASE) >gi 2130036 pir S61479

qlucose-1-phosphate adenylyltransferase (EC 2.7.7.27) small

chain B - barley >gi 1143502 emb CAA88450 (Z48563) ADP-glucose pyrophosphorylase small subunit [Hordeum

vulgare]

264720 Seq. No.

7525 1.R1011 Contig ID 5'-most EST tzu700205938.h1

Method BLASTX NCBI GI q2447107 BLAST score 818 E value 3.0e-87 Match length 349 % identity 47

NCBI Description (U42580) A638R [Paramecium bursaria Chlorella virus 1]

Seq. No. 264721

7528 1.R1011 Contig ID

LIB3078-056-Q1-K1-D2 5'-most EST

Seq. No. 264722

Contig ID 7529 1.R1011

LIB3150-101-P1-N1-H4 5'-most EST

Seq. No. 264723

Contig ID 7529 2.R1011

5'-most EST uC-zmflmo17263e06b1

264724 Seq. No.

7529 3.R1011 Contig ID 5'-most EST zuv700353580.hl

264725 Seq. No.

% identity

Contig ID 7532 1.R1011

5'-most EST uC-zmflb73120d06b1

37

Method BLASTX NCBI GI q1592812 BLAST score 173 E value 9.0e-12 Match length 127



```
NCBI Description (X95957) 22 kDa polypeptide [Nicotiana tabacum]
Seq. No. 264726
Contig ID 7532 2.R1011
```

5'-most EST LIB3060-028-Q1-K1-C4
Method BLASTX
NCBI GI g1550738
BLAST score 181
E value 8.0e-13
Match length 128

E value 8.0e-1
Match length 128
% identity 36

NCBI Description (Y08061) endomembrane-associated protein [Arabidopsis

thaliana] >gi_2982443_emb_CAA18251_ (AL022224)

endomembrane-associated protein [Arabidopsis thaliana]

Seq. No. 264727 Contig ID 7532 3

Contig ID 7532_3.R1011 5'-most EST tfd700571321.h1

Seq. No. 264728

Contig ID 7532_4.R1011 5'-most EST mwy700440308.h1

Seq. No. 264729

Contig ID 7532_5.R1011

5'-most EST LIB3062-017-Q1-K1-E9

Seq. No. 264730

Contig ID 7532_7.R1011

5'-most EST LIB3060-011-Q1-K1-F3

Method BLASTX
NCBI GI g1550738
BLAST score 179
E value 5.0e-13
Match length 74
% identity 53

NCBI Description (Y08061) endomembrane-associated protein [Arabidopsis

thaliana] >gi 2982443 emb CAA18251 (AL022224)

endomembrane-associated protein [Arabidopsis thaliana]

Seq. No. 264731

Contig ID 7533 1.R1011

5'-most EST LIB3068-059-Q1-K1-E12

Method BLASTX
NCBI GI g1352041
BLAST score 566
E value 1.0e-57
Match length 181
% identity 91

NCBI Description ATP SYNTHASE B CHAIN (SUBUNIT I) >gi_1363538_pir__S58548

H+-transporting ATP synthase (EC 3.6.1.34) chain I - maize

chloroplast >gi_902218_emb_CAA60282_ (X86563) ATPase I

subunit [Zea mays]

Seq. No. 264732

Contig ID 7535_1.R1011 5'-most EST xsy700217363.h1

36758

% identity



```
Method
                   BLASTX
NCBI GI
                   q4510363
BLAST score
                   652
E value
                   4.0e-68
Match length
                   134
% identity
                   (AC007017) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   264733
Seq. No.
                   7535 3.R1011
Contig ID
                   LIB3088-034-Q1-K1-H7
5'-most EST
                   264734
Seq. No.
                   7536 1.R1011
Contig ID
5'-most EST
                   LIB3150-040-Q1-N1-B12
                   BLASTX
Method
                   q3878960
NCBI GI
BLAST score
                   343
E value
                   7.0e-32
Match length
                   142
% identity
                   47
NCBI Description (Z49207) cDNA EST yk278a10.3 comes from this gene; cDNA EST
                   yk278a10.5 comes from this gene; cDNA EST yk486f8.5 comes
                   from this gene [Caenorhabditis elegans]
Seq. No.
                   264735
Contig ID
                   7536 2.R1011
5'-most EST
                   LIB3150-001-Q1-N1-B9
                   264736
Seq. No.
                   7538 1.R1011
Contig ID
                   LIB3068-050-Q1-K1-F9
5'-most EST
                   BLASTX
Method
                   g131148
NCBI GI
BLAST score
                   2702
E value
                   0.0e + 00
Match length
                   538
% identity
NCBI Description
                   PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2
                   >gi 72674 pir A2RZP7 photosystem I P700 apoprotein A2 -
                   rice chloroplast >gi_11981_emb_CAA33995_ (X15901) PSI P700 apoprotein A2 [Oryza sativa] >gi_226604_prf__1603356AA
                   photosystem I P700 apoprotein A2 [Oryza sativa]
Seq. No.
                   264737
                   7538 2.R1011
Contig ID
5'-most EST
                   LIB3068-012-Q1-K1-C5
Method
                   BLASTX
NCBI GI
                   q131148
BLAST score
                   924
E value
                   1.0e-100
Match length
                   207
```

82 NCBI Description PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2 >gi 72674 pir A2RZP7 photosystem I P700 apoprotein A2 -

rice chloroplast >qi 11981 emb CAA33995 (X15901) PSI P700



apoprotein A2 [Oryza sativa] >gi_226604_prf__1603356AA photosystem I P700 apoprotein A2 [Oryza sativa] 264738

Seq. No. 7541 1.R1011 Contig ID

LIB3062-040-Q1-K1-F3 5'-most EST

BLASTX Method NCBI GI q4263696 BLAST score 396 3.0e-38E value 174 Match length 47 % identity

(AC006223) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 264739 7542 1.R1011 Contig ID LIB36-021-Q1-E1-D8

5'-most EST BLASTX

Method NCBI GI q266607 600 BLAST score 1.0e-61 E value 160 Match length 75 % identity

NUCLEOSIDE DIPHOSPHATE KINASE II PRECURSOR (NDK II) (NDP NCBI Description

KINASE II) >gi_282832_pir__S28226 nucleoside-diphosphate kinase (EC 2.7.4.6) II - spinach >gi_218273_dbj_BAA02018_

(D11465) nucleoside diphosphate kinase II [Spinacia

oleracea]

264740 Seq. No.

7543 1.R1011 Contig ID wty700170858.hl 5'-most EST

264741 Seq. No.

7544 1.R1011 Contig ID

 $uC\text{-}z\overline{m}f1b73272c11b1$ 5'-most EST

BLASTX Method g116380 NCBI GI BLAST score 1962 0.0e+00E value 400 Match length 96 % identity

CHALCONE SYNTHASE C2 (NARINGENIN-CHALCONE SYNTHASE C2) NCBI Description

>gi_66554_pir__SYZMCC naringenin-chalcone synthase (EC 2.3.1.74) c2 - maize >gi_22218_emb_CAA42764 (X60205)

chalcone synthase [Zea mays]

264742 Seq. No.

7544 2.R1011 Contig ID xsy700210841.hl 5'-most EST

BLASTX Method g116380 NCBI GI 431 BLAST score 2.0e-42 E value 86 Match length 97 % identity

NCBI Description CHALCONE SYNTHASE C2 (NARINGENIN-CHALCONE SYNTHASE C2)



>gi_66554_pir__SYZMCC naringenin-chalcone synthase (EC
2.3.1.74) c2 - maize >gi_22218_emb_CAA42764_ (X60205)
chalcone synthase [Zea mays]

264743 Seq. No. 7544_3.R1011 Contig ID 5'-most EST uC-zmroteosinte017g09b1 Method BLASTX q116380 NCBI GI BLAST score 265 5.0e-23 E value Match length 51 % identity 100

NCBI Description CHALCONE SYNTHASE C2 (NARINGENIN-CHALCONE SYNTHASE C2) >gi_66554_pir__SYZMCC naringenin-chalcone synthase (EC 2.3.1.74) c2 - maize >gi 22218 emb CAA42764 (X60205)

chalcone synthase [Zea mays]

 Seq. No.
 264744

 Contig ID
 7549_1.R1011

 5'-most EST
 pmx700085331.h1

 Method
 BLASTX

 NCBI GI
 g585147

 BLAST score
 361

NCBI GI g585147 BLAST score 361 E value 7.0e-39 Match length 335 % identity 35

NCBI Description FLUG PROTEIN >gi_1078630 pir_A53186 flug protein - Emericella nidulans >gi 450258 (L27817) Flug [Emericella

nidulans]

Seq. No. 264745 Contig ID 7550 1.R1011

5'-most EST LIB3078-055-Q1-K1-H10

Method BLASTX
NCBI GI g1168863
BLAST score 203
E value 9.0e-16
Match length 75
% identity 55

NCBI Description CADMIUM INDUCED PROTEIN AS8 >gi_629507_pir__S47247 cadmium-induced protein - Arabidopsis thaliana

>gi 534902 emb CAA85363 (Z36896) cadmium induced protein

[Arabidopsis thaliana] >gi 2828282 emb CAA16696.1

(AL021687) cadmium-induced protein [Arabidopsis thaliana]

>gi 2832634 emb CAA16763 (AL021711) cadmium-induced

protein [Arabidopsis thaliana]

5'-most EST LIB3078-055-Q1-K1-H12

Method BLASTX
NCBI GI 93335366
BLAST score 144
E value 9.0e-09
Match length 64

Match length 64 % identity 41



```
NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]
                  264747
Seq. No.
                  7551 2.R1011
Contig ID
5'-most EST
                  xdb700340761.h1
                  264748
Seq. No.
                  7554 1.R1011
Contig ID
                  uC-zmrob73075e11b1
5'-most EST
                  BLASTX
Method
                  g2981439
NCBI GI
BLAST score
                   411
                   8.0e-40
E value
                  218
Match length
                   45
% identity
NCBI Description (AF051853) t-SNARE SED5 [Arabidopsis thaliana]
Seq. No.
                  264749
Contig ID
                  7555 1.R1011
5'-most EST
                  LIB36-020-Q1-E1-B8
Method
                  BLASTX
                  q4099835
NCBI GI
BLAST score
                   846
E value
                   1.0e-90
Match length
                   259
% identity
NCBI Description (U90266) bifunctional nuclease [Zinnia elegans]
                   264750
Seq. No.
                  7555 2.R1011
Contig ID
                  uC-zmflmo17301a01a1
5'-most EST
                   264751
Seq. No.
                   7555 4.R1011
Contig ID
                  hbs7\overline{0}1183049.h1
5'-most EST
Seq. No.
                   264752
                   7555 5.R1011
Contig ID
5'-most EST
                   LIB3137-016-Q1-K1-A4
Method
                   BLASTX
NCBI GI
                   g520582
BLAST score
                   163
E value
                   4.0e-11
                   67
Match length
                   52
% identity
NCBI Description (D37796) Ids3 [Hordeum vulgare]
                   264753
Seq. No.
                   7555 8.R1011
Contig ID
5'-most EST
                   uC-zmflmo17243f02a1
Method
                   BLASTX
                   q4099835
NCBI GI
BLAST score
                   244
E value
                   1.0e-20
Match length
                   77
% identity
```

36762

NCBI Description (U90266) bifunctional nuclease [Zinnia elegans]

Seq. No.

Contig ID

264760

7573_2.R1011



```
264754
Seq. No.
                  7556 1.R1011
Contig ID
                  tzu700202213.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g507158
BLAST score
                  1147
E value
                  1.0e-126
Match length
                  337
% identity
                  64
NCBI Description (U04815) PITSLRE alpha 1 [Homo sapiens]
                  264755
Seq. No.
                  7556 2.R1011
Contig ID
5'-most EST
                  uC-zmroteosinte032a03b1
                  BLASTX
Method
NCBI GI
                  q1082285
BLAST score
                  285
E value
                  4.0e-25
Match length
                  117
                  53
% identity
NCBI Description protein kinase (EC 2.7.1.37) cdc2-related PITSLRE alpha 2-3
                  - human
                  264756
Seq. No.
Contig ID
                  7564 1.R1011
                  LIB3078-055-Q1-K1-F7
5'-most EST
                  264757
Seq. No.
                  7569 1.R1011
Contig ID
5'-most EST
                  clt700043427.fl
Method
                  BLASTX
NCBI GI
                  g2911043
BLAST score
                  160
E value
                  1.0e-10
Match length
                  51
% identity
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
Seq. No.
                  264758
                  7569 2.R1011
Contig ID
                  clt700044218.f1
5'-most EST
Seq. No.
                  264759
                  7573 1.R1011
Contig ID
5'-most EST
                  LIB3066-013-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g3367568
BLAST score
                  748
E value
                  9.0e-89
Match length
                  256
% identity
                 (AL031135) protein kinase - like protein [Arabidopsis
NCBI Description
                  thaliana)
```

36763



60

% identity

```
5'-most EST
                  LIB3069-021-Q1-K1-E1
                  BLASTX
Method
                   g3860259
NCBI GI
                   181
BLAST score
                   6.0e-13
E value
                   72
Match length
                   65
% identity
                   (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                   264761
Seq. No.
                   7573 3.R1011
Contig ID
5'-most EST
                   xmt700257366.h1
                   BLASTX
Method
                   g3860259
NCBI GI
BLAST score
                   258
                   6.0e-22
E value
                   100
Match length
                   62
% identity
                   (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                   264762
Seq. No.
                   7580 1.R1011
Contig ID
5'-most EST
                   nwy700445261.h1
Method
                   BLASTX
                   g2351097
NCBI GI
BLAST score
                   1310
                   1.0e-145
E value
Match length
                   326
% identity
                   74
                  (AB006810) ATMRK1 [Arabidopsis thaliana]
NCBI Description
                   264763
Seq. No.
                   7583 1.R1011
Contig ID
                   xsy700212031.h1
5'-most EST
                   264764
Seq. No.
                   7585 1.R1011
Contig ID
                   LIB3156-021-Q1-K1-C5
5'-most EST
                   BLASTX
Method
                   q2244908
NCBI GI
                   760
BLAST score
                   7.0e-81
E value
                   195
Match length
                   74
% identity
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   264765
Seq. No.
Contig ID
                   7585 2.R1011
5'-most EST
                   LIB3136-011-Q1-K1-D9
                   BLASTX
Method
NCBI GI
                   q2244908
BLAST score
                   364
E value
                   1.0e-50
                   207
Match length
```

NCBI Description (Z97339) hypothetical protein [Arabidopsis thaliana]



```
264766
Seq. No.
Contig ID
                  7588 1.R1011
5'-most EST
                  LIB3060-047-Q1-K1-G5
Method
                  BLASTX
NCBI GI
                  g1170606
                  1114
BLAST score
                  1.0e-122
E value
Match length
                  222
                  100
% identity
                  ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                  >gi 629863 pir S45634 adenylate kinase (EC 2.7.4.3),
                  chloroplast - maize >gi 3114421 pdb 1ZAK A Chain A,
                  Adenylate Kinase From Maize In Complex With The Inhibitor
                  P1, P5-Bis (Adenosine-5'-)pentaphosphate (Ap5a)
                  >qi 3114422 pdb 1ZAK B Chain B, Adenylate Kinase From Maize
                  In Complex With The Inhibitor
                  P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)
Seq. No.
                  264767
                  7588 2.R1011
Contig ID
                  clt700042791.f1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1170606
BLAST score
                  387
                  3.0e - 37
E value
                  79
Match length
                  100
% identity
NCBI Description
                  ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE)
                  >gi 629863 pir S45634 adenylate kinase (EC 2.7.4.3),
                   chloroplast - maize >gi 3114421 pdb 1ZAK A Chain A,
                  Adenylate Kinase From Maize In Complex With The Inhibitor
                   P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)
```

>gi_3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor

P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)

264768 Seq. No. 7590 1.R1011 Contig ID $ypc7\overline{0}0804878.h1$ 5'-most EST BLASTX Method g2213884 NCBI GI 1330 BLAST score 1.0e-147 E value

388 Match length 68 % identity

(AF004166) 2-isopropylmalate synthase [Lycopersicon NCBI Description

pennellii]

Seq. No. 264769 Contig ID 7590 2.R1011 LIB3062-044-01-K1-H5 5'-most EST Method BLASTX NCBI GI q2213884

216 BLAST score 4.0e-18 E value 101 Match length 53 % identity



```
(AF004166) 2-isopropylmalate synthase [Lycopersicon
NCBI Description
                  pennellii]
                  264770
Seq. No.
                  7595 1.R1011
Contig ID
                  ntr700072913.h1
5'-most EST
                  BLASTX
Method
                  g4539292
NCBI GI
                  414
BLAST score
                  3.0e-40
E value
                  96
Match length
                  78
% identity
                  (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                  thaliana]
                  264771
Seq. No.
                  7595 2.R1011
Contig ID
                  LIB3150-020-Q1-N1-H5
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4539292
BLAST score
                  451
E value
                  5.0e-45
                  113
Match length
                  73
% identity
                  (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                  thaliana]
                  264772
Seq. No.
                  7595 4.R1011
Contig ID
5'-most EST
                   qmh700026842.f1
Seq. No.
                   264773
                   7597 1.R1011
Contig ID
                  LIB3079-052-Q1-K1-E12
5'-most EST
                   264774
Seq. No.
Contig ID
                   7600 1.R1011
                   LIB3078-055-Q1-K1-D6
5'-most EST
Method
                   BLASTX
NCBI GI
                   a3377797
BLAST score
                   601
E value
                   5.0e-62
Match length
                   185
% identity
                   (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                   by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                   H36046; coded for by A. thaliana cDNA T44067; coded for by
                   A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                   R90691 [Ara
Seq. No.
                   264775
Contig ID
                   7602 1.R1011
                   wyr700240602.hl
5'-most EST
```

36766

BLASTX

1873

g399213

0.0e + 00

Method NCBI GI

E value

BLAST score



Match length % identity

ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG NCBI Description

CD4B PRECURSOR >gi_100190_pir__B35905 CD4B protein - tomato >gi_170435 (M32604) ATP-dependent protease (CD4B)

[Lycopersicon esculentum]

264776 Seq. No.

7602 3.R1011 Contig ID

LIB3156-010-Q1-K1-E1 5'-most EST

BLASTX Method g461753 NCBI GI BLAST score 404 E value 3.0e-39 Match length 105 % identity

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

PRECURSOR >gi 419773 pir S31164 ATP-dependent ClpB

proteinase regulatory chain homolog precursor, chloroplast - garden pea >gi 169128 (L09547) nuclear encoded precursor

to chloroplast protein [Pisum sativum]

Seq. No. 264777

7602 4.R1011 Contig ID 5'-most EST bdu700382772.h1

Seq. No. 264778

Contig ID 7604 1.R1011

5'-most EST uC-zmroteosinte100d08b2

Method BLASTX NCBI GI q728970 BLAST score 163 E value 2.0e-10 Match length 355 23

% identity

NCBI Description MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX

TRANSPORTER 2) >gi_2119909_pir__ I39792 multidrug efflux transporter - Bacillus subtilis >gi_483941 (L32599) blt gene product [Bacillus subtilis] >gi 1303699 dbj BAA12355 (D84432) Blt [Bacillus subtilis] >gi_2635104_emb_CAB14600_ (Z99117) multidrug-efflux transporter [Bacillus subtilis]

Seq. No. 264779

Contig ID 7606 1.R1011

5'-most EST uC-zmrob73071a01b1

Method BLASTX NCBI GI g4415926 337 BLAST score 3.0e - 31E value Match length 277 % identity 34

NCBI Description (AC906282) unknown protein [Arabidopsis thaliana]

264780 Seq. No.

Contig ID 7609 1.R1011

5'-most EST uC-zmflmo17157e04a1



```
264781
Seq. No.
Contig ID
                  7612 1.R1011
                  LIB189-007-Q1-E1-G9
5'-most EST
                  BLASTX
Method
NCBI GI
                  q399213
                  2921
BLAST score
                  0.0e + 00
E value
Match length
                   664
% identity
                   86
                  ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
NCBI Description
                  CD4B PRECURSOR >gi 100190_pir__B35905 CD4B protein - tomato
                   >gi 170435 (M32604) ATP-dependent protease (CD4B)
                   [Lycopersicon esculentum]
Seq. No.
                   264782
                   7612 2.R1011
Contig ID
                   fwa700099434.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4105131
                   524
BLAST score
                   2.0e-53
E value
                   143
Match length
                   76
% identity
                  (AF043539) ClpC protease [Spinacia oleracea]
NCBI Description
Seq. No.
                   264783
                   7613 1.R1011
Contig ID
5'-most EST
                   pmx700090544.h1
Method
                   BLASTX
NCBI GI
                   q3128234
BLAST score
                   254
                   7.0e-29
E value
Match length
                   152
                   51
% identity
                  (AC004077) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   264784
Seq. No.
                   7619 1.R1011
Contig ID
                   LIB3159-003-Q1-K1-B10
5'-most EST
Method
                   BLASTX
                   g3319776
NCBI GI
                   396
BLAST score
                   3.0e-61
E value
Match length
                   142
                   85
% identity
                  (AJ007665) seryl-tRNA synthetase [Zea mays]
NCBI Description
                   264785
Seq. No.
                   7619 2.R1011
Contig ID
                   gct701174302.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3319776
                   383
BLAST score
                   1.0e-36
E value
                   79
Match length
```

91

% identity

NCBI Description



```
264786
Seq. No.
                  7619 3.R1011
Contig ID
                  LIB3078-054-Q1-K1-H5
5'-most EST
Method
                  BLASTX
                  q3319776
NCBI GI
BLAST score
                   385
                   6.0e-37
E value
Match length
                   81
                   91
% identity
                   (AJ007665) seryl-tRNA synthetase [Zea mays]
NCBI Description
                   264787
Seq. No.
                   7621 1.R1011
Contig ID
                   LIB3136-020-Q1-K1-C3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2146774
BLAST score
                   662
                   2.0e-69
E value
                   167
Match length
                   75
% identity
                   serine acetyltransferase (EC 2.3.1.30) Sat-52 - Arabidopsis
NCBI Description
                   thaliana >gi_905391 (U30298) serine acetyltransferase
                   [Arabidopsis thaliana]
                   264788
Seq. No.
                   7622 1.R1011
Contig ID
5'-most EST
                   tzu700206982.hl
Method
                   BLASTX
                   q3738322
NCBI GI
                   367
BLAST score
                   6.0e-35
E value
                   78
Match length
                   90
% identity
                   (AC005170) putative small nuclear ribonucleoprotein
NCBI Description
                   [Arabidopsis thaliana]
                   264789
Seq. No.
                   7622 2.R1011
Contig ID
                   xmt700267310.h1
5'-most EST
                   BLASTX
Method
                   g3738322
NCBI GI
                   366
BLAST score
                   9.0e-35
E value
                   79
Match length
                   90
% identity
                   (AC005170) putative small nuclear ribonucleoprotein
NCBI Description
                   [Arabidopsis thaliana]
                   264790
Seq. No.
                   7624 1.R1011
Contig ID
                   LIB3079-029-Q1-K1-A6
5'-most EST
Method
                   BLASTX
                   q4455223
NCBI GI
```

36769

452

201

7.0e-45

BLAST score

Match length

E value



```
% identity
                   (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   264791
Seq. No.
                   7627 1.R1011
Contig ID
                   LIB3\overline{0}78-055-Q1-K1-A2
5'-most EST
Method
                   BLASTX
                   g3249105
NCBI GI
BLAST score
                   222
                   1.0e-17
E value
Match length
                   144
% identity
                   35
                   (AC003114) Contains similarity to protein phosphatase 2C
NCBI Description
                   (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]
                   264792
Seq. No.
Contig ID
                   7630 1.R1011
                   uC-zmflb73190g03a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1730576
BLAST score
                   147
                   9.0e-09
E value
Match length
                   61
                   44
% identity
                   PROLINE IMINOPEPTIDASE (PROLYL AMINOPEPTIDASE)
NCBI Description
                   >gi_1084134_pir__JC4184 prolyl aminopeptidase (EC 3.4.11.5)
                   - Aeromonas sobria >gi 1236731 dbj BAA06380 (D30714)
                   prolyl aminopeptidase [Aeromonas sobria]
                   264793
Seq. No.
                   7637 1.R1011
Contig ID
                   LIB3078-054-Q1-K1-G5
5'-most EST
Method
                   BLASTX
                   g4335735
NCBI GI
BLAST score
                   426
                   1.0e-41
E value
Match length
                   119
% identity
                   71
                   (AC006248) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   264794
Seq. No.
Contig ID
                   7638 1.R1011
                   xdb7\overline{0}0338790.h1
5'-most EST
                   264795
Seq. No.
                   7644 1.R1011
Contig ID
5'-most EST
                   tfd700572550.h1
Method
                   BLASTX
                   q3335347
NCBI GI
BLAST score
                   1563
                   1.0e-174
E value
Match length
                   449
% identity
                   64
                   (AC004512) Contains similarity to ARI, RING finger protein
NCBI Description
```

gb_X98309 from Drosophila melanogaster. ESTs gb_T44383, gb_W43120, gb_N65868, gb_H36013, gb_AA042241, gb_T76869 and



gb_AA042359 come from this gene. [Arabidopsis thaliana]

264796 Seq. No. 7650_1.R1011 Contig ID wyr700236160.hl 5'-most EST BLASTX Method g1850546 NCBI GI 783 BLAST score 3.0e-83 E value 218 Match length

% identity 72 NCBI Description (U88045) syntaxin related protein AtVam3p [Arabidopsis

thaliana]

Seq. No. 264797
Contig ID 7650_2.R1011

5'-most EST LIB143-064-Q1-E1-C8

Method BLASTX
NCBI GI g1850546
BLAST score 183
E value 2.0e-13
Match length 83
% identity 48

% identity 48 NCBI Description (U88045) syntaxin related protein AtVam3p [Arabidopsis

thaliana]

Seq. No. 264798 Contig ID 7652 1.R1011

5'-most EST LIB3078-054-Q1-K1-F2

Seq. No. 264799 Contig ID 7656_1.R1011

5'-most EST LIB3078-054-Q1-K1-E12

5'-most EST LIB3060-013-Q1-K1-D7

Seq. No. 264801 Contig ID 7659_1.R1011

5'-most EST uC-zmflmo17236d11b1

Seq. No. 264802

Contig ID 7659_3.R1011 5'-most EST fwa700097268.h1

Method BLASTX
NCBI GI g2673913
BLAST score 529
E value 2.0e-60
Match length 182
% identity 63

NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]

 Seq. No.
 264803

 Contig ID
 7661_1.R1011

5'-most EST LIB3062-037-Q1-K1-C4

Method BLASTX



g1168537 NCBI GI BLAST score 1019 1.0e-111 E value 222 Match length 86 % identity

ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732 NCBI Description

aspartic proteinase (EC 3.4.23.-) - rice

>gi 218143 dbj BAA02242 (D12777) aspartic proteinase

[Oryza sativa]

264804 Seq. No. 7661 2.R1011 Contig ID

uC-zmroteosintel18g09b1 5'-most EST

BLASTX Method NCBI GI g1168537 BLAST score 1129 1.0e-124 E value Match length 236 90 % identity

ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732 NCBI Description

aspartic proteinase (EC 3.4.23.-) - rice

>gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase

[Oryza sativa]

264805 Seq. No. 7661 4.R1011 Contig ID

 $uC-z\overline{m}flb73286f02b1$ 5'-most EST

Method BLASTX g1168537 NCBI GI 661 BLAST score 4.0e-75 E value

Match length 164 84 % identity

ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732 NCBI Description

aspartic proteinase (EC 3.4.23.-) - rice

>gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase

[Oryza sativa]

264806 Seq. No.

7661_5.R1011 Contig ID 5'-most EST uC-zmflb73290q01b1

BLASTX Method NCBI GI g1168537 750 BLAST score 1.0e-79 E value Match length 175 80 % identity

NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732

aspartic proteinase (EC 3.4.23.-) - rice

>gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase

[Oryza sativa]

Seq. No. 264807

7666 1.R1011 Contig ID

uC-zmflMo17014d03b1 5'-most EST

BLASTN Method NCBI GI g3821780



BLAST score 36 E value 5.0e-10 Match length 36 % identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 264808 Contig ID 7666_2.R1011

5'-most EST uC-zmflmo17070a02a1

Seq. No. 264809 Contig ID 7666_3.R1011

5'-most EST uC-zmflmo17067e10b1

Seq. No. 264810 Contig ID 7672_1.R1011

5'-most EST uC-zmroteosinte046h07b1

Method BLASTX
NCBI GI g2914708
BLAST score 295
E value 3.0e-26

Match length 79 % identity 66

NCBI Description (AC003974) hypothetical protein [Arabidopsis thaliana]

>qi 3298553 (AC004681) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 264811

Contig ID 7675 1.R1011

5'-most EST uC-zmroteosinte021h11b1

Method BLASTX
NCBI GI g3450842
BLAST score 847
E value 1.0e-90
Match length 329
% identity 53

NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza

sativa]

Seq. No. 264812

Contig ID 7675_2.R1011

5'-most EST LIB3157-015-Q1-K1-B5

Seq. No. 264813

Contig ID 7676_1.R1011 5'-most EST ypc700804376.h1

Method BLASTX
NCBI GI g4580461
BLAST score 278
E value 2.0e-24
Match length 114
% identity 44

NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 264814

Contig ID 7676 2.R1011

5'-most EST LIB3150-051-Q1-N1-D3



```
Method
                  BLASTX
                  g4580461
NCBI GI
                  834
BLAST score
                   2.0e-89
E value
                   198
Match length
                   74
% identity
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                   264815
Seq. No.
                   7676 3.R1011
Contig ID
                   ntr700075093.h1
5'-most EST
Method
                   BLASTX
                   g4580461
NCBI GI
                   339
BLAST score
                   1.0e-31
E value
Match length
                   82
                   74
% identity
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                   264816
Seq. No.
                   7676 4.R1011
Contig ID
                   xmt700263705.h1
5'-most EST
Method
                   BLASTX
                   g4580461
NCBI'GI
                   202
BLAST score
                   2.0e-15
E value
                   48
Match length
% identity
                   73
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                   264817
Seq. No.
                   7677 1.R1011
Contig ID
                   LIB3078-054-Q1-K1-B6
5'-most EST
                   BLASTX
Method
                   g2494261
NCBI GI
                   817
BLAST score
                   1.0e-87
E value
Match length
                   209
                   74
% identity
                  ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
NCBI Description
                   >gi_99903_pir__S21567 translation elongation factor Tu
                   precursor - soybean chloroplast >gi 18776_emb_CAA46864_
                   (X66062) EF-Tu [Glycine max] >gi_448921_prf__1918220A
                   elongation factor Tu [Glycine max]
                   264818
Seq. No.
Contig ID
                   7679 1.R1011
5'-most EST
                   zuv700354934.h1
                   BLASTX
Method
                   g1731146
NCBI GI
BLAST score
                   422
                   6.0e-41
E value
```

Match length 202 % identity 44

NCBI Description HYPOTHETICAL 42.1 KD PROTEIN ZK1307.9 IN CHROMOSOME III >gi 3881615 emb CAA87435 (Z47358) similar to YJU2 protein

[Caenorhabditis elegans]



 Seq. No.
 264819

 Contig ID
 7679 3.R1011

 5'-most EST
 xdb700342078.h1

 Seq. No.
 264820

 Contig ID
 7680 1.R1011

 5'-most EST
 uC-zmflmo17242c12b1

Method BLASTX
NCBI GI g1724110
BLAST score 956
E value 1.0e-103
Match length 326
% identity 57

NCBI Description (U79770) cinnamyl-alcohol dehydrogenase Eli3

[Mesembryanthemum crystallinum]

Method BLASTX
NCBI GI g2980793
BLAST score 667
E value 1.0e-69
Match length 211
% identity 60

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 264822 Contig ID 7683_1.R1011

5'-most EST LIB3137-009-Q1-K1-E10

Method BLASTX
NCBI GI g3513727
BLAST score 1053
E value 1.0e-115
Match length 307
% identity 68

NCBI Description (AF080118) contains similarity to TPR domains (Pfam:

TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative

protein [Arabidopsis Thaliana]

Seq. No. 264823

Contig ID 7686_1.R1011

5'-most EST uC-zmflmo17335c11b1

Seq. No. 264824

Contig ID 7687_1.R1011

5'-most EST uC-zmroteosinte017h04b1

Seq. No. 264825

Contig ID 7693_1.R1011

5'-most EST LIB3078-054-Q1-K1-A1

Method BLASTX
NCBI GI g2864610
BLAST score 327



E value 5.0e-30 Match length 108 % identity 56

NCBI Description (AL021811) putative protein [Arabidopsis thaliana] >gi_4049336_emb_CAA22561_ (AL034567) putative protein

[Arabidopsis thaliana]

Seq. No. 264826 Contig ID 7694_1.R1011

5'-most EST LIB3078-054-Q1-K1-A10

Method BLASTX
NCBI GI g4455280
BLAST score 402
E value 4.0e-39
Match length 93
% identity 67

NCBI Description (AL035527) putative protein [Arabidopsis thaliana]

Seq. No. 264827 Contig ID 7696_1.R1011

5'-most EST uC-zmflmo17313d07b1

Method BLASTX
NCBI GI g2911044
BLAST score 327
E value 9.0e-36
Match length 215
% identity 47

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 264828

Contig ID 7696_2.R1011

5'-most EST LIB3069-055-Q1-K1-C5

5'-most EST uC-zmflmo17223b11b1

Method BLASTX
NCBI GI g1705677
BLAST score 3583
E value 0.0e+00
Match length 777
% identity 89

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG

>gi_2118115_pir__S60112 cell division control protein CDC48
homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell

division cycle protein [Arabidopsis thaliana]

 Seq. No.
 264830

 Contig ID
 7697_2.R1011

 5'-most EST
 pmx700091431.h1

Method BLASTX
NCBI GI g1705677
BLAST score 440
E value 2.0e-43
Match length 131
% identity 70

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG



>gi_2118115_pir__S60112 cell division control protein CDC48
homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell
division cycle protein [Arabidopsis thaliana]

 Seq. No.
 264831

 Contig ID
 7697_3.R1011

 5'-most EST
 uer700579090.h1

Method BLASTX
NCBI GI g1705677
BLAST score 443
E value 5.0e-62
Match length 157
% identity 82

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG

>gi_2118115_pir__S60112 cell division control protein CDC48
homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell

division cycle protein [Arabidopsis thaliana]

Seq. No. 264832 Contig ID 7697_4.R1011

5'-most EST LIB3069-022-Q1-K1-C6

Method BLASTX
NCBI GI g1705677
BLAST score 475
E value 1.0e-47
Match length 100
% identity 91

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG

>gi_2118115_pir__S60112 cell division control protein CDC48
homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell

division cycle protein [Arabidopsis thaliana]

Seq. No. 264833

Contig ID 7697_7.R1011

5'-most EST uC-zmflb73188b10b1

Method BLASTX
NCBI GI g1705678
BLAST score 359
E value 8.0e-34
Match length 109
% identity 73

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING

PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213) valosin-containing protein [Glycine max]

Seq. No. 264834

Contig ID 7700_1.R1011

5'-most EST uC-zmroteosinte027g01b1

Seq. No. 264835

Contig ID 7703 1.R1011

5'-most EST uC-zmflb73115q02a1

Method BLASTN
NCBI GI g3821780
BLAST score 34
E value 3.0e-09
Match length 34



% identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No.

264836

Contig ID 5'-most EST 7703 2.R1011 tzu700201628.hl

Seq. No.

264837

Contiq ID

7703 3.R1011

5'-most EST

LIB189-020-Q1-E1-G1

Seq. No.

264838

Contig ID

7704 1.R1011

5'-most EST

LIB3079-041-Q1-K1-D10

Method

BLASTX

NCBI GI BLAST score g4325372 295

E value

5.0e-26

Match length

214

% identity NCBI Description 39 (AF128396) contains similarity to protein disulfide

isomerases [Arabidopsis thaliana]

Seq. No.

264839

Contig ID

7704 2.R1011

5'-most EST

uC-zmflmo17126b07b1

Method NCBI GI BLAST score BLASTX g4325372

E value

302 5.0e-27

Match length

221

% identity

38

NCBI Description

(AF128396) contains similarity to protein disulfide

isomerases [Arabidopsis thaliana]

Seq. No.

264840

7706 1.R1011

Contig ID 5'-most EST

uC-zmflmo17366e04a1

Seq. No.

264841

Contig ID

7706 2.R1011

5'-most EST

gct701167845.h1

Seq. No.

264842

Contig ID

7709 1.R1011

5'-most EST

lhp700053459.rl BLASTX

Method NCBI GI

g3258238

BLAST score

159

E value Match length 3.0e-10

190

% identity

23

NCBI Description

(AP000007) 224aa long hypothetical protein [Pyrococcus

horikoshii]

Seq. No.

264843

Contig ID

7712_1.R1011



fwa700097532.h1 5'-most EST BLASTX Method g2598049 NCBI GI 880 BLAST score 1.0e-94 E value 224 Match length 76 % identity (Y15269) chloroplast drought-induced stress protein, 34 kD) NCBI Description [Solanum tuberosum] 264844 Seq. No. 7712 2.R1011 Contig ID LIB3066-054-Q1-K1-D4 5'-most EST BLASTX Method g2632088 NCBI GI BLAST score 267 3.0e-23 E value Match length 95 60 % identity (Y15489) Plastid-lipid-Associated Protein [Nicotiana NCBI Description tabacum] 264845 Seq. No. 7712 3.R1011 Contig ID uC-zmflmo17322e10a1 5'-most EST BLASTX Method g2598049 NCBI GI BLAST score 203 7.0e-16 E value Match length 53 72 % identity (Y15269) chloroplast drought-induced stress protein, 34 kD) NCBI Description [Solanum tuberosum] 264846 Seq. No. 7713 1.R1011 Contig ID 5'-most EST LIB3078-053-Q1-K1-F6 Method BLASTX a3738334 NCBI GI 293 BLAST score 7.0e-26 E value Match length 354 33 % identity (AC005170) unknown protein [Arabidopsis thaliana] NCBI Description 264847 Seq. No. Contig ID 7719 1.R1011 5'-most EST LIB3062-020-Q1-K1-H3 264848 Seq. No. 7719 2.R1011 Contig ID fwa700101930.hl 5'-most EST

Seq. No. 264849 Contig ID 7722_1.R1011

5'-most EST LIB84-001-Q1-E1-C6

Method BLASTX



NCBI GI q2829751 BLAST score 212 1.0e-16 E value Match length 114 39 % identity MACROPHAGE MIGRATION INHIBITORY FACTOR HOMOLOG (BMMIF) NCBI Description >gi_1850559 (U88035) macrophage migration inhibitory factor [Brugia malayi] >gi_2190976 (AF002699) macrophage migration inhibitory factor [Brugia malayi] 264850 Seq. No. 7723 1.R1011 Contig ID LIB3078-053-Q1-K1-F10 5'-most EST BLASTX Method g3777598 NCBI GI 417 BLAST score 1.0e-40 E value 108 Match length % identity 80 (AF095707) 30S ribosomal protein S17 [Oryza sativa] NCBI Description 264851 Seq. No. 7726 1.R1011 Contig ID nbm700471492.hl 5'-most EST BLASTX Method g2244847 NCBI GI 363 BLAST score 9.0e - 34E value Match length 515 % identity 28 (Z97337) hydroxyproline-rich glycoprotein homolog NCBI Description [Arabidopsis thaliana] 264852 Seq. No. 7726 5.R1011 Contig ID LIB3067-005-Q1-K1-G8 5'-most EST 264853 Seq. No. Contig ID 7730 1.R1011 uC-zmroteosinte062c09b1 5'-most EST BLASTX Method g3212116 NCBI GI 278 BLAST score 3.0e-24E value 138 Match length 43 % identity

NCBI Description (Y17393) prefoldin subunit 2 [Mus musculus]

 Seq. No.
 264854

 Contig ID
 7733_1.R1011

 5'-most EST
 LIB3067-049-Q1-K1-G2

 Method
 BLASTX

 NCBI GI
 g4008006

BLAST score 580 E value 2.0e-59 Match length 192 % identity 57



(AF084034) receptor-like protein kinase [Arabidopsis NCBI Description thaliana] 264855 Seq. No. 7733 2.R1011 Contig ID uC-zmflb73017b07b1 5'-most EST Method BLASTX g4008006 NCBI GI 457 BLAST score 1.0e-45 E value 144 Match length % identity 61 (AF084034) receptor-like protein kinase [Arabidopsis NCBI Description thaliana] 264856 Seq. No. 7737 1.R1011 Contig ID clt700045605.f1 5'-most EST BLASTX Method q4115379 NCBI GI 385 BLAST score 8.0e-37 E value 204 Match length 45 % identity (AC005967) putative carbonyl reductase [Arabidopsis NCBI Description thaliana] Seq. No. 264857 7738 1.R1011 Contig ID LIB3069-051-Q1-K1-G12 5'-most EST BLASTX Method g4262154 NCBI GI 458 BLAST score E value 3.0e-45266 Match length 45 % identity (AC005275) putative protein phosphatase regulatory subunit NCBI Description [Arabidopsis thaliana] 264858 Seq. No. 7740 1.R1011 Contig ID 5'-most EST LIB3068-038-Q1-K1-F1 Method BLASTX q133933 NCBI GI 1154 BLAST score 1.0e-126 E value

E value 1.06
Match length 224
% identity 100

NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S3

>gi_1363605 pir__ S58590 ribosomal protein S3 - maize
chloroplast >gi_12469 emb_CAA68427_ (Y00340) ribosomal
protein S3 [Zea mays] >gi_902260_emb_CAA60324_ (X86563)

ribosomal protein S3 [Zea mays]

Seq. No. 264859 Contig ID 7743 1.R1011

5'-most EST LIB3078-053-Q1-K1-D8



```
264860
Seq. No.
                  7743 2.R1011
Contig ID
                  xsy700209740.hl
5'-most EST
                   264861
Seq. No.
                   7744 1.R1011
Contig ID
                   uC-zmflb73051f07b1
5'-most EST
                   264862
Seq. No.
                   7744 2.R1011
Contig ID
                   xdb7\overline{0}0337147.h1
5'-most EST
                   264863
Seq. No.
                   7746 1.R1011
Contig ID
                   clt700045173.f1
5'-most EST
                   BLASTX
Method
                   q1651654
NCBI GI
BLAST score
                   276
                   6.0e-24
E value
                   142
Match length
                   39
% identity
                  (D90899) hypothetical protein [Synechocystis sp.]
NCBI Description
                   264864
Seq. No.
                   7757 1.R1011
Contig ID
                   LIB83-010-Q1-E1-G3
5'-most EST
Seq. No.
                   264865
                   7759 1.R1011
Contig ID
                   LIB3067-019-Q1-K1-G8
5'-most EST
                   BLASTX
Method
                   g1155068
NCBI GI
BLAST score
                   266
                   3.0e-24
E value
                   146
Match length
                   45
% identity
                   (X94976) cell wall-plasma membrane linker protein [Brassica
NCBI Description
                   napus]
                   264866
Seq. No.
                   7759 2.R1011
Contig ID
                   pmx700088766.hl
5'-most EST
                   BLASTX
Method
                   g2244874
NCBI GI
                   270
BLAST score
                   8.0e-25
E value
Match length
                   141
                    52
 % identity
NCBI Description (Z97338) coll wall protein homolog [Arabidopsis thaliana]
                    264867
 Seq. No.
                    7759 4.R1011
Contig ID
                    wty700168145.hl
 5'-most EST
                    264868
 Seq. No.
```

7760 1.R1011

Contig ID



5'-most EST rvt700548735.h1 Method BLASTX q1723176 NCBI GI BLAST score 254 1.0e-21 E value 163 Match length 39 % identity HYPOTHETICAL 22.4 KD PROTEIN SLL0615 NCBI Description >gi_1001617_dbj_BAA10348_ (D64002) transmembrane protein FT27 [Synechocystis sp.] >gi 1256592 (U38892) similar to Mus musculus transmembrane protein (clone pFT27); Method: conceptual translation supplied by author; ORF206 [Synechocystis sp.] 264869 Seq. No. Contig ID 7763 1.R1011 gct701180465.hl 5'-most EST Method BLASTX g3402719 NCBI GI BLAST score 452 1.0e-44 E value Match length 112 74 % identity (AC004261) unknown protein [Arabidopsis thaliana] NCBI Description 264870 Seq. No. 7770 1.R1011 Contig ID 5'-most EST uC-zmflmo17273h12b1 Method BLASTX q3850588 NCBI GI 187 BLAST score 4.0e-13E value 466 Match length % identity 21 (AC005278) Contains similarity to gb AB011110 KIAA0538 NCBI Description protein from Homo sapiens brain and to phospholipid-binding domain C2 PF_00168. ESTs gb_AA585988 and gb_T04384 come from this gene. [Arabidopsis thaliana] 264871 Seq. No. 7770 2.R1011 Contig ID uC-zmflb73272d02a1 5'-most EST 264872 Seq. No. 7770 3.R1011 Contig ID 5'-most EST LIB143-004-Q1-E1-D3

Seq. No. 264873

Contig ID 7772_1.R1011 5'-most EST yd1700405307.h1

Method BLASTX
NCBI GI g4309969
BLAST score 802
E value 2.0e-85
Match length 259
% identity 57

NCBI Description (AC002983) putative phosphoglyceride transfer protein

% identity



[Arabidopsis thaliana]

```
264874
Seq. No.
                  7774 1.R1011
Contig ID
                  xmt700257314.h1
5'-most EST
                  BLASTX
Method
                  q4406775
NCBI GI
BLAST score
                  282
                  2.0e-24
E value
                  388
Match length
                  26
% identity
                  (AC006836) unknown protein [Arabidopsis thaliana]
NCBI Description
                  264875
Seq. No.
                  7774 2.R1011
Contig ID
5'-most EST
                  LIB3078-052-Q1-K1-F11
Seq. No.
                  264876
                  7774 3.R1011
Contig ID
                  LIB83-013-Q1-E1-A5
5'-most EST
                   264877
Seq. No.
                  7779 1.R1011
Contig ID
                   LIB3078-052-Q1-K1-F7
5'-most EST
                   BLASTX
Method
                   q4539351
NCBI GI
BLAST score
                   953
                   1.0e-107
E value
Match length
                   307
% identity
                   67
                  (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                   264878
Seq. No.
                   7779_2.R1011
Contig ID
                   uC-zmflb73129b08a1
5'-most EST
                   BLASTX
Method
                   g4539351
NCBI GI
                   282
BLAST score
                   3.0e-25
E value
                   65
Match length
                   80
% identity
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
                   264879
Seq. No.
                   7780 1.R1011
Contig ID
                   LIB3078-052-Q1-K1-F9
5'-most EST
                   264880
Seq. No.
                   7783_1.R1011
Contig ID
                   LIB36-013-Q1-E1-C5
5'-most EST
                   BLASTN
Method
                   q4185305
NCBI GI
BLAST score
                   248
                   1.0e-137
E value
                   392
Match length
                   91
```

36784

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21

Seq. No.

264887



(sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete cds; and unknown genes

```
Seq. No.
                   264881
                   7784 1.R1011
Contig ID
                   fwa700101448.h1
5'-most EST
                   BLASTX
Method
                  g3292814
NCBI GI
BLAST score
                   919
                   2.0e-99
E value
                   248
Match length
                  71
% identity
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
Seq. No.
                   264882
Contig ID
                   7784 2.R1011
5'-most EST
                  LIB36-013-Q1-E1-G1
Method
                  BLASTX
                   a3292814
NCBI GI
BLAST score
                   833
                   4.0e-89
E value
Match length
                   215
% identity
                   75
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
                   264883
Seq. No.
Contig ID
                   7784 3.R1011
5'-most EST
                   tfd700572530.h1
                   BLASTX
Method
                   g3292814
NCBI GI
BLAST score
                   193
E value
                   2.0e-14
Match length
                   43
                   81
% identity
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
Seq. No.
                   264884
                   7784 4.R1011
Contig ID
5'-most EST
                   LIB189-014-Q1-E1-F5
Method
                   BLASTX
NCBI GI
                   g3292814
BLAST score
                   347
E value
                   1.0e-32
Match length
                   86
% identity
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
Seq. No.
                   264885
Contig ID
                   7788 1.R1011
5'-most EST
                   dyk700105386.h1
Seq. No.
                   264886
Contig ID
                   7788 4.R1011
                   uC-zmflmo17011f03b1
5'-most EST
```



```
Contig ID
                   7788 6.R1011
5'-most EST
                   kem700612289.h1
                   264888
Seq. No.
                   7789 1.R1011
Contig ID
                   uC-zmflmo17175c10b1
5'-most EST
                   BLASTX
Method
                   g2144098
NCBI GI
                   488
BLAST score
                   1.0e-48
E value
Match length
                   271
                   41
% identity
                   SC2 - rat >gi 256994 bbs 115268 (S45663) SC2=synaptic
NCBI Description
                   glycoprotein [rats, brain, Peptide, 308 aa] [Rattus sp.]
                   264889
Seq. No.
                   7789 2.R1011
Contig ID
                   LIB3156-003-Q1-K1-E2
5'-most EST
                   BLASTX
Method
                   q2144098
NCBI GI
                   334
BLAST score
                   7.0e-31
E value
                   159
Match length
                   47
% identity
                   SC2 - rat >gi 256994 bbs 115268 (S45663) SC2=synaptic
NCBI Description
                   glycoprotein [rats, brain, Peptide, 308 aa] [Rattus sp.]
Seq. No.
                   264890
                   7791 1.R1011
Contig ID
                   LIB3078-052-Q1-K1-D8
5'-most EST
                   264891
Seq. No.
                   7794 1.R1011
Contig ID
                   clt700044781.f1
5'-most EST
                   264892
Seq. No.
Contig ID
                   7800 1.R1011
5'-most EST
                   LIB84-002-Q1-E1-C9
Method
                   BLASTX
NCBI GI
                   a1730981
BLAST score
                   195
E value
                   2.0e-14
Match length
                   167
% identity
                   HYPOTHETICAL 41.0 KD PROTEIN IN NUCB-AROD INTERGENIC REGION
NCBI Description
                   >gi_1303788_dbj_BAA12444_ (D84432) YqeH [Bacillus subtilis]
>gi_2635013_emb_CAB14509_ (Z99117) similar to hypothetical
                   proteins [Bacillus subtilis]
                    264893
Seq. No.
                   7801 1.R1011
Contig ID
```

5'-most EST uC-zmflb73054c03b1

Method BLASTX
NCBI GI g399900
BLAST score 489
E value 1.0e-48
Match length 255



% identity 46 HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT5 (HD-ZIP PROTEIN 5) NCBI Description (HD-ZIP PROTEIN ATHB-1) >gi_99659_pir__S16325 homeotic

protein Athb-1 - Arabidopsis thaliana

>gi_16329_emb_CAA41625_ (X58821) Athb-1 protein

[Arabidopsis thaliana]

264894 Seq. No. 7801 2.R1011 Contig ID

uC-zmroteosinte002b06b1 5'-most EST

Seq. No. 264895 7802 1.R1011 Contig ID

LIB3137-058-Q1-K1-H6 5'-most EST

Method BLASTX NCBI GI q1352881 147 BLAST score 7.0e-09 E value 123 Match length 31 % identity

HYPOTHETICAL 15.7 KD PROTEIN IN NUP85-SSC1 INTERGENIC NCBI Description

REGION >gi 1078266 pir S57063 probable membrane protein

YJR044c - yeast (Saccharomyces cerevisiae) >gi 1015699_emb_CAA89572_ (Z49544) ORF YJR044c [Saccharomyces cerevisiae] >gi 1197072 (L36344) ORF;

putative [Saccharomyces cerevisiae]

Seq. No. 264896

7810 1.R1011 Contig ID pmx700088774.hl 5'-most EST

BLASTX Method g133872 NCBI GI 1113 BLAST score 1.0e-131 E value 375 Match length 66 % identity

NCBI Description 30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1) >gi_282838_pir__S26494 ribosomal protein S1, chloroplast spinach >gi_322404_pir__A44121 small subunit ribosomal protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_ (X66135) ribosomal protein S1 [Spinacia oleracea] >gi_170143 (M82923) chloroplast ribosomal protein S1

[Spinacia oleracea]

264897 Seq. No. 7813_1.R1011 Contig ID

5'-most EST LIB83-006-Q1-E1-C9

Method BLASTX NCBI GI q2809245 BLAST score 430 E value 3.0e-42Match length 106 % identity 76

(AC002560) F21B7.14 [Arabidopsis thaliana] NCBI Description

264898 Seq. No. Contig ID 7813 2.R1011



```
LIB3078-024-Q1-K1-E4
5'-most EST
Method
                  BLASTX
                  q2809245
NCBI GI
BLAST score
                  394
                  6.0e - 38
E value
Match length
                  104
                  71
% identity
NCBI Description (AC002560) F21B7.14 [Arabidopsis thaliana]
                  264899
Seq. No.
                  7813 3.R1011
Contig ID
                  clt700044727.fl
5'-most EST
                  264900
Seq. No.
                   7814 1.R1011
Contig ID
                  uC-zmflmo17190a12b1
5'-most EST
                   264901
Seq. No.
Contig ID
                   7814 3.R1011
                   uC-zmflb73025f02a1
5'-most EST
                   264902
Seq. No.
                   7818 1.R1011
Contig ID
                   LIB3150-006-Q1-N1-A7
5'-most EST
                   BLASTX
Method
                   g3763927
NCBI GI
                   939
BLAST score
                   1.0e-101
E value
Match length
                   285
% identity
                   65
                  (AC004450) putative carboxyphosphoenolpyruvate mutase
NCBI Description
                   [Arabidopsis thaliana]
                   264903
Seq. No.
                   7818 2.R1011
Contig ID
                   LIB143-013-Q1-E1-G9
 5*-most EST
 Seq. No.
                   264904
                   7820 1.R1011
 Contig ID
                   LIB189-023-Q1-E1-A2
 5'-most EST
                   BLASTX
Method
                   g2224810
 NCBI GI
                   754
 BLAST score
                   6.0e-80
 E value
                   251
 Match length
 % identity
 NCBI Description (Z97022) cysteine proteinase [Hordeum vulgare]
                   264905
 Seq. No.
                   7827 1.R1011
 Contig ID
 5'-most EST
                   LIB36-015-Q1-E1-G4
                   BLASTX
 Method
                   q1653463
 NCBI GI
                   158
 BLAST score
```

36788

2.0e-10

72

46

E value

Match length

% identity



```
NCBI Description (D90913) hydrogenase component [Synechocystis sp.]
                  264906
Seq. No.
                  7829 1.R1011
Contig ID
                  uC-zmflb73232h06b1
5'-most EST
                  BLASTX
Method
                  q4314378
NCBI GI
                  447
BLAST score
                  2.0e-62
E value
                  334
Match length
                  41
% identity
                  (AC006232) putative lipase [Arabidopsis thaliana]
NCBI Description
                  264907
Seq. No.
                  7831 1.R1011
Contig ID
                  fdz701161833.hl
5'-most EST
                  BLASTX
Method
                  q2492514
NCBI GI
BLAST score
                  1361
E value
                  1.0e-151
                  283
Match length
                   95
% identity
                  CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
NCBI Description
                  >qi 1483215 emb CAA68141 (X99808) chloroplast FtsH
                  protease [Arabidopsis thaliana]
                   264908
Seq. No.
                   7831 2.R1011
Contig ID
5'-most EST
                  LIB3088-002-Q1-K1-E12
                   264909
Seq. No.
                   7833 1.R1011
Contig ID
                   uC-zmflb73126q05b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2369766
BLAST score
                   865
                   9.0e-93
E value
Match length
                   322
                   55
% identity
NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]
Seq. No.
                   264910
                   7833 2.R1011
Contig ID
                   uC-zmflmo17152b01b1
5'-most EST
                   BLASTX
Method
                   g2369766
NCBI GI
```

885 BLAST score

4.0e-95 E value 301 Match length % identity 62

(AJ001304) hypothetical protein [Citrus x paradisi] NCBI Description

264911 Seq. No. 7833 4.R1011 Contig ID uC-zmflmo17250e06a1 5'-most EST

264912 Seq. No.



```
7835 1.R1011
Contig ID
                   cat700016830.r2
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4510381
BLAST score
                   207
                   1.0e-15
E value
                   145
Match length
% identity
                    39
                   (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   264913
                   7835 2.R1011
Contig ID
                   rvt7\overline{0}0553108.h1
5'-most EST
Seq. No.
                    264914
                    7837 1.R1011
Contig ID
                    ntr700076058.h1
5'-most EST
                    BLASTX
Method
NCBI GI
                    q1345683
                    2492
BLAST score
                    0.0e + 00
E value
                    496
Match length
                    93
% identity
                    CATALASE ISOZYME 3 >gi_487045_pir__S37379 catalase (EC
NCBI Description
                    1.11.1.6) 3 - maize >g\overline{i}_16843\overline{7} (L\overline{05}934) catalase [Zea mays]
                    264915
Seq. No.
                    7837 2.R1011
Contig ID
5'-most EST
                    LIB3060-030-Q1-K1-F3
Method
                    BLASTX
                    q1345683
NCBI GI
                    953
BLAST score
                    1.0e-103
E value
Match length
                    226
                    81
% identity
NCBI Description CATALASE ISOZYME 3 >gi_487045_pir__S37379 catalase (EC
                    1.11.1.6) 3 - maize >g\overline{i}_{1}16843\overline{7} (L05934) catalase [Zea mays]
                    264916
Seq. No.
                    7837 3.R1011
Contig ID
5'-most EST
                    gct701167703.h1
                    BLASTX
Method
                    g4039152
NCBI GI
                    165
BLAST score
                    4.0e-11
E value
                    36
Match length
                    81
% identity
                    (AF104221) low temperature and salt responsive protein
NCBI Description
                    LTI6B [Arabidopsis thaliana] >gi_4325219_gb_AAD17303_
                    (AF122006) hydrophobic protein [Arabidopsis thaliana]
                    264917
 Seq. No.
```

7837 4.R1011 Contig ID

LIB3150-069-P2-K1-G3 5'-most EST

BLASTX Method q4490737 NCBI GI 610 BLAST score



```
2.0e-76
E value
Match length
                   292
                   57
% identity
                   (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   264918
                   7837 5.R1011
Contig ID
                   fC-z\overline{m}le700433471a4
5'-most EST
                   BLASTX
Method
                   g231689
NCBI GI
                   2626
BLAST score
                   0.0e+00
E value
                   493
Match length
                   99
% identity
                   CATALASE ISOZYME 2 >gi_100861_pir__S18819 catalase (EC
NCBI Description
                   1.11.1.6) - maize >gi_22234_emb_CAA38588_ (X54819) catalase
                   [Zea mays]
                   264919
Seq. No.
                   7837 6.R1011
Contig ID
                   uC-zmflb73191d03b1
5'-most EST
                   BLASTN
Method
                   g21856
NCBI GI
BLAST score
                   54
                   4.0e-21
E value
                   179
Match length
                   83
% identity
                   Wheat rDNA 25S-18S intergenic region EcoRI-BamHI fragment
NCBI Description
                   264920
Seq. No.
                   7837 7.R1011
Contig ID
                    fC-zmle700428273r2
5'-most EST
                   BLASTX
Method
                   g168433
NCBI GI
                    196
BLAST score
                    4.0e-15
E value
                    38
Match length
                    100
 % identity
NCBI Description (J02976) catalase [Zea mays]
                    264921
 Seq. No.
                    7837 8.R1011
 Contig ID
                    uC-z\overline{m}flb73192h11b1
 5'-most EST
                    BLASTX
 Method
                    g2149640
 NCBI GI
                    324
 BLAST score
                    1.0e-29
 E value
 Match length
                    81
 % identity
 NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]
                    264922
 Seq. No.
                    7837 10.R1011
 Contig ID
                    qct701173035.h2
 5'-most EST
```

Contig ID 7837_12.R1011

Seq. No.

264923



5'-most EST uC-zmflb73325e09a1

Method BLASTX
NCBI GI g4039153
BLAST score 168
E value 2.0e-11
Match length 36
% identity 75

NCBI Description (AF104221) low temperature and salt responsive protein

LTI6A [Arabidopsis thaliana] >gi_4325217_gb_AAD17302_(AF122005) hydrophobic protein [Arabidopsis thaliana]

Seq. No. 264924

Contig ID 7837_13.R1011

5'-most EST uC-zmroteosinte084g09b1

Method BLASTX
NCBI GI 94039152
BLAST score 165
E value 3.0e-11
Match length 36
% identity 81

NCBI Description (AF104221) low temperature and salt responsive protein

LTI6B [Arabidopsis thaliana] >gi_4325219_gb_AAD17303_

(AF122006) hydrophobic protein [Arabidopsis thaliana]

Seq. No. 264925

Contig ID 7837_14.R1011

5'-most EST uC-zmflmo17131d07b1

Method BLASTX
NCBI GI g1345683
BLAST score 287
E value 2.0e-25
Match length 62
% identity 89

NCBI Description CATALASE ISOZYME 3 >gi_487045_pir__S37379 catalase (EC

1.11.1.6) 3 - maize $> g\overline{i}_1 = 168437$ (LO5934) catalase [Zea mays]

Seq. No. 264926

Contig ID 7837_15.R1011

5'-most EST LIB3068-050-Q1-K1-B6

Method BLASTN
NCBI GI g22274
BLAST score 81
E value 2.0e-37
Match length 81
% identity 100

NCBI Description Maize 26S - 17S rDNA spacer region from Black Mexican Sweet

(BMS) suspension cells

Seq. No. 264927

Contig ID 7837_16.R1011 5'-most EST nwy700445520.h1

Seq. No. 264928

Contig ID 7837_18.R1011 5'-most EST gwl700616485.h1

Method BLASTX NCBI GI g2190992

NCBI GI

BLAST score

g505100

253



```
343
BLAST score
                  3.0e-32
E value
                  107
Match length
                  67
% identity
NCBI Description (AF004358) glutathione S-transferase TSI-1 [Aegilops
                  tauschii]
                  264929
Seq. No.
                  7837 19.R1011
Contig ID
5'-most EST
                  uC-zmrob73034c08a1
Method
                  BLASTN
                  g169818
NCBI GI
BLAST score
                  159
                  3.0e-84
E value
Match length
                  260
                  92
% identity
NCBI Description Rice 25S ribosomal RNA gene
                  264930
Seq. No.
                  7847 1.R1011
Contig ID
5'-most EST
                 pmx700089777.h1
Method
                  BLASTX
NCBI GI
                  g3096939
BLAST score
                  391
E value
                  1.0e-37
Match length
                  114
% identity
                  64
NCBI Description (AL023094) putative protein [Arabidopsis thaliana]
                  264931
Seq. No.
Contig ID
                  7853 1.R1011
5'-most EST
                  LIB3069-029-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g4503527
BLAST score
                  882
E value
                  8.0e-95
Match length
                  370
                  44
% identity
NCBI Description UNKNOWN >gi 1778051 (U62583) Prt1 homolog [Homo sapiens]
                  264932
Seq. No.
                  7853 2.R1011
Contig ID
5'-most EST
                  uer7\overline{0}0578687.h1
Method
                  BLASTN
NCBI GI
                 q172952
BLAST score
                  42
E value
                  2.0e-14
Match length
                  46
                  98
% identity
NCBI Description S.cerevisiae Arg-tRNA-3 and Asp-tRNA genes, clone pjb18u
Seq. No.
                  264933
Contig ID
                  7854 1.R1011
5'-most EST
                  LIB3078-051-Q1-K1-F7
                  BLASTX
Method
```



```
9.0e-22
E value
Match length
                  118
% identity
                   49
                  (D31886) KIAA0066 [Homo sapiens]
NCBI Description
                   264934
Seq. No.
                   7860 1.R1011
Contig ID
                   nbm700471484.h1
5'-most EST
                   BLASTX
Method
                   g3413886
NCBI GI
BLAST score
                   589
                   3.0e-60
E value
Match length
                   418
                   35
% identity
                   (AB007931) KIAA0462 protein [Homo sapiens]
NCBI Description
Seq. No.
                   264935
Contig ID
                   7861 1.R1011
                   LIB3078-051-Q1-K1-D4
5'-most EST
                   BLASTX
Method
                   g2586083
NCBI GI
BLAST score
                   155
                   3.0e-10
E value
Match length
                   99
                   36
% identity
                   (U72725) receptor kinase-like protein [Oryza
NCBI Description
                   longistaminata]
Seq. No.
                   264936
                   7861 2.R1011
Contig ID
                   LIB189-002-Q1-E1-C8
5'-most EST
                   BLASTX
Method
                   g2586081
NCBI GI
                   229
BLAST score
                   2.0e-18
E value
                   132
Match length
                   10
% identity
                   (U72725) receptor kinase-like protein [Oryza
NCBI Description
                   longistaminata]
                   264937
Seq. No.
                   7864_1.R1011
Contig ID
                   LIB84-028-Q1-E1-G3
 5'-most EST
                   BLASTX
Method
                   g4127456
NCBI GI
                    718
BLAST score
                    1.0e-75
 E value
Match length
                    208
                    66
 % identity
                   (AJ010818) Cpn21 protein [Arabidopsis thaliana]
 NCBI Description
                    264938
 Seq. No.
                    7866 1.R1011
 Contig ID
```

Seq. No. 264938
Contig ID 7866_1.R1011
5'-most EST wty700165373.h1
Method BLASTX
NCBI GI g1167953

BLAST score



E value 1.0e-106
Match length 306
% identity 63
NCBI Description (U43496) putative 32.6 kDa jasmonate-induced protein [Hordeum vulgare] >gi_2465426 (AF021256) 32 kDa protein [Hordeum vulgare]

Seq. No. 264939

Contig ID 7866_2.R1011 5'-most EST LIB3T37-062-Q1-K1-B8

Method BLASTX
NCBI GI g1167953
BLAST score 562
E value 1.0e-57
Match length 153

Match length 153 % identity 68

NCBI Description (U43496) putative 32.6 kDa jasmonate-induced protein [Hordeum vulgare] >gi 2465426 (AF021256) 32 kDa protein

[Hordeum vulgare]

Seq. No. 264940 Contig ID 7867_1.R1011

5'-most EST LIB143-001-Q1-E1-E8

Method BLASTX
NCBI GI g3913733
BLAST score 997
E value 1.0e-108
Match length 258
% identity 71

NCBI Description HYDROXYACYLGLUTATHIONE HYDROLASE CYTOPLASMIC ISOZYME

(GLYOXALASE II) (GLX II) >gi_1924921_emb_CAA69644_ (Y08357) hydroxyacylglutathione hydrolase [Arabidopsis thaliana]

Seq. No. 264941

Contig ID 7869 1.R1011

5'-most EST LIB3\overline{1}50-006-Q1-N1-G10

Seq. No. 264942

Contig ID 7875_2.R1011 5'-most EST xsy700208311.h1

Method BLASTX
NCBI GI g119958
BLAST score 144
E value 6.0e-09
Match length 95
% identity 40

NCBI Description FERREDOXIN III PRECURSOR (FD III) >gi_168473 (M73831)

ferredoxin [Zea mays] >gi_1864001_dbj_BAA19251_ (AB001387)

Fd III [Zea mays] >gi_444686_prf__1907324C

ferredoxin: ISOTYPE=III [Zea mays]

Seq. No. 264943

Contig ID 7880_1.R1011 5'-most EST cyk700050662.f1

Method BLASTX
NCBI GI g2129473
BLAST score 239

36795

ż



E value 2.0e-26
Match length 148
% identity 49

NCBI Description arabinogalactan-like protein - loblolly pine >gi_607774 (U09556) arabinogalactan-like protein [Pinus taeda]

Seq. No. 264944

Contig ID 7886 1.R1011

5'-most EST LIB143-045-Q1-E1-A3

Method BLASTX
NCBI GI g3341685
BLAST score 355
E value 2.0e-33
Match length 104
% identity 68

NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 264945

Contig ID 7886_2.R1011 5'-most EST hvj700622270.h1

Method BLASTX
NCBI GI g3341685
BLAST score 364
E value 2.0e-34
Match length 123
% identity 64

NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 264946

Contig ID 7889 1.R1011

5'-most EST uC-zmflb73307g05b1

 Seq. No.
 264947

 Contig ID
 7889_2.R1011

 5'-most EST
 dyk700102572.h1

Seq. No. 264948

Contig ID 7895_1.R1011 5'-most EST qmh700026075.f1

Seq. No. 264949

Contig ID 7896 1.R1011

5'-most EST uC-zmflb73012h08b1

Method BLASTX
NCBI GI g3421413
BLAST score 1270
E value 1.0e-140
Match length 267
% identity 88

NCBI Description (AF081922) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa] >gi_3421415 (AF081923) protein

phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

 Seq. No.
 264950

 Contig ID
 7897_1.R1011

 5'-most EST
 nbm700474325.h1

Method BLASTX

Match length

NCBI Description

% identity

76



```
NCBI GI
                   q3252856
BLAST score
                   1449
                   1.0e-161
E value
Match length
                   337
                   82
% identity
                   (AF020425) glutamate decarboxylase isozyme 1 [Nicotiana
NCBI Description
                   tabacum]
                   264951
Seq. No.
                   7903 1.R1011
Contig ID
                   hbs7\overline{0}1185555.h1
5'-most EST
Method
                   BLASTX
                   q3005702
NCBI GI
BLAST score
                   169
                   8.0e-12
E value
Match length
                   101
                   41
% identity
                  (AF054989) unknown [Homo sapiens]
NCBI Description
                   264952
Seq. No.
                   7904 1.R1011
Contig ID
5'-most EST
                   nwy700444568.h1
Method
                   BLASTX
NCBI GI
                   q4432860
                   210
BLAST score
                   4.0e-16
E value
Match length
                   97
% identity
                   45
                  (AC006300) putative glucose-induced repressor protein
NCBI Description
                   [Arabidopsis thaliana]
                   264953
Seq. No.
Contig ID
                   7905 1.R1011
5'-most EST
                   LIB3078-050-Q1-K1-H12
                   264954
Seq. No.
Contig ID
                   7909 1.R1011
5'-most EST
                   LIB3078-050-Q1-K1-H5
                   BLASTX
Method
                   g2244996
NCBI GI
BLAST score
                   249
E value
                   4.0e-21
Match length
                   140
                   37
% identity
                   (Z97341) similarity to a membrane-associated salt-inducible
NCBI Description
                   protein [Arabidopsis thaliana]
Seq. No.
                   264955
                   7919_1.R1011
Contig ID
5'-most EST
                   LIB3078-040-Q1-K1-H10
Method
                   BLASTX
NCBI GI
                   q3885513
BLAST score
                   277
                   3.0e-24
E value
```

36797

(AF084201) similar to chloroplast 50S ribosomal protein L31

5'-most EST



[Medicago sativa]

```
264956
Seq. No.
Contig ID
                  7921 1.R1011
                  LIB84-007-Q1-E1-D12
5'-most EST
                  BLASTX
Method
                  q4512694
NCBI GI
BLAST score
                   291
                   1.0e-25
E value
                   150
Match length
                   43
% identity
                  (AC006569) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   264957
Contig ID
                   7921 2.R1011
5'-most EST
                   fdz701160934.h1
Seq. No.
                   264958
                   7926 1.R1011
Contig ID
                   LIB3068-033-Q1-K1-B10
5'-most EST
                   BLASTX
Method
                   g1731181
NCBI GI
BLAST score
                   167
                   3.0e-12
E value
                   97
Match length
                   46
% identity
                   HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II
NCBI Description
                   >gi 3874230 emb CAA90107_ (Z49909) weak similarity with a
                   B. Flavum translocation protein (Swiss Prot accession
                   number P38376); cDNA EST yk220e10.5 comes from this gene
                   [Caenorhabditis elegans]
                   264959
Seq. No.
                   7927 1.R1011
Contig ID
                   LIB3078-050-Q1-K1-D7
5'-most EST
                   BLASTX
Method
                   g1877026
NCBI GI
                   228
BLAST score
                   8.0e-19
E value
                   55
Match length
                   80
% identity
                  (D78336) ribosomal protein S19 [Oryza sativa]
NCBI Description
                   264960
Seq. No.
                   7928 1.R1011
Contig ID
                   uC-zmflmo17023e06b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2244839
                   351
BLAST score
                   4.0e-33
E value
                   165
Match length
                   42
% identity
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   264961
Seq. No.
                   7930 1.R1011
Contig ID
```

uC-zmflmo17339c03b1



BLASTX Method g4506753 NCBI GI 1235 BLAST score 1.0e-136 E value 331 Match length 72 % identity TATA binding protein interacting protein 49 kDa NCBI Description >gi_3132308_dbj_BAA28169_ (AB012122) TIP49 [Homo sapiens] >gi_3243035 (AF070735) RuvB-like protein RUVBL1 [Homo sapiens] >gi_3892584_emb_CAA08986_ (AJ010058) Nuclear matrix protein NMP238 [Homo sapiens] >gi_4151525 (AF099084) Pontin52 [Homo sapiens] 264962 Seq. No. 7937 1.R1011 Contig ID LIB36-004-Q1-E1-C8 5'-most EST BLASTX Method g2911057 NCBI GI 846 BLAST score 8.0e-91 E value 200 Match length 77 % identity (AL021961) caffeoyl-CoA O-methyltransferase - like protein NCBI Description [Arabidopsis thaliana] 264963 Seq. No. 7937 2.R1011 Contig ID xsy700212016.h1 5'-most EST BLASTX Method g2911057 NCBI GI 647 BLAST score 9.0e-68 E value 140 Match length 89 % identity (AL021961) caffeoyl-CoA O-methyltransferase - like protein NCBI Description [Arabidopsis thaliana] Seq. No. 264964 7937 3.R1011 Contig ID 5'-most EST LIB3067-026-Q1-K1-A10 BLASTX Method g2911057 NCBI GI 450 BLAST score 1.0e-44 E value 100 Match length % identity (AL021961) caffeoyl-CoA O-methyltransferase - like protein NCBI Description [Arabidopsis thaliana] 264965 Seq. No. 7937 4.R1011 Contig ID LIB3079-010-Q1-K1-C4 5'-most EST

Method BLASTX

NCBI GI g1575436 BLAST score 356 1.0e-33 E value Match length 88



% identity (U62734) caffeoyl-CoA O-methyltransferase 2 [Nicotiana NCBI Description tabacum] Seq. No. 264966 7937 5.R1011 Contig ID wyr700237247.hl 5'-most EST Method BLASTN q5091496 NCBI GI BLAST score 54 2.0e-21 E value 141 Match length 92 % identity Oryza sativa genomic DNA, chromosome 6, clone P0680A03, NCBI Description complete sequence Seq. No. 264967 7942 1.R1011 Contig ID 5'-most EST LIB3078-050-Q1-K1-D6 BLASTX Method NCBI GI g2832619 BLAST score 189 4.0e-23 E value Match length 105 51 % identity (AL021711) major intrinsic protein (MIP) - like [Arabidopsis NCBI Description thaliana] 264968 Seq. No. 7943 1.R1011 Contig ID uC-zmrob73012g11b1 5'-most EST Method BLASTX g1237250 NCBI GI BLAST score 825 2.0e-88 E value 249 Match length 63 % identity NCBI Description (X96784) cytochrome P450 [Nicotiana tabacum] 264969 Seq. No. 7950 1.R1011 Contig ID LIB3078-050-Q1-K1-C7 5'-most EST 264970 Seq. No. 7952 1.R1011 Contig ID uC-zmflmo17267b08b1 5'-most EST BLASTX Method NCBI GI q4582436 BLAST score 1732 0.0e + 00E value 579 Match length 61 % identity (AC007196) unknown protein [Arabidopsis thaliana] NCBI Description 264971

Seq. No. 7952 2.R1011 Contig ID

5'-most EST uC-zmflMo17013f11b1



```
BLASTX
Method
                  g4582436
NCBI GI
BLAST score
                  262
                  2.0e-22
E value
                  73
Match length
                  70
% identity
                  (AC007196) unknown protein [Arabidopsis thaliana]
NCBI Description
                  264972
Seq. No.
Contig ID
                  7952 3.R1011
                  uC-zmflb73337c11a1
5'-most EST
                  264973
Seq. No.
Contig ID
                  7955 1.R1011
                  LIB3150-012-Q1-N1-D10
5'-most EST
                  264974
Seq. No.
                  7955 2.R1011
Contig ID
5'-most EST
                  LIB3153-010-Q1-K1-E12
                  264975
Seq. No.
                  7969 1.R1011
Contig ID
                  LIB3150-103-P2-K1-B6
5'-most EST
                  264976
Seq. No.
                  7972 1.R1011
Contig ID
                  uC-zmflb73118e07b1
5'-most EST
                  BLASTX
Method
                   q1001649
NCBI GI
BLAST score
                   625
                   7.0e-65
E value
                   314
Match length
                   43
% identity
                  (D64002) DNA gyrase A subunit [Synechocystis sp.]
NCBI Description
                   264977
Seq. No.
Contig ID ·
                   7973 1.R1011
5'-most EST
                   ymt700224806.h1
                   BLASTX
Method
NCBI GI
                   g3342823
BLAST score
                   957
                   1.0e-103
E value
                   180
Match length
                   95
% identity
                  (AF076955) eukaryotic translation initiation factor p28
NCBI Description
                   subunit [Zea mays]
                   264978
Seq. No.
                   7973 2.R1011
Contig ID
                   uC-zmflb73192d02b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3342823
                   421
BLAST score
                   2.0e-41
E value
                   81
Match length
```

36801

NCBI Description (AF076955) eukaryotic translation initiation factor p28

100

% identity

Match length

% identity

254

51



subunit [Zea mays]

```
264979
Seq. No.
                  7973 4.R1011
Contig ID
                  LIB3180-059-P2-M1-A12
5'-most EST
                  BLASTN
Method
NCBI GI
                  q3342822
                  181
BLAST score
                  2.0e-97
E value
                  294
Match length
                  95
% identity
                  Zea mays eukaryotic translation initiation factor p28
NCBI Description
                  subunit (eIFiso-4E) mRNA, complete cds
                  264980
Seq. No.
                  7973 5.R1011
Contig ID
                  tfd700575054.h1
5'-most EST
Method
                  BLASTX
                  q3342823
NCBI GI
                  207
BLAST score
                  2.0e-16
E value
                  56
Match length
% identity
                  73
                  (AF076955) eukaryotic translation initiation factor p28
NCBI Description
                  subunit [Zea mays]
                  264981
Seq. No.
                  7977 1.R1011
Contig ID
                  LIB3078-049-Q1-K1-H10
5'-most EST
                  BLASTX
Method
                   q3668080
NCBI GI
BLAST score
                   683
                   8.0e-72
E value
                   219
Match length
                   64
% identity
                  (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   264982
                   7979 1.R1011
Contig ID
                  LIB3078-049-Q1-K1-H12
5'-most EST
Method
                   BLASTX
                   g1785488
NCBI GI
                   322
BLAST score
E value
                   1.0e-29
                   97
Match length
                   64
% identity
                  (D14590) flavonoid 3',5'-hydroxylase [Campanula medium]
NCBI Description
Seq. No.
                   264983
                   7982 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17193g12b1
Method
                   BLASTX
NCBI GI
                   q1176658
BLAST score
                   329
E value
                   6.0e-59
```



NCBI Description HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II

>gi_726363 (U23168) No definition line found

[Caenorhabditis elegans]

Seq. No. 264984

Contig ID 7982_2.R1011

5'-most EST uC-zmflmo17355f12a1

Seq. No. 264985

Contig ID 7982_3.R1011 5'-most EST xmt700262492.h1

Seq. No. 264986

Contig ID 7983_1.R1011 5'-most EST cat700020072.r1

Seq. No. 264987

Contig ID 7983_2.R1011 5'-most EST ymt700219546.h1

Seq. No. 264988

Contig ID 7984_1.R1011

5'-most EST uC-zmroteosinte103e09b2

Method BLASTX
NCBI GI g3287270
BLAST score 724
E value 1.0e-76

Match length 253 % identity 59

NCBI Description (Y09533) involved in starch metabalism [Solanum tuberosum]

Seq. No. 264989

Contig ID 7991_1.R1011

5'-most EST LIB3078-049-Q1-K1-F2

Seq. No. 264990

Contig ID 7991_2.R1011

5'-most EST uC-zmflb73144f02b1

Seq. No. 264991

Contig ID 7991_3.R1011

5'-most EST LIB3078-027-Q1-K1-D8

Seq. No. 264992

Contig ID 7992_1.R1011

5'-most EST LIB3060-007-Q1-K1-G1

Method BLASTX
NCBI GI g2213632
BLAST score 369
E value 2.0e-40
Match length 142

% identity 61

NCBI Description (AC000103) F21J9.24 [Arabidopsis thaliana]

Seq. No. 264993

Contig ID 7997_1.R1011

5'-most EST uC-zmflmo170113g07b1

% identity

NCBI Description

54

bicolor]



```
BLASTX
Method
NCBI GI
                   g2213626
BLAST score
                   344
                   4.0e-32
E value
Match length
                   117
                   49
% identity
                  (AC000103) F21J9.18 [Arabidopsis thaliana]
NCBI Description
                   264994
Seq. No.
                   7997 2.R1011
Contig ID
                   LIB3060-016-Q1-K1-A9
5'-most EST
                   BLASTX
Method
                   g2213626
NCBI GI
BLAST score
                   430
                   5.0e-42
E value
Match length
                   225
                   42
% identity
                   (AC000103) F21J9.18 [Arabidopsis thaliana]
NCBI Description
                   264995
Seq. No.
                   8003 1.R1011
Contig ID
                   LIB3078-049-Q1-K1-F11
5'-most EST
                   BLASTX
Method
                   g3236254
NCBI GI
                   277
BLAST score
                   4.0e-24
E value
                   110
Match length
                   52
% identity
                   (AC004684) unknown protein [Arabidopsis thaliana]
NCBI Description
                   264996
Seq. No.
                   8004 1.R1011
Contig ID
                   ymt700220809.h1
5'-most EST
                   BLASTX
Method
                   g4539352
NCBI GI
                   258
BLAST score
                   3.0e-22
E value
                   175
Match length
                   35
% identity
                   (AL035539) putative protein [Arabidopsis thaliana]
NCBI Description
                   264997
Seq. No.
                   8007 1.R1011
Contig ID
                   uC-zmflmo17202e05b1
5'-most EST
                   264998
Seq. No.
                   8008_1.R1011
Contig ID
5'-most EST
                   uC-zmflb73079e04b2
                   BLASTX
Method
NCBI GI
                   q3256035
                   1238
BLAST score
                   1.0e-136
E value
Match length
                   438
```

(Y14274) putative serine/threonine protein kinase [Sorghum



```
264999
Seq. No.
                   8009 1.R1011
Contig ID
                   LIB3078-049-Q1-K1-D9
5'-most EST
                   265000
Seq. No.
                   8010 1.R1011
Contiq ID
                   LIB3079-032-Q1-K1-A12
5'-most EST
                   BLASTX
Method
                   q3914658
NCBI GI
BLAST score
                   542
                   3.0e-55
E value
Match length
                   142
% identity
                   68
                   50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_1694974_emb_CAA70851_ (Y09635) plastid ribosomal
                   protein [Arabidopsis thaliana]
                   265001
Seq. No.
                   8011 1.R1011
Contig ID
                   LIB3\overline{0}69-049-Q1-K1-B2
5'-most EST
                   265002
Seq. No.
                   8015 1.R1011
Contig ID
                   LIB36-003-Q1-E1-D9
5'-most EST
                   BLASTX
Method
                   g4467116
NCBI GI
BLAST score
                   211
E value
                   2.0e-16
Match length
                   152
                   32
% identity
                   (AL035538) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   265003
Seq. No.
                   8015 2.R1011
Contig ID
                   LIB189-013-Q1-E1-B12
5'-most EST
                   265004
Seq. No.
                   8017 1.R1011
Contig ID
                   uC\text{-}z\bar{m}flmo17176e08b1
5'-most EST
                   BLASTX
Method
                   g2982243
NCBI GI
                   232
BLAST score
                   6.0e-41
E value
                   151
Match length
                   60
% identity
NCBI Description (AF051204) hypothetical protein [Picea mariana]
Seq. No.
                   265005
                   8017 2.R1011
Contig ID
                   LIB3078-049-Q1-K1-E9
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2982243
```

BLAST score 241 3.0e - 30

E value 133 Match length % identity

NCBI Description (AF051204) hypothetical protein [Picea mariana]

Seq. No.

```
8021 1.R1011
Contig ID
5'-most EST
                  yyf700348972.h1
Method
                  BLASTN
                  g5091496
NCBI GI
BLAST score
                  36
                  2.0e-10
E value
                  56
Match length
                   91
% identity
                  Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
NCBI Description
                   complete sequence
                   265007
Seq. No.
                   8021 2.R1011
Contig ID
                   LIB3067-038-Q1-K1-F12
5'-most EST
Method
                   BLASTN
                   g5091496
NCBI GI
BLAST score
                   52
                   5.0e-20
E value
Match length
                   100
                   88
% identity
                   Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
NCBI Description
                   complete sequence
                   265008
Seq. No.
                   8023 1.R1011
Contig ID
5'-most EST
                   LIB3059-043-Q1-K1-C8
Method
                   BLASTX
                   q3980383
NCBI GI
                   290
BLAST score
                   1.0e-25
E value
                   72
Match length
% identity
                   72
                  (AC004561) unknown protein [Arabidopsis thaliana]
NCBI Description
                   265009
Seq. No.
                   8023 2.R1011
Contig ID
5'-most EST
                   wyr700240281.h1
                   BLASTX
Method
                   g3980383
NCBI GI
                   303
BLAST score
                   2.0e-27
E value
                   66
Match length
                   80
 % identity
NCBI Description (AC004561) unknown protein [Arabidopsis thaliana]
                   265010
Seq. No.
                   8024 1.R1011
Contig ID
                   xmt700258320.h1
 5'-most EST
                   BLASTX
Method
                   g2062167
NCBI GI
 BLAST score
                   1070
                    1.0e-117
 E value
                   320
Match length
 % identity
                   (AC001645) Proline-rich protein APG isolog [Arabidopsis
 NCBI Description
```



49

% identity

thaliana]

Seq. No. 265011 Contig ID 8025 1.R1011 5'-most EST nwy700446664.hl BLASTX Method NCBI GI g4263509 BLAST score 612 2.0e-63 E value Match length 152 72 % identity (AC004044) hypothetical protein [Arabidopsis thaliana] NCBI Description 265012 Seq. No. Contig ID 8027 1.R1011 5'-most EST uC-zmflmo17201c02b1 Seq. No. 265013 8027 2.R1011 Contig ID 5'-most EST wyr700239281.h1 265014 Seq. No. Contig ID 8027 3.R1011 5'-most EST uC-zmflmo17040b01b1 BLASTX Method NCBI GI g3287695 BLAST score 149 E value 4.0e-09 Match length 37 % identity 76 (AC003979) Similar to hypothetical protein C34B7.2 NCBI Description gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis thaliana] 265015 Seq. No. 8032 1.R1011 Contig ID uC-zmflmo17283f01b1 5'-most EST Method BLASTX g575605 NCBI GI BLAST score 694 8.0e-73 E value 291 Match length % identity 49 (D42065) cationic peroxidase isozyme 40K precursor NCBI Description [Nicotiana tabacum] 265016 Seq. No. Contig ID 8032_2.R1011 LIB3150-076-P1-N1-A8 5'-most EST Method BLASTX g3928088 NCBI GI 153 BLAST score E value 6.0e-10 Match length 63

36807

NCBI Description (AC005770) putative peroxidase [Arabidopsis thaliana]



```
265017
Seq. No.
                  8032 3.R1011
Contig ID
                  uC-zmflb73111f11a1
5'-most EST
                  265018
Seq. No.
                  8033 1.R1011
Contig ID
                  fdz701164177.h1
5'-most EST
                  BLASTX
Method
                  a3445204
NCBI GI
                  196
BLAST score
                  7.0e-15
E value
                   64
Match length
                  59
% identity
                  (AC004786) putative GTP-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                   265019
Seq. No.
                   8034 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17127b08a1
                   265020
Seq. No.
                   8035 1.R1011
Contig ID
                   ceu700430360.h1
5'-most EST
                   BLASTX
Method
                   q3355717
NCBI GI
BLAST score
                   864
                   4.0e-93
E value
                   177
Match length
                   94
% identity
NCBI Description (Y13053) seryl-tRNA synthetase [Zea mays]
                   265021
Seq. No.
Contig ID
                   8037 1.R1011
                   LIB3156-002-Q1-K1-C2
5'-most EST
Method
                   BLASTX
                   g3510256
NCBI GI
BLAST score
                   304
                   2.0e-27
E value
Match length
                   123
% identity
                   44
NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]
                   265022
Seq. No.
                   8038 1.R1011
Contig ID
                   ntr700074243.h1
5'-most EST
                   BLASTX
Method
                   g3874057
NCBI GI
                   157
BLAST score
                   8.0e-10
E value
                   72
Match length
                   47
 % identity
NCBI Description (Z78536) similar to RNA binding protein [Caenorhabditis
                   elegans]
                   265023
Seq. No.
                   8038 2.R1011
Contig ID
                   qmh700027150.f1
 5'-most EST
```



```
265024
Seq. No.
                  8038 3.R1011
Contig ID
                  yyf700349322.h1
5'-most EST
                   BLASTX
Method
                  g1934994
NCBI GI
BLAST score
                   161
                   8.0e-11
E value
                   83
Match length
                   40
% identity
                   (Y12424) SGRP-1 [Solanum commersonii]
NCBI Description
Seq. No.
                   265025
                   8040 1.R1011
Contig ID
5'-most EST
                   ymt700219322.h1
                   265026
Seq. No.
                   8041 1.R1011
Contiq ID
                   LIB3279-005-P1-K1-B8
5'-most EST
                   BLASTX
Method
                   g4510363
NCBI GI
                   648
BLAST score
                   1.0e-67
E value
Match length
                   148
% identity
                   82
                   (AC007017) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   265027
Seq. No.
                   8042 1.R1011
Contig ID
                   uwh700207141.h1
5'-most EST
                   BLASTX
Method
                   g3776578
NCBI GI
                   292
BLAST score
                   8.0e-26
E value
                   132
Match length
                   39
% identity
                   (AC005388) ESTs gb_F13915 and gb_F13916 come from this
NCBI Description
                   gene. [Arabidopsis thaliana]
                   265028
Seq. No.
                   8050 1.R1011
Contig ID
                   uC-zmflb73028e01b1
5'-most EST
                   265029
Seq. No.
                   8051 1.R1011
Contig ID
5'-most EST
                   LIB3078-049-Q1-K1-B4
Method
                   BLASTX
                   g1922938
NCBI GI
                   240
BLAST score
                   3.0e-20
E value
                   75
Match length
 % identity
                    60
```

Seq. No. 265030

NCBI Description

CO7A9.11 (gb_Z29094). [Arabidopsis thaliana]

(AC000106) Similar to Caenorhabditis hypothetical protein



```
8052 1.R1011
Contig ID
5'-most EST
                  rvt700550855.h1
Method
                  BLASTX
NCBI GI
                  q1730771
                  298
BLAST score
                  3.0e-26
E value
                  355
Match length
                  27
% identity
                  HYPOTHETICAL 110.9 KD PROTEIN IN SPC98-TOM70 INTERGENIC
NCBI Description
                  REGION >gi 2132752_pir _S63064 probable membrane protein
                  YNL123w - yeast (Saccharomyces cerevisiae)
                  >gi_1183950_emb_CAA93384_ (Z69382) N1897 [Saccharomyces
                  cerevisiae] >gi 1302054 emb CAA96004 (Z71399) ORF YNL123w
                  [Saccharomyces cerevisiae]
                  265031
Seq. No.
                  8052 2.R1011
Contig ID
                  uC-zmflmo17185e02b1
5'-most EST
                  BLASTX
Method
                  q1730771
NCBI GI
                  201
BLAST score
                  3.0e-15
E value
                  147
Match length
                  35
% identity
                  HYPOTHETICAL 110.9 KD PROTEIN IN SPC98-TOM70 INTERGENIC
NCBI Description
                  REGION >gi_2132752_pir__S63064 probable membrane protein
                  YNL123w - yeast (Saccharomyces cerevisiae)
                  >gi 1183950_emb_CAA93384_ (Z69382) N1897 [Saccharomyces
                   cerevisiae] >gi 1302054 emb CAA96004 (Z71399) ORF YNL123w
                   [Saccharomyces cerevisiae]
                  265032
Seq. No.
                  8053 1.R1011
Contig ID
                  uC-zmflmo17159d09b1
5'-most EST
Method
                  BLASTX
                  g4587577
NCBI GI
BLAST score
                  347
                   3.0e-32
E value
Match length
                  123
% identity
                   56
                  (AC006550) F1003.17 [Arabidopsis thaliana]
NCBI Description
                   265033
Seq. No.
Contig ID
                   8054 1.R1011
5'-most EST
                   LIB36-013-Q1-E1-D7
Method
                   BLASTX
NCBI GI
                   g3021532
BLAST score
                   1062
                   1.0e-116
E value
Match length
                   239
% identity
                   83
                  (AJ001772) glucose-6-phosphate dehydrogenase [Nicotiana
```

265034 Seq. No.

NCBI Description

8056 1.R1011 Contig ID zuv700354793.h1 5'-most EST

tabacum]



```
Method
                    BLASTX
                    g4506013
NCBI GI
                    455
BLAST score
                    7.0e-45
E value
Match length
                    299
                    34
% identity
                    protein phosphatase 1, regulatory subunit 7
NCBI Description
                    >gi_2136139_pir__S68209 sds22 protein homolog - human
                    >gi_1085028_emb_CAA90626_ (Z50749) yeast sds22 homolog
[Homo sapiens] >gi_4633067_gb_AAD26611.1_ (AF067136)
protein phosphatase-1 regulatory subunit 7 alpha1 [Homo
                    sapiens] >gi 1585165_prf__2124310A sds22 gene [Homo
                    sapiens]
                    265035
Seq. No.
                    8058 1.R1011
Contig ID
                    LIB189-006-Q1-E1-F4
5'-most EST
Method
                    BLASTX
                    q3334441
NCBI GI
                    289
BLAST score
                    2.0e-25
E value
                    207
Match length
                    35
% identity
                    HYPOTHETICAL 47.9 KD PROTEIN T517.9 IN CHROMOSOME II
NCBI Description
                    >gi 2642161 (AC003000) hypothetical protein [Arabidopsis
                    thaliana]
Seq. No.
                    265036
                    8060 1.R1011
Contig ID
                    LIB3079-052-Q1-K1-G6
5'-most EST
                    BLASTX
Method
                    g1881585
NCBI GI
                     267
BLAST score
                     3.0e-23
E value
                     98
Match length
                     53
% identity
                    (U72489) remorin [Solanum tuberosum]
NCBI Description
                     265037
Seq. No.
                     8061 1.R1011
Contig ID
                     wty700167307.h1
5'-most EST
                     BLASTX
Method
                     q729051
NCBI GI
BLAST score
                     658
                     7.0e-69
E value
                     160
Match length
                     79
% identity
                     CALTRACTIN (CENTRIN) >gi 444342_prf__1906390A
NCBI Description
                     caltractin-like protein [Atriplex nummularia]
                     265038
Seq. No.
                     8061 2.R1011
Contig ID
```

5'-most EST LIB3061-008-Q1-K1-E9

Method BLASTX
NCBI GI g729051
BLAST score 495
E value 7.0e-50



Match length 121 % identity CALTRACTIN (CENTRIN) >gi_444342_prf__1906390A NCBI Description caltractin-like protein [Atriplex nummularia] 265039 Seq. No. 8062 1.R1011 Contig ID 5'-most EST ceu700428173.h1 265040 Seq. No. 8065 1.R1011 Contig ID wty700169212.h1 5'-most EST Method BLASTX g4539454 NCBI GI BLAST score 497 8.0e-50 E value Match length 125 74 % identity (ALO49500) contains EST gb:AA728416 [Arabidopsis thaliana] NCBI Description 265041 Seq. No. 8071 1.R1011 Contig ID LIB3060-028-Q1-K1-C7 5'-most EST Method BLASTX NCBI GI g3559935 BLAST score 648 2.0e-67 E value 199 Match length % identity 60 (AJ005253) ClpP protease [Mus musculus] NCBI Description >gi 4454289_emb_CAA09966_ (AJ012249) ClpP protease [Mus musculus] Seq. No. 265042 8071 2.R1011 Contig ID LIB3062-013-Q1-K1-E12 5'-most EST BLASTX Method g3559935 NCBI GI BLAST score 342 4.0e-32 E value 86 Match length 74 % identity NCBI Description (AJ005253) ClpP protease [Mus musculus] >gi 4454289 emb CAA09966 (AJ012249) ClpP protease [Mus musculus] 265043 Seq. No. 8072_1.R1011 Contig ID $yyf7\overline{0}0351544.h1$ 5'-most EST BLASTX Method

NCBI GI q3341697 BLAST score 157 4.0e-10 E value

> 173 48

Match length

% identity

NCBI Description (AC003672) hypothetical protein [Arabidopsis thaliana]



```
265044
Seq. No.
                  8072 2.R1011
Contig ID
                  dyk700102154.h1
5'-most EST
                  BLASTX
Method
                  q3341697
NCBI GI
                   290
BLAST score
                   1.0e-25
E value
                   80
Match length
                   66
% identity
                   (AC003672) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   265045
Seq. No.
                   8073 1.R1011
Contig ID
                   fwa700100876.h1
5'-most EST
                   BLASTX
Method
                   q3914666
NCBI GI
BLAST score
                   769
                   1.0e-81
E value
Match length
                   220
                   70
% identity
                   CHLOROPLAST 50S RIBOSOMAL PROTEIN L4 PRECURSOR
NCBI Description
                   >gi 2791998 emb CAA74895 (Y14566) ribosomal protein L4
                   [Arabidopsis thaliana] > gi 2792000 emb CAA74894 (Y14565)
                   ribosomal protein L4 [Arabidopsis thaliana]
                   265046
Seq. No.
                   8077 1.R1011
Contig ID
                   zla700380425.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2459445
                   369
BLAST score
                   1.0e-34
E value
Match length
                   238
                   37
% identity
                   (AC002332) putative ribonucleoprotein [Arabidopsis
NCBI Description
                   thaliana]
                   265047
Seq. No.
Contig ID
                   8078 1.R1011
                   ypc700799809.h1
5'-most EST
                   BLASTX
Method
                   q3169012
NCBI GI
                   892
BLAST score
                   2.0e-96
E value
Match length
                   203
                   81
% identity
                   (AJ002610) putative calmodulin binding transporter protein
NCBI Description
                   [Hordeum vulgare]
                   265048
Seq. No.
                   8080 1.R1011
Contig ID
                   LIB189-027-Q1-E1-D7
5'-most EST
```

265049 Seq. No. 8084 1.R1011 Contig ID pmx700082323.h1 5'-most EST

BLASTN Method



```
NCBI GI
                  g3821780
BLAST score
                  36
                  2.0e-10
E value
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  265050
Seq. No.
                  8084 4.R1011
Contig ID
                  rvt700548546.hl
5'-most EST
                  265051
Seq. No.
Contig ID
                  8086 1.R1011
                  xmt700265809.h1
5'-most EST
                  265052
Seq. No.
                  8088 1.R1011
Contig ID
5'-most EST
                  LIB3116-032-P1-K1-A2
Method
                  BLASTX
                  q1698670
NCBI GI
                  1293
BLAST score
                   1.0e-151
E value
                   269
Match length
                   96
% identity
                  (U66241) S-like RNase [Zea mays]
NCBI Description
                   265053
Seq. No.
                   8088 3.R1011
Contig ID
5'-most EST
                   LIB3136-057-Q1-K1-E5
Method
                   BLASTN
                   q1698669
NCBI GI
                   217
BLAST score
                   1.0e-118
E value
Match length
                   357
                   97
% identity
NCBI Description Zea mays S-like RNase (kin1) mRNA, complete cds
                   265054
Seq. No.
                   8090 1.R1011
Contig ID
                   ymt700224272.h1
5'-most EST
                   BLASTX
Method
                   g4218120
NCBI GI
                   755
BLAST score
                   4.0e-80
E value
                   271
Match length
                   54
% identity
NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis
                   thaliana]
```

Seq. No. 265055 8095_1.R1011 Contig ID LIB3078-048-Q1-K1-C4 5'-most EST BLASTX Method q3287270 NCBI GI 342 BLAST score

1.0e-32 E value Match length 84

79 % identity (Y09533) involved in starch metabalism [Solanum tuberosum] NCBI Description 265056 Seq. No. 8096 1.R1011 Contig ID LIB3062-018-Q1-K1-C2 5'-most EST Method BLASTX NCBI GI a4097573 BLAST score 486 1.0e-48 E value 134 Match length % identity 66 NCBI Description (U64917) GMFP7 [Glycine max] Seq. No. 265057 Contig ID 8096 2.R1011 LIB3066-051-Q1-K1-A12 5'-most EST Method BLASTX NCBI GI q4467145 BLAST score 517 2.0e-52 E value Match length 155 % identity 65 NCBI Description (AL035540) farnesylated protein (ATFP6) [Arabidopsis thaliana] Seq. No. 265058 8096 3.R1011 Contig ID wyr700237207.hl 5'-most EST Method BLASTX NCBI GI q4467145 BLAST score 158 E value 1.0e-10 Match length 65 % identity 51 NCBI Description (AL035540) farnesylated protein (ATFP6) [Arabidopsis thaliana] 265059

Seq. No. 265059 Contig ID 8096_4.R1011 5'-most EST qmh700027327.f1

Seq. No. 265060 Contig ID 8097 1.R1011

5'-most EST LIB3078-048-Q1-K1-C6

Method BLASTX
NCBI GI g2252856
BLAST score 426
E value 7.0e-42
Match length 128
% identity 60

NCBI Description (AF013294) No definition line found [Arabidopsis thaliana]

Seq. No. 265061

Contig ID 8105_1.R1011

5'-most EST uC-zmflb73059c06a2

Method BLASTN



```
g22429
NCBI GI
BLAST score
                   52
                   5.0e-20
E value
Match length
                  123
                  85
% identity
                  Maize pseudo-Gpal pseudogene for glyceraldehyde-3-phosphate
NCBI Description
                  dehydrogenase subunit A
                   265062
Seq. No.
                   8105 2.R1011
Contig ID
                   LIB3067-053-Q1-K1-E6
5'-most EST
Seq. No.
                   265063
                   8105_3.R1011
Contig ID
                   uC-zmf1b73279d05a2
5'-most EST
                   BLASTN
Method
                   q22429
NCBI GI
BLAST score
                   59
E value
                   3.0e-24
                   150
Match length
                   85
% identity
                  Maize pseudo-Gpa1 pseudogene for glyceraldehyde-3-phosphate
NCBI Description
                   dehydrogenase subunit A
                   265064
Seq. No.
                   8105 4.R1011
Contig ID
                   uC-zmflb73022b07b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1778093
BLAST score
                   802
                   2.0e-85
E value
Match length
                   332
                   48
% identity
                   (U64902) putative sugar transporter; member of major
NCBI Description
                   facilitative superfamily; integral membrane protein [Beta
                   vulgaris]
                   265065
Seq. No.
Contig ID
                   8105 5.R1011
                   uC-zmflmo17151f08a1
5'-most EST
                   265066
Seq. No.
                   8105 7.R1011
Contig ID
                   LIB3069-006-Q1-K1-F1
5'-most EST
                   BLASTN
Method
                   g22123
NCBI GI
                   51
BLAST score
                   2.0e-19
E value
                   135
Match length
                   42
% identity
                  Maize alcohol dehydrogenase 1 gene (Adh1-1S)
NCBI Description
```

Seq. No. 265067 Contig ID 8111 1.R1011

5'-most EST LIB3078-048-Q1-K1-B6

Method BLASTX NCBI GI g4581108



BLAST score 247 E value 4.0e-21 Match length 111 % identity 48

NCBI Description (AC005825) putative chloroplast outer membrane protein 86,also very similar to GTP-inding protein from pea

(GB:L36857) [Arabidopsis thaliana]

Seq. No. 265069

Contig ID 8122_1.R1011 5'-most EST gct701175274.h1

Seq. No. 265070

Contig ID 8124_1.R1011

5'-most EST LIB3062-001-Q1-K2-C12

Method BLASTX
NCBI GI g3334201
BLAST score 520
E value 1.0e-52
Match length 164
% identity 61

NCBI Description GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_1724106

(U79768) glycine cleavage system protein H precursor

[Mesembryanthemum crystallinum]

Seq. No. 265071

Contig ID 8126 1.R1011

5'-most EST uC-zmroteosinte062d03b1

Method BLASTX
NCBI GI g2773404
BLAST score 661
E value 4.0e-69
Match length 284
% identity 49

NCBI Description (AF041255) pyridoxal kinase [Sus scrofa]

Seq. No. 265072

Contig ID 8128_1.R1011

5'-most EST uC-zmflMo17092b11b1

Method BLASTX
NCBI GI g4263704
BLAST score 220
E value 2.0e-17
Match length 87
% identity 43

NCBI Description (AC006223) putative sugar starvation-induced protein

[Arabidopsis thaliana]

Seq. No. 265073 Contig ID 8128 2

Contig ID 8128_2.R1011 5'-most EST uC-zmflmo17306e03b1

Method BLASTX
NCBI GI g4263704



BLAST score 513 E value 9.0e-52 Match length 223 % identity 45

NCBI Description (AC006223) putative sugar starvation-induced protein

[Arabidopsis thaliana]

Seq. No. 265074

Contig ID 8128_4.R1011 5'-most EST xsy700210030.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 265075

Contig ID 8128_6.R1011 5'-most EST pmx700082326.h1

Seq. No. 265076

Contig ID 8128_8.R1011 5'-most EST xmt700264671.h1

Seq. No. 265077

Contig ID 8129_1.R1011

5'-most EST LIB3068-007-Q1-K1-F10

Method BLASTX
NCBI GI g3287877
BLAST score 239
E value 1.0e-19
Match length 93
% identity 49

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 1 (LTP 1) (MAJOR

ALLERGEN)

Seq. No. 265078 Contig ID 8129_2.R1011

5'-most EST LIB3067-022-Q1-K1-D2

Seq. No. 265079 Contig ID 8129 3.R1011

5'-most EST uC-zmflb73237c04b2

Method BLASTX
NCBI GI g2497746
BLAST score 221
E value 1.0e-17
Match length 94
% identity 46

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR (LTP 2)

>gi 951334 (U31766) lipid transfer protein precursor [Oryza

satīva]

Seq. No. 265080 Contig ID 8135_1.R1011

Seq. No.

Contig ID



```
5'-most EST
                  LIB3078-047-Q1-K1-F4
                  265081
Seq. No.
Contig ID
                  8137 1.R1011
5'-most EST
                  LIB3078-047-Q1-K1-G1
                  265082
Seq. No.
                  8139 1.R1011
Contig ID
                  xmt700260305.h2
5'-most EST
                  BLASTX
Method
                  g1326163
NCBI GI
                  368
BLAST score
E value
                  1.0e-34
                  174
Match length
                  45
% identity
                  (U54704) stress related protein PvSRP [Phaseolus vulgaris]
NCBI Description
                  265083
Seq. No.
Contig ID
                  8139 2.R1011
                  fdz701164761.h1
5'-most EST
                  265084
Seq. No.
                  8141 1.R1011
Contig ID
5'-most EST
                  LIB3279-013-P1-K1-G2
                  BLASTX
Method
                  g3116122
NCBI GI
                  272
BLAST score
                   3.0e-23
E value
Match length
                   366
% identity
                   22
                  (AL023287) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                   265085
Seq. No.
Contig ID
                   8141 2.R1011
                  LIB3115-014-P1-K1-D9
5'-most EST
Method
                   BLASTN
                   g2645165
NCBI GI
BLAST score
                   69
E value
                   3.0e - 30
Match length
                   85
                   95
% identity
NCBI Description Oryza sativa mRNA, similar to ribosomal protein
                   265086
Seq. No.
                   8141 3.R1011
Contig ID
                   ntr700075612.h1
5'-most EST
                   BLASTN
Method
                   g407800
NCBI GI
                   42
BLAST score
                   3.0e-14
E value
                   46
Match length
% identity
NCBI Description G.hirsutum mRNA for ribosomal protein 41, large subunit
                   (RL41)
                   265087
```

8143 1.R1011



LIB84-030-Q1-E1-C2 5'-most EST Method BLASTX NCBI GI g228403 BLAST score 576 2.0e-59 E value 132 Match length % identity 84 glycolate oxidase [Lens culinaris] NCBI Description 265088 Seq. No. 8143 2.R1011 Contig ID 5'-most EST LIB189-014-Q1-E1-B2 Method BLASTX g2554675 NCBI GI 161 BLAST score 5.0e-11 E value Match length 39 74 % identity Three-Dimensional Structure Of Glycolate Oxidase With Bound NCBI Description Active-Site Inhibitors >gi_2624594_pdb_1AL7_ Three-Dimensional Structures Of Glycolate Oxidase With Bound Active-Site Inhibitors 265089 Seq. No. 8151 1.R1011 Contig ID $qw17\overline{0}0614978.h1$ 5'-most EST Seq. No. 265090 Contig ID 8158 1.R1011 LIB3078-047-Q1-K1-C12 5'-most EST 265091 Seq. No. 8159 1.R1011 Contig ID uC-zmroteosinte104b02b2 5'-most EST 265092 Seq. No. 8163 1.R1011 Contig ID uC-zmflb73074e12a1 5'-most EST Seq. No. 265093 8163 2.R1011 Contig ID LIB3059-039-Q1-K1-C7 5'-most EST BLASTX Method g3236242 NCBI GI 354 BLAST score 2.0e-33 E value 104 Match length % identity (AC004684) putative ribosomal protein L36 [Arabidopsis NCBI Description thaliana]

Seq. No. 265094
Contig ID 8163_3.R1011
5'-most EST uC-zmflb73144f09b1
Method BLASTX
NCBI GI g3236242

254

BLAST score



```
1.0e-21
E value
Match length
                   80
                   66
% identity
                   (AC004684) putative ribosomal protein L36 [Arabidopsis
NCBI Description
                   thaliana]
                   265095
Seq. No.
                   8163 6.R1011
Contig ID
5'-most EST
                   wty700168541.hl
                   265096
Seq. No.
                   8164 1.R1011
Contig ID
                   LIB3\overline{1}37-017-Q1-K1-C1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3821254
BLAST score
                   1690
                   0.0e + 00
E value
Match length
                   417
% identity
                   77
                   (AJ007789) geranylgeranyl reductase [Nicotiana tabacum]
NCBI Description
                   265097
Seq. No.
                   8165 1.R1011
Contig ID
                   LIB3116-002-Q1-K1-F10
5'-most EST
                   265098
Seq. No.
                   8167 1.R1011
Contig ID
                   LIB3078-047-Q1-K1-A1
5'-most EST
Method
                   BLASTX
                   q496164
NCBI GI
                   980
BLAST score
                   1.0e-106
E value
                   219
Match length
% identity
                   86
                   (L26305) ribosome-inactivating protein [Zea mays]
NCBI Description
                   >gi 1096509_prf__2111429A ribosome-inactivating protein
                   [Zea mays]
                   265099
Seq. No.
                   8170 1.R1011
Contig ID
                   LIB3078-038-Q1-K1-C10
5'-most EST
                   265100
Seq. No.
                   8171 1.R1011
Contig ID
                   mwy700438766.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3914667
BLAST score
                    387
                    3.0e-37
E value
Match length
                   89
                   83
```

% identity NCBI Description

50S RIBOSOMAL PROTEIN L28, CHLOROPLAST PRECURSO ?

>gi 2459427 (AC002332) putative chloroplast 50s ribosomal

protein L28 [Arabidopsis thaliana]

265101 Seq. No. Contig ID 8172_1.R1011

Contig ID

5'-most EST



```
5'-most EST
                  LIB3078-047-Q1-K1-A4
                  265102
Seq. No.
                  8174 1.R1011
Contig ID
                  fwa700099206.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2911053
BLAST score
                  571
                  2.0e-66
E value
                  233
Match length
                  58
% identity
                  (AL021961) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  265103
Seq. No.
                   8182 1.R1011
Contig ID
5'-most EST
                  LIB3078-046-Q1-K1-G3
                   265104
Seq. No.
Contig ID
                   8184 1.R1011
                  hvj700619190.h1
5'-most EST
                   BLASTX
Method
                   q4056480
NCBI GI
BLAST score
                   686
E value
                   2.0e-72
Match length
                   180
                   72
% identity
                  (AC005896) putative adenylate kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   265105
                   8184 2.R1011
Contig ID
                   LIB3059-046-Q1-K1-H2
5'-most EST
Method
                   BLASTX
                   g3402678
NCBI GI
BLAST score
                   446
                   4.0e-44
E value
                   127
Match length
                   66
% identity
                  (AC004697) putative adenylate kinase [Arabidopsis thaliana]
NCBI Description
                   265106
Seq. No.
                   8194 1.R1011
Contig ID
                   LIB3078-046-Q1-K1-F5
5'-most EST
Seq. No.
                   265107
                   8195 1.R1011
Contig ID
                   LIB3060-034-Q1-K1-G1
5'-most EST
                   BLASTX
Method
                   g3068714
NCBI GI
                   513
BLAST score
                   2.0e-51
E value
                   333
Match length
% identity
                  (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
                   265108
Seq. No.
```

36822

8196 1.R1011

LIB3060-054-Q1-K1-B12



```
Method
                  BLASTX
                  q3334376
NCBI GI
BLAST score
                  869
                  1.0e-93
E value
                  168
Match length
                  99
% identity
                  THIOREDOXIN M-TYPE PRECURSOR (TRX-M) >gi_725276 (L40957)
NCBI Description
                  thioredoxin M [Zea mays]
                  265109
Seq. No.
                  8196 2.R1011
Contig ID
                  LIB3078-001-Q1-K1-F4
5'-most EST
                  BLASTX
Method
                  g3334376
NCBI GI
BLAST score
                  732
                  1.0e-77
E value
                  156
Match length
                  91
% identity
                  THIOREDOXIN M-TYPE PRECURSOR (TRX-M) >gi_725276 (L40957)
NCBI Description
                  thioredoxin M [Zea mays]
                  265110
Seq. No.
                  8196 4.R1011
Contig ID
                  LIB189-013-Q1-E1-F11
5'-most EST
                  BLASTX
Method
                  g3334376
NCBI GI
                  207
BLAST score
                  3.0e-16
E value
                  65
Match length
                  63
% identity
                  THIOREDOXIN M-TYPE PRECURSOR (TRX-M) >gi 725276 (L40957)
NCBI Description
                  thioredoxin M [Zea mays]
                  265111
Seq. No.
                  8196 5.R1011
Contig ID
5'-most EST
                   ceu700425101.h1
Method
                   BLASTN
                   g725275
NCBI GI
                   54
BLAST score
E value
                   9.0e-22
                   76
Match length
                   93
% identity
NCBI Description Zea mays thioredoxin M mRNA, complete cds
                   265112
Seq. No.
                   8197 1.R1011
Contig ID
5'-most EST
                   LIB3078-046-Q1-K1-D2
Method
                   BLASTX
NCBI GI
                   g3549680
BLAST score
                   175
                   3.0e-12
E value
Match length
                   107
% identity
                   36
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
```

36823

265113

8198 1.R1011

Seq. No.

Contig ID



```
wty700168518.h1
5'-most EST
                   BLASTX
Method
                   g2208962
NCBI GI
BLAST score
                   376
                   9.0e-36
E value
                  93
Match length
                   80
% identity
                   (Y10118) signal recognition particle subunit 14 [Oryza
NCBI Description
                   sativa]
                   265114
Seq. No.
                   8199 1.R1011
Contig ID
                   LIB3078-046-Q1-K1-D5
5'-most EST
                   BLASTX
Method
                   g3080390
NCBI GI
BLAST score
                   252
                   1.0e-21
E value
Match length
                   124
                   58
% identity
                   (AL022603) putative protein [Arabidopsis thaliana]
NCBI Description
                   265115
Seq. No.
Contig ID
                   8201 1.R1011
                   fC-zmle700438809r4
5'-most EST
                   265116
Seq. No.
                   8201 2.R1011
Contig ID
5'-most EST
                   uC-zmrob73006e03b1
Method
                   BLASTX
                   g3551523
NCBI GI
                   315
BLAST score
                   2.0e-28
E value
                   242
Match length
                   34
% identity
                  (AB017026) oxysterol-binding protein [Mus musculus]
NCBI Description
                   265117
Seq. No.
Contig ID
                   8201 4.R1011
5'-most EST
                   wty700169334.h1
                   265118
Seq. No.
                   8201 5.R1011
Contig ID
                   uC-zmromo17030f02a1
5'-most EST
                   265119
Seq. No.
                   8203 1.R1011
Contig ID
5'-most EST
                   xjt700096229.hl
Method
                   BLASTX
NCBI GI
                   q3292849
                   1440
BLAST score
                   1.0e-160
E value
Match length
                   329
% identity
                   (AJ007582) arginine methyltransferase [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No. 265120



```
Contig ID
                  8204 1.R1011
                  LIB3078-046-Q1-K1-E2
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4508068
BLAST score
                  266
                  3.0e-23
E value
                  92
Match length
% identity
                   60
                  (AC005882) 3063 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  265121
                   8213 1.R1011
Contig ID
5'-most EST
                  LIB3078-046-Q1-K1-C4
                   265122
Seq. No.
                   8216 1.R1011
Contig ID
5'-most EST
                   LIB3069-054-Q1-K1-G5
                   BLASTX
Method
NCBI GI
                   q1723176
                   258
BLAST score
                   7.0e-22
E value
                   175
Match length
                   35
% identity
                   HYPOTHETICAL 22.4 KD PROTEIN SLL0615
NCBI Description
                   >gi_1001617_dbj_BAA10348_ (D64002) transmembrane protein
                   FT27 [Synechocystis sp.] >gi_1256592 (U38892) similar to
                   Mus musculus transmembrane protein (clone pFT27); Method:
                   conceptual translation supplied by author; ORF206
                   [Synechocystis sp.]
                   265123
Seq. No.
                   8217 1.R1011
Contig ID
                   LIB83-004-Q1-E2-H5
5'-most EST
Method
                   BLASTX
                   g4454032
NCBI GI
                   550
BLAST score
                   4.0e-56
E value
Match length
                   215
                   50
% identity
                  (AL035394) putative protein [Arabidopsis thaliana]
NCBI Description
                   265124
Seq. No.
                   8217 3.R1011
Contig ID
                   wyr7\overline{0}0239714.h1
5'-most EST
                   BLASTX
Method
                   g4454032
NCBI GI
                   241
BLAST score
                   3.0e-20
E value
                   90
Match length
                   51
% identity
                  (AL035394) putative protein [Arabidopsis thaliana]
NCBI Description
```

 Seq. No.
 265125

 Contig ID
 8217_4.R1011

 5'-most EST
 gct701174323.h1

Seq. No. 265126



```
Contig ID
                  8237 1.R1011
                  uC-zmflmo17174f01b1
5'-most EST
                  BLASTN
Method
NCBI GI
                  q3821780
BLAST score
                  36
                  4.0e-10
E value
                  48
Match length
% identity
                  67
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                  265127
Seq. No.
                  8238 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17320f11a1
                  265128
Seq. No.
                  8239 1.R1011
Contig ID
5'-most EST
                  LIB3078-012-Q1-K1-E1
                   265129
Seq. No.
Contig ID
                   8248 1.R1011
5'-most EST
                  uC-zmflb73169a11b2
                   BLASTX
Method
                   g3941720
NCBI GI
BLAST score
                   398
                   3.0e-38
E value
                   184
Match length
                   48
% identity
                   (AF087021) tyrosyl-tRNA synthetase; tyrosine--tRNA ligase
NCBI Description
                   [Bos taurus]
                   265130
Seq. No.
                   8249 1.R1011
Contig ID
                   yyf700352308.h1
5'-most EST
Method
                   BLASTX
                   q4586058
NCBI GI
                   728
BLAST score
                   1.0e-76
E value
                   421
Match length
% identity
                   41
                  (AC007020) unknown protein [Arabidopsis thaliana]
NCBI Description
                   265131
Seq. No.
                   8252 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73132e04b1
Method
                   BLASTX
                   g1168978
NCBI GI
BLAST score
                   1142
                   1.0e-125
E value
                   216
Match length
                   100
% identity
                   PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP)
NCBI Description
                   >gi 1363574_pir__S58576 clpP protein - maize chloroplast
                   >gi_902246_emb_CAA60310_ (X86563) clpP [Zea mays]
```

Seq. No. 265132 Contig ID 8252 2.R1011

5'-most EST LIB3068-035-Q1-K1-H11



Method BLASTX NCBI GI g140281 BLAST score 457 7.0e-45E value Match length 146 67 % identity NCBI Description Seq. No. 265133

HYPOTHETICAL 16.8 KD PROTEIN (ORF 143)

>gi 81821 pir__S05717 hypothetical protein 143 - soybean chloroplast >gi 11577 emb CAA30522 (X07675) ORF 143

[Glycine max]

8255 1.R1011 Contig ID

LIB3078-045-Q1-K1-C1 5'-most EST

Method BLASTX NCBI GI q3885882 964 BLAST score E value 1.0e-104 198 Match length

% identity 91

(AF093629) inorganic pyrophosphatase [Oryza sativa] NCBI Description

Seq. No. 265134

8255 2.R1011 Contig ID

LIB3279-059-P1-K1-B5 5'-most EST

Method BLASTX q3885882 NCBI GI BLAST score 458 E value 1.0e-45 Match length 111 82 % identity

(AF093629) inorganic pyrophosphatase [Oryza sativa] NCBI Description

265135 Seq. No.

8258 1.R1011 Contig ID

LIB189-020-Q1-E1-E2 5'-most EST

Seq. No. 265136

Contig ID 8263 1.R1011

LIB3067-058-Q1-K1-F3 5'-most EST

BLASTX Method NCBI GI g4512216 BLAST score 561 1.0e-57 E value 151 Match length 79 % identity

(AB004882) response regulator [Zea mays] NCBI Description

265137 Seq. No. Contig ID 8264_1.R1011 uC-zmrob73036b05b1 5'-most EST

Seq. No. 265138 8264 2.R1011 Contig ID 5'-most EST cjh700193220.hl

Seq. No. 265139



```
Contig ID
                  8264 7.R1011
                  rvt700549313.h1
5'-most EST
Seq. No.
                  265140
Contig ID
                  8272 1.R1011
5'-most EST
                  LIB83-012-Q1-E1-G8
Seq. No.
                  265141
Contig ID
                  8273 1.R1011
5'-most EST
                  LIB3152-022-P1-K1-G12
                  BLASTX
Method
NCBI GI
                   g4038034
BLAST score
                   421
                   3.0e-41
E value
Match length
                   91
% identity
NCBI Description
                  (AC005936) unknown protein [Arabidopsis thaliana]
Seq. No.
                   265142
                   8273 2.R1011
Contig ID
5'-most EST
                   LIB3069-048-Q1-K1-D6
                   BLASTX
Method
NCBI GI
                   q4038034
BLAST score
                   419
                   6.0e-41
E value
Match length
                   91
                   86
% identity
NCBI Description
                  (AC005936) unknown protein [Arabidopsis thaliana]
Seq. No.
                   265143
                   8280 1.R1011
Contig ID
                   uwc700155571.h1
5'-most EST
Seq. No.
                   265144
                   8281 1.R1011
Contig ID
                   mwy700440585.h1
5'-most EST
Method
                   BLASTX
                   g3928150
NCBI GI
BLAST score
                   253
E value
                   4.0e-39
                   98
Match length
                   90
% identity
                  (AJ131049) hypothetical protein [Cicer arietinum]
NCBI Description
                   265145
Seq. No.
                   8282 1.R1011
Contig ID
                   LIB3150-099-P1-N1-E1
5'-most EST
Method
                   BLASTX
                   g4587525
NCBI GI
BLAST score
                   838
E value
                   2.0e-89
                   340
Match length
                   50
% identity
```

NCBI Description (AC007060) Contains the PF_00650 CRAL/TRIO

phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene.

[Arabidopsis thaliana]

E value

Match length

% identity

3.0e-13

113



```
265146
Seq. No.
                  8283 1.R1011
Contig ID
                  LIB143-013-Q1-E1-C8
5'-most EST
                  BLASTN
Method
                  g1944204
NCBI GI
BLAST score
                  52
                  6.0e-20
E value
                  68
Match length
                  94
% identity
NCBI Description Oryza sativa mRNA for RicMT, complete cds
                  265147
Seq. No.
                  8283 2.R1011
Contig ID
                  LIB3069-055-Q1-K1-H5
5'-most EST
Method
                  BLASTN
                  g1944204
NCBI GI
BLAST score
                  56
                  2.0e-22
E value
Match length
                   68
                   96
% identity
NCBI Description Oryza sativa mRNA for RicMT, complete cds
                   265148
Seq. No.
                   8283 3.R1011
Contig ID
                  LIB143-046-Q1-E1-F9
5'-most EST
Method
                  BLASTN
NCBI GI
                   g296593
BLAST score
                   52
                   3.0e-20
E value
                   72
Match length
                   93
% identity
NCBI Description H. vulgare pZE40 gene
                   265149
Seq. No.
                   8283 4.R1011
Contig ID
5'-most EST
                   LIB143-013-Q1-E1-G2
                   265150
Seq. No.
                   8283 6.R1011
Contig ID
                   hvj700619958.hl
5'-most EST
                   265151
Seq. No.
                   8284 1.R1011
Contig ID
                   uC-zmflb73147b11b1
5'-most EST
Seq. No.
                   265152
Contig ID
                   8292 1.R1011
5'-most EST
                   uC-zmflmo17023e10b1
                   BLASTX
Method
NCBI GI
                   q3193298
BLAST score
                   185
```

36829

NCBI Description (AF069298) T14P8.17 gene product [Arabidopsis thaliana]

NCBI Description



```
265153
Seq. No.
Contig ID
                  8292 2.R1011
                  LIB3137-050-Q1-K1-F8
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3193285
BLAST score
                  157
                  2.0e-10
E value
Match length
                  85
                  35
% identity
                  (AF069298) T14P8.18 gene product [Arabidopsis thaliana]
NCBI Description
                  265154
Seq. No.
Contig ID
                  8292 3.R1011
5'-most EST
                  uC-zmflb73155e06a1
                  265155
Seq. No.
Contig ID
                  8308 1.R1011
5'-most EST
                  uC-zmflmo17312b02b1
Method
                  BLASTX
NCBI GI
                  q1076748
BLAST score
                  1083
                   1.0e-118
E value
                   279
Match length
% identity
                   80
                  major intrinsic protein - rice >gi 440869 dbj BAA04257_
NCBI Description
                   (D17443) major intrinsic protein [Oryza sativa]
                   265156
Seq. No.
Contig ID
                   8313 1.R1011
                  LIB3062-045-Q1-K1-E4
5'-most EST
                   265157
Seq. No.
                   8314 1.R1011
Contig ID
                   cyk700050927.f1
5'-most EST
                   BLASTX
Method
                   g3201971
NCBI GI
                   153
BLAST score
                   1.0e-09
E value
Match length
                   131
% identity
                   37
                  (AF068333) hypothetical secretory protein SH27A precursor
NCBI Description
                   [Oryza sativa]
Seq. No.
                   265158
                   8317 1.R1011
Contig ID
5'-most EST
                   LIB3279-006-P1-K1-F1
                   265159
Seq. No.
                   8317 2.R1011
Contig ID
                   LIB3279-006-P1-K1-C5
5'-most EST
                   BLASTX
Method
                   g2459445
NCBI GI
BLAST score
                   631
                   2.0e-65
E value
Match length
                   197
% identity
                   62
```

(AC002332) putative ribonucleoprotein [Arabidopsis



thaliana]

```
265160
Seq. No.
                   8317 3.R1011
Contig ID
5'-most EST
                   dyk700104342.hl
                   265161
Seq. No.
Contig ID
                   8317 4.R1011
                   LIB3182-005-P2-M1-B5
5'-most EST
                   BLASTX
Method
                   g2459445
NCBI GI
                   421
BLAST score
E value
                   2.0e-41
                   150
Match length
                   37
% identity
                   (AC002332) putative ribonucleoprotein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   265162
                   8319 1.R1011
Contig ID
                   yyf700350515.h1
5'-most EST
                   BLASTX
Method
                   g2497543
NCBI GI
BLAST score
                   2111
                   0.0e+00
E value
Match length
                   493
                   83
% identity
                   PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_542061_pir__S41379
NCBI Description
                   pyruvate kinase - common tobacco >gi_444023_emb_CAA82628_
                   (Z29492) pyruvate kinase [Nicotiana tabacum]
                   265163
Seq. No.
                   8319 2.R1011
Contiq ID
                   xmt7\overline{0}0260513.h1
5'-most EST
                   BLASTX
Method
                   g322787
NCBI GI
                   341
BLAST score
                   6.0e-32
E value
                   87
Match length
                   77
% identity
NCBI Description pyruvate kinase (EC 2.7.1.40), cytosolic - potato
                   265164
Seq. No.
                   8321 1.R1011
Contig ID
                   uwc700152516.h1
5'-most EST
                   265165
Seq. No.
                   8322_1.R1011
Contig ID
                   ntr700072454.h1
5'-most EST
                   BLASTX
Method
                   q3122234
NCBI GI
                   280
BLAST score
                   8.0e-25
E value
Match length
                   123
                   50
% identity
NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT
```

(EIF-2-BETA) (P38) >gi_2306768 (U87163) eIF-2 beta subunit



[Triticum aestivum]

Seq. No. 265166 Contig ID 8331_1.R1011

5'-most EST LIB3137-020-Q1-K1-F2

Seq. No. 265167

Contig ID 8332 1.R1011

5'-most EST LIB189-009-Q1-E1-H5

Method BLASTX
NCBI GI g3914005
BLAST score 711
E value 6.0e-75
Match length 143
% identity 100

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586

(U85494) LON1 protease [Zea mays]

Seq. No. 265168

Contig ID 8332_2.R1011

5'-most EST uC-zmflb73054g10b1

Method BLASTX
NCBI GI g3914005
BLAST score 1953
E value 0.0e+00
Match length 482
% identity 95

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586

(U85494) LON1 protease [Zea mays]

Seq. No. 265169
Contig ID 8337 2.R1011

5'-most EST LIB3137-013-Q1-K1-C9

Seq. No. 265170

Contig ID 8339_1.R1011 5'-most EST tzu700202801.h1

Seq. No. 265171

Contig ID 8339_2.R1011 5'-most EST nbm700471759.h1

Method BLASTX
NCBI GI g3367596
BLAST score 709
E value 6.0e-75
Match length 215
% identity 60

NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 265172

Contig ID 8344_1.R1011

5'-most EST LIB3059-043-Q1-K1-A6

Method BLASTX
NCBI GI g168699
BLAST score 432
E value 1.0e-42
Match length 106

E value

Match length

2.0e-49 151



```
% identity
                   86
                  (M60836) zein [Zea mays]
NCBI Description
                  265173
Seq. No.
                  8344 2.R1011
Contig ID
5'-most EST
                  LIB3118-010-Q1-K1-E4
                  BLASTX
Method
NCBI GI
                  g82660
BLAST score
                  500
E value
                   2.0e-50
                  171
Match length
% identity
                   65
                  19K zein precursor (clone ZG31A) - maize (fragment)
NCBI Description
                   >gi_809117_emb_CAA24720_ (V01473) zein [Zea mays]
Seq. No.
                   265174
                  8344 3.R1011
Contig ID
                  LIB3059-047-Q1-K1-B11
5'-most EST
                  BLASTX
Method
                   g168701
NCBI GI
BLAST score
                   527
                   3.0e-53
E value
                   303
Match length
% identity
                   67
NCBI Description
                  (M60837) zein [Zea mays]
Seq. No.
                   265175
                   8344 4.R1011
Contig ID
                   LIB3<u>1</u>51-020-Q1-K1-E9
5'-most EST
Method
                   BLASTX
NCBI GI
                   q629861
                   439
BLAST score
                   2.0e-43
E value
Match length
                   128
                   73
% identity
NCBI Description
                  zein Zdl, 19K - maize >gi_535020 emb_CAA47639 (X67203)
                   zein Zd1 (19 kDa zein) [Zea mays]
Seq. No.
                   265176
Contig ID
                   8344 5.R1011
5'-most EST
                   LIB3151-026-Q1-K1-A5
Method
                   BLASTN
NCBI GI
                   q1808685
BLAST score
                   97
E value
                   8.0e-47
Match length
                   197
% identity
                   87
NCBI Description S.stapfianus pSD.39 mRNA
Seq. No.
                   265177
                   8344 9.R1011
Contig ID
                   LIB3180-053-P2-M1-H2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q168701
BLAST score
                   490
```



```
% identity
                  70
                  (M60837) zein [Zea mays]
NCBI Description
                  265178
Seq. No.
                  8344 11.R1011
Contig ID
                  ypc700800373.h1
5'-most EST
Method
                  BLASTX
                  g141605
NCBI GI
                  221
BLAST score
                  5.0e-18
E value
Match length
                  48
                  96
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >qi 168680 (M12145) 19 kDa zein protein [Zea mays]
                  265179
Seq. No.
Contig ID
                  8344 13.R1011
                  LIB3152-034-P1-K1-H10
5'-most EST
Method
                  BLASTX
NCBI GI
                  q168701
BLAST score
                  233
                  3.0e-19
E value
Match length
                  67
                  73
% identity
                  (M60837) zein [Zea mays]
NCBI Description
Seq. No.
                  265180
Contig ID
                  8344 15.R1011
                  LIB3059-019-Q1-K1-H4
5'-most EST
Method
                  BLASTN
NCBI GI
                  q168677
                  145
BLAST score
                  8.0e-76
E value
                  272
Match length
                  92
% identity
                  Maize 19 kDa zein mRNA, clone cZ19C1, complete cds
NCBI Description
                  265181
Seq. No.
                  8344 16.R1011
Contig ID
5'-most EST
                  LIB3061-015-Q1-K1-C7
                  BLASTN
Method
                  g168700
NCBI GI
                   147
BLAST score
                   7.0e-77
E value
                  171
Match length
                   96
% identity
NCBI Description Z.mays zein mRNA, complete cds
                   265182
Seq. No.
                   8344 18.R1011
Contig ID
```

LIB3078-039-Q1-K1-E2 5'-most EST

BLASTX Method NCBI GI q1808686 230 BLAST score

1.0e-32 E value 136 Match length



% identity 55

NCBI Description (Y10783) hypothetical protein [Sporobolus stapfianus]

Seq. No. 265183

Contig ID 8344 20.R1011

5'-most EST LIB3059-005-Q1-K1-F3

Method BLASTN
NCBI GI g168673
BLAST score 189
E value 1.0e-102
Match length 245
% identity 95

NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds

Seq. No. 265184

Contig ID 8351_1.R1011 5'-most EST nbm700473983.h1

Method BLASTX
NCBI GI 94507857
BLAST score 386
E value 1.0e-36
Match length 426
% identity 29

NCBI Description Herpes virus-associated ubiquitin-specific protease

>gi_2501460_sp_Q93009_UBPH_HUMAN PROBABLE UBIQUITIN

CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) >gi 1545952 emb CAA96580 (F72400) have a received and the relation of the protection of the relation of

(Z72499) herpesvirus associated ubiquitin-specific protease

(HAUSP) [Homo sapiens]

Seq. No. 265185

Contig ID 8351_2.R1011

5'-most EST uC-zmflb73013g10b1

Seq. No. 265186

Contig ID 8351 3.R1011

5'-most EST LIB3067-033-Q1-K1-B8

Seq. No. 265187 Contig ID 8352 1.R1011

5'-most EST LIB3150-043-Q1-N1-G11

Seq. No. 265188

Contig ID 8355_1.R1011

5'-most EST uC-zmflb73073h07b3

Seq. No. 265189

Contig ID 8357_1.R1011 5'-most EST LIB3078-054-Q1-K1-G4

Method BLASTX
NCBI GI g3510542
BLAST score 186
E value 2.0e-13

E value 2.06 Match length 152 % identity 34



```
(AF038949) intracellular pathogenesis-related protein
NCBI Description
                  PinmIII [Pinus monticola]
                  265190
Seq. No.
                  8360 1.R1011
Contig ID
                  LIB3069-011-Q1-K1-B8
5'-most EST
                  BLASTX
Method
                  g2495703
NCBI GI
                  568
BLAST score
                  5.0e-58
E value
                  284
Match length
% identity
                  43
                  HYPOTHETICAL PROTEIN KIAA0126 >gi 1469175 dbj BAA09475
NCBI Description
                  (D50916) The KIAA0126 gene is partially related to a yeast
                  gene. [Homo sapiens]
                  265191
Seq. No.
                  8360 2.R1011
Contig ID
                  uC-zmflb73274e12b1
5'-most EST
Method
                  BLASTX
                  g2495703
NCBI GI
                  277
BLAST score
E value
                  3.0e-24
Match length
                  140
                  49
% identity
                  HYPOTHETICAL PROTEIN KIAA0126 >gi 1469175 dbj BAA09475
NCBI Description
                  (D50916) The KIAA0126 gene is partially related to a yeast
                  gene. [Homo sapiens]
                  265192
Seq. No.
                  8363 1.R1011
Contig ID
                  LIB3151-059-Q1-K1-H12
5'-most EST
                  BLASTX
Method
                  g3080435
NCBI GI
BLAST score
                  1592
                  1.0e-178
E value
                  419
Match length
% identity
                  72
                  (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
                  265193
Seq. No.
                  8364 1.R1011
Contig ID
5'-most EST
                  wty700171119.hl
                  BLASTX
Method
                  q2668492
NCBI GI
                   222
BLAST score
E value
                   6.0e-18
```

Match length 75 % identity

(D89981) metal-transporting P-type ATPase [Arabidopsis NCBI Description

thaliana]

265194 Seq. No. 8370 1.R1011 Contig ID

5'-most EST LIB3067-045-Q1-K1-F6

Seq. No. 265195



8372 1.R1011 Contig ID 5'-most EST

uC-zmf1b73217a02b2

BLASTX Method g4262149 NCBI GI 368 BLAST score 8.0e - 35E value 176 Match length 43 % identity

(AC005275) putative xyloglucan endotransglycosylase NCBI Description

[Arabidopsis thaliana]

265196 Seq. No.

8372 2.R1011 Contig ID

LIB3136-011-Q1-K1-G7 5'-most EST

BLASTX Method NCBI GI q4262149 175 BLAST score 9.0e-13E value 45 Match length 58 % identity

(AC005275) putative xyloglucan endotransglycosylase NCBI Description

[Arabidopsis thaliana]

265197 Seq. No.

8380 1.R1011 Contig ID

5'-most EST uC-zmflmo17153h05b1

BLASTX Method NCBI GI g4325372 535 BLAST score 4.0e-54E value 261 Match length % identity 51

(AF128396) contains similarity to protein disulfide NCBI Description

isomerases [Arabidopsis thaliana]

265198 Seq. No.

Contig ID 8380 2.R1011

uC-zmflMo17009c12b1 5'-most EST

265199 Seq. No.

8380 3.R1011 Contig ID

5'-most EST uC-zmflmo17123a09a1

265200 Seq. No.

8381 1.R1011 Contig ID

5'-most EST uC-zmflmo17039b04b1

Seq. No. 265201

Contig ID 8382 1.R1011

5'-most EST LIB3067-049-Q1-K1-B8

265202 Seq. No.

Contig ID 8387 1.R1011

uC-zmflmo17068c01b2 5'-most EST

Method BLASTX g4049353 NCBI GI BLAST score 1208



E value 1.0e-133 Match length 472 51 % identity (AL034567) putative protein [Arabidopsis thaliana] NCBI Description 265203 Seq. No. 8387 3.R1011 Contig ID 5'-most EST uwc700152327.h1 BLASTX Method NCBI GI g4630748 BLAST score 374 3.0e-36 E value Match length 81 85 % identity (AC007236) putative anion exchange protein 3 [Arabidopsis NCBI Description thaliana] Seq. No. 265204 Contig ID 8393 1.R1011 5'-most EST LIB3060-052-Q1-K1-A9 265205 Seq. No. 8395 1.R1011 Contig ID 5'-most EST LIB3067-048-Q1-K1-D1 BLASTX Method q4220476 NCBI GI BLAST score 1423 1.0e-158 E value Match length 437 % identity (AC006069) ribophorin I-like protein [Arabidopsis thaliana] NCBI Description 265206 Seq. No. 8397 1.R1011 Contig ID pmx700085660.h1 5'-most EST BLASTX Method g2673917 NCBI GI 1091 BLAST score E value 1.0e-119 Match length 339 32 % identity (AC002561) putative ATP-dependent RNA helicase [Arabidopsis NCBI Description thaliana] 265207 Seq. No. 8397 2.R1011 Contig ID $uC-z\overline{m}flmo17249e11a1$ 5'-most EST Method BLASTX g2673917 NCBI GI

BLAST score 170 4.0e-12 E value 44 Match length 68 % identity

(AC002561) putative ATP-dependent RNA helicase [Arabidopsis NCBI Description

thaliana]

Seq. No. 265208



Contig ID 8399_1.R1011 5'-most EST LIB3150-098-P1-N1-A5

 Seq. No.
 265209

 Contig ID
 8401_1.R1011

 5'-most EST
 uC-zmflB73045f02b1

Method BLASTX
NCBI GI g3914557
BLAST score 1021
E value 1.0e-111
Match length 193
% identity 99

NCBI Description RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED PROTEIN) >gi 1155265 (U40219) possible apospory-associated

protein [Pennisetum ciliare]

Seq. No. 265210 Contig ID 8401 2.R1011

Contig ID 8401_2.R1011 5'-most EST LIB3182-002-P1-M1-E7

Method BLASTX
NCBI GI g3914557
BLAST score 680
E value 1.0e-71

E value 1.0e-Match length 131 % identity 99

NCBI Description RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED

PROTEIN) >gi_1155265 (U40219) possible apospory-associated

protein [Pennisetum ciliare]

Seq. No. 265211

Contig ID 8401_4.R1011 5'-most EST pmx700085735.h1

Method BLASTX
NCBI GI g3914557
BLAST score 373
E value 5.0e-36
Match length 74
% identity 100

NCBI Description RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED

PROTEIN) >gi_1155265 (U40219) possible apospory-associated

protein [Pennisetum ciliare]

Seq. No. 265212

Contig ID 8401_5.R1011

5'-most EST uC-zmflb73204b11b1

Method BLASTX
NCBI GI g3914557
BLAST score 173
E value 5.0e-23
Match length 63
% identity 97

NCBI Description RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED

PROTEIN) >gi_1155265 (U40219) possible apospory-associated

protein [Pennisetum ciliare]

Seq. No. 265213 Contig ID 8401 7.R1011



```
5'-most EST
                  LIB3078-038-Q1-K1-H9
Method
                  BLASTX
NCBI GI
                  q3914557
BLAST score
                   375
                   9.0e-36
E value
Match length
                  74
                   96
% identity
                  RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED
NCBI Description
                  PROTEIN) >qi 1155265 (U40219) possible apospory-associated
                  protein [Pennisetum ciliare]
Seq. No.
                  265214
                  8401 9.R1011
Contig ID
                  LIB3088-032-Q1-K1-F10
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3914557
                   231
BLAST score
E value
                   3.0e-24
Match length
                  72
% identity
                   86
                  RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED
NCBI Description
                   PROTEIN) >gi 1155265 (U40219) possible apospory-associated
                  protein [Pennisetum ciliare]
Seq. No.
                  265215
                  8402 1.R1011
Contig ID
5'-most EST
                   cat7\overline{0}0020719.r1
Method
                  BLASTX
NCBI GI
                  q4646202
BLAST score
                   402
                   4.0e-39
E value
Match length
                  145
% identity
                   57
NCBI Description
                  (AC007230) ESTs gb H76289 and gb H76537 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                   265216
Contig ID
                   8405 1.R1011
5'-most EST
                  uC-zmflb73178g04b1
Method
                  BLASTX
                  g2145356
NCBI GI
BLAST score
                   2112
E value
                   0.0e+00
Match length
                   647
                   63
% identity
NCBI Description
                   (Y11122) HD-Zip protein [Arabidopsis thaliana] >gi 3132474
                   (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]
Seq. No.
                   265217
Contig ID
                   8405 2.R1011
```

5'-most EST uC-zmflmo17370f01a1 Method BLASTX

NCBI GI g2145356 BLAST score 203 E value 4.0e-16 Match length 51 % identity 71



(Y11122) HD-Zip protein [Arabidopsis thaliana] >gi_3132474 NCBI Description (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana] 265218 Seq. No. Contig ID 8405 3.R1011 uer700582709.h1 5'-most EST Seq. No. 265219 8407 1.R1011 Contig ID LIB3078-036-Q1-K1-E9 5'-most EST BLASTX Method NCBI GI g4063751 BLAST score 169 2.0e-11 E value Match length 98 36 % identity (AC005851) putative white protein [Arabidopsis thaliana] NCBI Description >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana] 265220 Seq. No. 8407 2.R1011 Contig ID LIB3136-013-Q1-K1-A5 5'-most EST Method BLASTX NCBI GI q4063751 BLAST score 421 6.0e-41E value Match length 337 % identity 30 (AC005851) putative white protein [Arabidopsis thaliana] NCBI Description >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana] 265221 Seq. No. 8409 1.R1011 Contig ID LIB3150-086-P1-N1-A5 5'-most EST BLASTX Method NCBI GI g2245131 BLAST score 275 6.0e-24 E value 223 Match length % identity (Z97344) hypothetical protein [Arabidopsis thaliana] NCBI Description 265222 Seq. No. 8410 1.R1011 Contig ID $ceu7\overline{0}0429252.h1$ 5'-most EST BLASTX Method g2293006 NCBI GI BLAST score 244 2.0e-20 E value 118 Match length % identity NCBI Description (AJ000977) hypothetical protein [Rhodobacter sphaeroides]

Seq. No. 265223 Contig ID 8411_1.R1011

% identity



5'-most EST xmt700265908.h1 BLASTX Method g3785977 NCBI GI BLAST score 585 4.0e-60 E value 299 Match length % identity 41 (AC005560) putative growth regulator protein [Arabidopsis NCBI Description thaliana] 265224 Seq. No. Contig ID 8416 1.R1011 uC-zmflb73161c11b2 5'-most EST Method BLASTX NCBI GI q2245066 BLAST score 358 8.0e-34 E value Match length 113 % identity 64 (Z97342) Beta-Amylase [Arabidopsis thaliana] NCBI Description 265225 Seq. No. Contig ID 8416 2.R1011 LIB3066-054-Q1-K1-G8 5'-most EST Method BLASTX g2245066 NCBI GI 366 BLAST score E value 1.0e-34 Match length 119 64 % identity (Z97342) Beta-Amylase [Arabidopsis thaliana] NCBI Description Seq. No. 265226 8416 3.R1011 Contig ID $xyt7\overline{0}0343673.h1$ 5'-most EST BLASTX Method NCBI GI g2245066 BLAST score 487 1.0e-67 E value 147 Match length % identity 78 (Z97342) Beta-Amylase [Arabidopsis thaliana] NCBI Description 265227 Seq. No. 8417 1.R1011 Contig ID wty700162617.h1 5'-most EST Seq. No. 265228 Contig ID 8423 1.R1011 pmx700087812.h1 5'-most EST BLASTX Method q728882 NCBI GI BLAST score 877 2.0e-94 E value Match length 178

36842

NCBI Description ADP-RIBOSYLATION FACTOR 3 >gi_541846 pir__S41938



ADP-ribosylation factor 3 - Arabidopsis thaliana >gi_453191_emb_CAA54564_ (X77385) ADP-ribosylation factor 3 [Arabidopsis thaliana]

 Seq. No.
 265229

 Contig ID
 8423_2.R1011

 5'-most EST
 xdb700339168.h1

Seq. No. 265230 Contig ID 8423_3.R1011

5'-most EST LIB3117-012-Q1-K1-H6

Method BLASTX
NCBI GI g728882
BLAST score 443
E value 5.0e-55
Match length 150
% identity 76

NCBI Description ADP-RIBOSYLATION FACTOR 3 >gi_541846_pir__S41938

ADP-ribosylation factor 3 - Arabidopsis thaliana

>gi_453191_emb_CAA54564_ (X77385) ADP-ribosylation factor 3

[Arabidopsis thaliana]

Seq. No. 265231

Contig ID 8428_1.R1011

5'-most EST LIB3157-017-Q1-K1-H5

Method BLASTX
NCBI GI g4220535
BLAST score 434
E value 8.0e-43
Match length 95
% identity 85

NCBI Description (AL035356) clathrin coat assembly like protein [Arabidopsis

thaliana]

Seq. No. 265232

Contig ID 8428_2.R1011 5'-most EST xjt700095891.h1

Method BLASTX
NCBI GI g4220535
BLAST score 869
E value 1.0e-93
Match length 226
% identity 76

NCBI Description (AL035356) clathrin coat assembly like protein [Arabidopsis

thaliana]

Seq. No. 265233 Contig ID 8433_1.R1011

5'-most EST LIB3078-038-Q1-K1-A5

Method BLASTX
NCBI GI g3746067
BLAST score 713
E value 2.0e-75
Match length 229
% identity 62

NCBI Description (AC005311) hypothetical protein [Arabidopsis thaliana]



Seq. No. 265234

Contig ID 8434_1.R1011

5'-most EST uC-zmflmo17286g03b1

Seq. No. 265235

Contig ID 8434_2.R1011 5'-most EST mwy700438365.h1

Seq. No. 265236

Contig ID 8434 5.R1011

5'-most EST uC-zmflmo17133c09b1

Seq. No. 265237

Contig ID 8434 6.R1011

5'-most EST uC-zmflmo17264b12a1

Seq. No. 265238

Contig ID 8435_1.R1011 5'-most EST qmh700029232.f1

Method BLASTX
NCBI GI g294668
BLAST score 1135
E value 1.0e-161
Match length 358
% identity 82

NCBI Description (L13242) beta-ketoacyl-ACP synthase [Ricinus communis]

Seq. No. 265239

Contig ID 8435_2.R1011

5'-most EST LIB3150-114-P2-K1-H6

Seq. No. 265240

Contig ID 8435_3.R1011 5'-most EST xdb700340794.h1

Seq. No. 265241

Contig ID 8439_1.R1011

5'-most EST uC-zmflb73376c06a2

Method BLASTX
NCBI GI g478409
BLAST score 332
E value 9.0e-45
Match length 157
% identity 57

NCBI Description peroxidase (EC 1.11.1.7), cationic - adzuki bean

>gi_218328_dbj_BAA01950_ (D11337) peroxidase [Vigna

angularis]

Seq. No. 265242

Contig ID 8442_1.R1011 5'-most EST pmx700083233.h1

Method BLASTX
NCBI GI g2498731
BLAST score 1105
E value 1.0e-121
Match length 352
% identity 62



```
NCBI Description
                  PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
                   >gi_1362013_pir__S57611 zeta-crystallin homolog -
                   Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)
                   zeta-crystallin homologue [Arabidopsis thaliana]
Seq. No.
                   265243
                   8443 1.R1011
Contig ID
5'-most EST
                   LIB3078-038-Q1-K1-B6
                   265244
Seq. No.
                   8445 1.R1011
Contig ID
5'-most EST
                   LIB36-003-Q1-E1-B1
Method
                   BLASTX
NCBI GI
                   q267120
                   478
BLAST score
                   1.0e-47
E value
Match length
                   172
                   58
% identity
                   THIOREDOXIN F-TYPE PRECURSOR (TRX-F) >gi 100070 pir S20929
NCBI Description
                   thioredoxin f precursor - garden pea
                   >gi 20907 emb CAA45098 (X63537) thioredoxin F [Pisum
                   sat\overline{i}vum] \overline{>}gi_1388086 (\overline{U}35830) thioredoxin f [Pisum sativum]
                   265245
Seq. No.
Contig ID
                   8445 2.R1011
5'-most EST
                   nwy700447436.h1
                   BLASTX
Method
                   g3202022
NCBI GI
BLAST score
                   476
E value
                   2.0e-47
Match length
                   114
% identity
                   80
                  (AF069314) thioredoxin F precursor [Mesembryanthemum
NCBI Description
                   crystallinum]
Seq. No.
                   265246
Contig ID
                   8445 3.R1011
5'-most EST
                   LIB189-010-Q1-E1-F4
Method
                   BLASTX
NCBI GI
                   q3202022
BLAST score
                   335
E value
                   4.0e-31
Match length
                   78
                   78
% identity
NCBI Description
                  (AF069314) thioredoxin F precursor [Mesembryanthemum
                   crystallinum]
                   265247
Seq. No.
                   8445 5.R1011
                   mwy700442550.h1
```

Contig ID 5'-most EST

Seq. No. 265248

8455 1.R1011 Contig ID

5'-most EST LIB3061-022-Q1-K1-B2

BLASTX Method NCBI GI g4455302 BLAST score 723



E value 2.0e-76 Match length 223 % identity 62

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 265249

Contig ID 8455_2.R1011

5'-most EST uC-zmf1B73004b09b1

Method BLASTX
NCBI GI g4455302
BLAST score 324
E value 1.0e-29
Match length 142
% identity 49

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 265250

Contig ID 8456 1.R1011

5'-most EST LIB3078-037-Q1-K1-H2

Seq. No. 265251

Contig ID 8457 1.R1011

5'-most EST LIB3078-037-Q1-K1-H3

Seq. No. 265252

Contig ID 8463_1.R1011 5'-most EST tzu700206072.h1

Method BLASTX
NCBI GI g2499551
BLAST score 254
E value 2.0e-21

E value 2.0 Match length 93 % identity 54

NCBI Description PUTATIVE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-PHOSPHATASE

>gi_1001408_dbj_BAA10030_ (D63999) low molecular weight
phosphotyrosine protein phosphatase [Synechocystis sp.]

Seq. No. 265253

Contig ID 8467_1.R1011

5'-most EST LIB3150-045-Q1-N1-D7

Method BLASTX
NCBI GI g2293568
BLAST score 415
E value 2.0e-40
Match length 85
% identity 89

NCBI Description (AF012897) HvB12D homolog [Oryza sativa]

Seq. No. 265254 Contig ID 8467 2.R1011

5'-most EST LIB3078-027-Q1-K1-H2

Method BLASTX
NCBI GI g2293568
BLAST score 382
E value 1.0e-36
Match length 78
% identity 91



NCBI Description (AF012897) HvB12D homolog [Oryza sativa]

Seq. No. 265255

Contig ID 8467_3.R1011 5'-most EST cjh700193058.h1

Method BLASTX
NCBI GI g2293568
BLAST score 198
E value 3.0e-15
Match length 42
% identity 86

NCBI Description (AF012897) HvB12D homolog [Oryza sativa]

Seq. No. 265256

Contig ID 8473 1.R1011

5'-most EST LIB3078-037-Q1-K1-F6

Seq. No. 265257

Contig ID 8474 1.R1011

5'-most EST uC-zmrob73019g06b1

Method BLASTX
NCBI GI g3242714
BLAST score 165
E value 3.0e-11
Match length 157
% identity 28

NCBI Description (AC003040) hypersensitivity-related protein [Arabidopsis

thaliana]

Seq. No. 265258

Contig ID 8482 1.R1011

5'-most EST uC-zmflmo17013c02b1

Seq. No. 265259

Contig ID 8482_2.R1011

5'-most EST LIB3137-001-Q1-K1-G9

Seq. No. 265260

Contig ID 8483_1.R1011 5'-most EST tfd700574047.h1

Method BLASTX
NCBI GI g4539305
BLAST score 874
E value 1.0e-105
Match length 278
% identity 64

NCBI Description (AL049480) putative protein [Arabidopsis thaliana]

Seq. No. 265261

Contig ID 8486_1.R1011 5'-most EST wty700164083.h1

Seq. No. 265262

Contig ID 8486 4.R1011

5'-most EST uC-zmflmo17155e05b1

Seq. No. 265263



```
8489 1.R1011
Contig ID
                  nbm700471556.h1
5'-most EST
                  BLASTX
Method
                  q4567201
NCBI GI
                  154
BLAST score
                  3.0e-09
E value
                  234
Match length
% identity
                  (AC007168) putative aspartate aminotransferase [Arabidopsis
NCBI Description
                  thaliana]
                  265264
Seq. No.
Contig ID
                  8493 1.R1011
                  uwc700152090.h1
5'-most EST
                  BLASTX
Method
                  q632500
NCBI GI
                  318
BLAST score
                   3.0e-29
E value
Match length
                   118
% identity
                   (U17394) polyadenylation factor 64 kDa subunit [Xenopus
NCBI Description
                   laevis]
                   265265
Seq. No.
                   8494 1.R1011
Contig ID
                   LIB3062-011-Q1-K1-C8
5'-most EST
                   BLASTX
Method
                   q282430
NCBI GI
BLAST score
                   380
                   1.0e-36
E value
                   136
Match length
                   52
% identity
                   leucine--tRNA ligase (EC 6.1.1.4) - Bacillus subtilis
NCBI Description
                   >qi 143148 (M88581) transfer RNA-Leu synthetase [Bacillus
                   subtilis]
                   265266
Seq. No.
                   8496 1.R1011
Contig ID
5'-most EST
                   LIB3078-037-Q1-K1-B4
Method
                   BLASTX
NCBI GI
                   g3776015
                   258
BLAST score
                   2.0e-39
E value
                   148
Match length
                   58
% identity
                   (AJ010471) RNA helicase [Arabidopsis thaliana]
NCBI Description
                   >gi_4249378_gb_AAD14475_ (AC005966) Identical to
                   gb_AJ010471 mRNA for DEAD box RNA helicase (RH22) from
                   Arabidopsis thaliana. EST gb_Y11191 comes from this gene.
                   [Arabidopsis thaliana]
                   265267
Seq. No.
                   8497 1.R1011
Contig ID
                   zuv700353143.h1
5'-most EST
```

36848

265268

8501 1.R1011

Seq. No.

Contig ID

E value

Match length

1.0e-18

61



5'-most EST LIB3070-006-Q1-N1-D4 Seq. No. 265269 8502 1.R1011 Contig ID uC-zmflmo17201e04b1 5'-most EST Method BLASTX NCBI GI g4455223 BLAST score 987 1.0e-107 E value Match length 280 68 % identity (AL035440) putative DNA binding protein [Arabidopsis NCBI Description thaliana] Seq. No. 265270 Contig ID 8505 1.R1011 xsy700214827.h1 5'-most EST Method BLASTX q3096922 NCBI GI BLAST score 358 1.0e-33 E value Match length 82 % identity 84 (AL023094) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 265271 8506 1.R1011 Contig ID 5'-most EST LIB3078-036-Q1-K1-G5 Method BLASTX g3096931 NCBI GI 319 BLAST score 4.0e-29 E value Match length 112 54 % identity (AL023094) putative ribosomal protein S16 [Arabidopsis NCBI Description thaliana] Seq. No. 265272 8507 1.R1011 Contig ID pmx700089637.h1 5'-most EST BLASTX Method NCBI GI g2459417 BLAST score 1499 E value 1.0e-167 Match length 501 65 % identity (AC002332) putative pre-mRNA splicing factor PRP19 NCBI Description [Arabidopsis thaliana] Seq. No. 265273 8507 2.R1011 Contig ID uC-zmflB73006e10b1 5'-most EST Method BLASTX g2341025 NCBI GI BLAST score 228



% identity (AC000104) F19P19.2 [Arabidopsis thaliana] NCBI Description 265274 Seq. No. 8507 3.R1011 Contig ID tzu700204559.h1 5'-most EST BLASTX Method g2459417 NCBI GI BLAST score 277 1.0e-24 E value Match length 72 75 % identity (AC002332) putative pre-mRNA splicing factor PRP19 NCBI Description [Arabidopsis thaliana] 265275 Seq. No. 8514 1.R1011 Contig ID ymt700223457.h1 5'-most EST BLASTX Method q549061 NCBI GI 1170 BLAST score 1.0e-128 E value 378 Match length 60 % identity T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA) NCBI Description (CCT-ZETA-1) >gi_631655_pir__S43063 CCT (chaperonin containing TCP-1) zeta chain - mouse >gi_468554_emb_CAA83432_ (Z31557) CCT (chaperonin containing TCP-1) zeta subunit [Mus musculus] 265276 Seq. No. 8515 1.R1011 Contig ID 5'-most EST LIB84-007-Q1-E1-E10 BLASTX Method NCBI GI q2894565 BLAST score 208 E value 3.0e-16 Match length 88 50 % identity (AL021890) heat shock protein - like [Arabidopsis thaliana] NCBI Description 265277 Seq. No. 8515 2.R1011 Contig ID 5'-most EST wyr700243427.hl 265278 Seq. No. Contig ID 8529 1.R1011 5'-most EST uC-zmf1b73116b12b2 Method BLASTX NCBI GI q3021268 BLAST score 338 E value 2.0e-31 175 Match length % identity 44 (AL022347) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 265279



8538 1.R1011 Contig ID $nwy7\overline{0}0447591.h1$ 5'-most EST 265280 Seq. No.

8543 1.R1011 Contig ID 5'-most EST uC-zmroteosinte040d01b1

265281 Seq. No.

8546 1.R1011 Contig ID

5'-most EST LIB3158-011-Q1-K1-H4

Method BLASTX NCBI GI g2499551 BLAST score 149 E value 9.0e-12 Match length 69

% identity 57

PUTATIVE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-PHOSPHATASE NCBI Description

>qi 1001408 dbj BAA10030 (D63999) low molecular weight phosphotyrosine protein phosphatase [Synechocystis sp.]

Seq. No. 265282 Contig ID 8546 3.R1011

5'-most EST LIB3078-035-Q1-K1-H11

Method BLASTX q2499551 NCBI GI BLAST score 154 E value 4.0e-10 Match length 47 % identity 60

PUTATIVE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-PHOSPHATASE NCBI Description

>gi 1001408 dbj BAA10030 (D63999) low molecular weight phosphotyrosine protein phosphatase [Synechocystis sp.]

265283 Seq. No.

Contig ID 8549 1.R1011 5'-most EST xyt700343023.h1

Method BLASTX NCBI GI q2811226 524 BLAST score 5.0e-53 E value Match length 156 70 % identity

(AF042669) fimbrin 2 [Arabidopsis thaliana] >gi 2811232 NCBI Description

(AF042671) fimbrin 2 [Arabidopsis thaliana]

Seq. No. 265284

Contig ID 8555 1.R1011

5'-most EST uC-zmflb73151d09b1

265285 Seq. No.

Contig ID 8555 2.R1011

5'-most EST uC-zmflmo17150f11a1

Seq. No. 265286

Contig ID 8558 1.R1011

5'-most EST uC-zmflmo17277a08b1

Method BLASTX

Seq. No.

Contig ID

265292

8573 1.R1011



```
NCBI GI
                   q1916290
                   265
BLAST score
E value
                   1.0e-22
Match length
                   165
                   40
% identity
                  (U89876) ALY [Mus musculus]
NCBI Description
                   265287
Seq. No.
                   8558 2.R1011
Contig ID
                   LIB3061-034-Q1-K1-G12
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1916290
BLAST score
                   252
                   4.0e-21
E value
Match length
                   165
% identity
                   39
                  (U89876) ALY [Mus musculus]
NCBI Description
                   265288
Seq. No.
                   8558 3.R1011
Contig ID
                   uer700577029.h1
5'-most EST
Seq. No.
                   265289
                   8565 1.R1011
Contig ID
                   LIB3062-041-Q1-K1-H9
5'-most EST
Method
                   BLASTX
                   g1001650
NCBI GI
BLAST score
                   174
E value
                   3.0e-12
Match length
                   64
                   50
% identity
                  (D64002) hypothetical protein [Synechocystis sp.]
NCBI Description
                   265290
Seq. No.
                   8571 1.R1011
Contig ID
5'-most EST
                   xmt7\overline{0}0262622.h1
Method
                   BLASTX
                   q4127456
NCBI GI
BLAST score
                   825
                   3.0e-88
E value
                   224
Match length
                   71
% identity
                  (AJ010818) Cpn21 protein [Arabidopsis thaliana]
NCBI Description
                   265291
Seq. No.
Contig ID
                   8572 1.R1011
5'-most EST
                   uC-zmroB73030h09b1
Method
                   BLASTX
NCBI GI
                   q1064931
BLAST score
                   680
                   2.0e-71
E value
Match length
                   190
% identity
                   64
NCBI Description
                  (X92965) cyclin A-like protein [Nicotiana tabacum]
```



```
uC-zmflb73096f12b1
5'-most EST
                  265293
Seq. No.
                  8577 1.R1011
Contig ID
5'-most EST
                  LIB83-002-Q1-E1-G12
                  265294
Seq. No.
Contig ID
                  8578 1.R1011
                  LIB3078-035-Q1-K1-B8
5'-most EST
                  BLASTX
Method
                  g4335751
NCBI GI
                  713
BLAST score
                  2.0e-75
E value
                  200
Match length
                  63
% identity
                  (AC006284) putative methyltransferase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  265295
                  8583 1.R1011
Contig ID
                  LIB3078-035-Q1-K1-C8
5'-most EST
                  BLASTX
Method
                  q3183077
NCBI GI
                  310
BLAST score
                  2.0e-28
E value
                  124
Match length
                  51
% identity
                  PROBABLE 1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE
NCBI Description
                   (DHNA-OCTAPRENYLTRANSFERASE) >gi_1653114_dbj_BAA18030
                   (D90911) menaquinone biosynthesis protein [Synechocystis
                   sp.]
                   265296
Seq. No.
                   8589 1.R1011
Contig ID
                  LIB3078-034-Q1-K1-G9
5'-most EST
Seq. No.
                   265297
                   8591 1.R1011
Contig ID
5'-most EST
                   LIB83-002-Q1-E1-A7
Method
                   BLASTX
NCBI GI
                   q3287270
BLAST score
                   854
                   8.0e-92
E value
Match length
                   188
                   85
% identity
NCBI Description (Y09533) involved in starch metabalism [Solanum tuberosum]
Seq. No.
                   265298
                   8593 1.R1011
Contig ID
                   LIB3088-041-Q1-K1-A7
5'-most EST
                   265299
Seq. No.
                   8593 4.R1011
Contig ID
                   uC-zmflb73395h11a2
5'-most EST
```

36853

265300

8595 1.R1011

Seq. No.

Contig ID



5'-most EST LIB3068-062-Q1-K1-E3 Method BLASTX

NCBI GI g129871
BLAST score 183
E value 4.0e-13
Match length 37
% identity 100
NCBI Description CYTOCHRO

CYTOCHROME B6-F COMPLEX SUBUNIT 5 > gi_65644_pir_WMRZ4 cytochrome b6-f complex 4.2K protein - rice chloroplast > gi_100947_pir_A32159_plastoquinol--plastocyanin reductase (EC 1.10.99.1) chain V - maize chloroplast

>gi_2147243_pir__\$68166 cytochrome b6-f complex chain 5 -

beet chloroplast >gi_12006_emb_CAA33967_ (X15901)

cytochrome b /f complex subunit 5 [Oryza sativa] >gi_342588 (J04502) cytochrome b6-f complex subunit 5 (petE) [Zea mays] >gi_533296_dbj_BAA07216_ (D38019) cytochrome b6/f complex subunit 5 [Beta vulgaris] >gi_533302_dbj_BAA07222_ (D38020) cytochrome b6/f complex subunit 5 [Beta trigyna] >gi_533304_dbj_BAA07223_ (D38021) cytochrome b6/f complex subunit 5 [Beta webbiana] >gi_860888_emb_CAA60964_ (X87636)

cytochrome b6-f complex subunit 5 [Beta vulgaris]
>gi 860894 emb CAA60969 (X87637) petG [Beta vulgaris]
>gi 902240 emb CAA60304 (X86563) cytochrome b /f complex
subunit 5 [Zea mays] >gi 2612818 emb CAA75627 (Y15429)
cytochrome b6/f-complex subunit V [Populus deltoides]
>gi 2924268 emb CAA77420 (Z00044) cytochrome b/f complex
subunit V [Nicotiana tabacum] >gi 226628 prf 1603356BB

cytochrome b/f complex 5 [Oryza sativa]

Seq. No. 265301

Contig ID 8597 1.R1011

5'-most EST LIB3078-034-Q1-K1-G10

Seq. No. 265302 Contig ID 8604_1.R1011

Method BLASTX
NCBI GI g2673912
BLAST score 467
E value 2.0e-46
Match length 144
% identity 62

NCBI Description (AC002561) unknown protein [Arabidopsis thaliana]

Seq. No. 265303 Contig ID 8607 1.R1011

5'-most EST LIB36-012-Q1-E1-G10

Method BLASTX
NCBI GI g2494275
BLAST score 308
E value 4.0e-28
Match length 82
% identity 70

NCBI Description ELONGATION FACTOR P (EF-P) >gi_1399829 (U59235) elongation

factor P [Synechococcus PCC7942]

Seq. No. 265304



Contig ID 8610 1.R1011 5'-most EST

uC-zmflmo17312g10b1

BLASTX Method NCBI GI q3367536 BLAST score 536 2.0e-54 E value 118 Match length % identity 90

(AC004392) Contains similarity to symbiosis-related like NCBI Description

> protein F1N20.80 gi 2961343 from A. thaliana BAC gb AL022140. EST gb T04695 comes from this gene.

[Arabidopsis thaliana]

265305 Seq. No.

8610 2.R1011 Contig ID

uC-zmflmo17262f01b1 5'-most EST

Method BLASTX q4581162 NCBI GI BLAST score 540 4.0e-55 E value Match length 119 87 % identity

(AC006220) putative symbiosis-related protein [Arabidopsis NCBI Description

thaliana]

265306 Seq. No.

8610 4.R1011 Contig ID

5'-most EST uC-zmrob73036g02b1

Method BLASTX q4581162 NCBI GI 333 BLAST score 3.0e-49E value Match length 120

% identity 86

(AC006220) putative symbiosis-related protein [Arabidopsis NCBI Description

thaliana]

265307 Seq. No.

8610 5.R1011 Contig ID wty700168724.h1 5'-most EST

BLASTX Method g3367536 NCBI GI BLAST score 143 5.0e-09 E value 33 Match length 82 % identity

(ACO04392) Contains similarity to symbiosis-related like NCBI Description

protein F1N20.80 gi_2961343 from A. thaliana BAC gb_AL022140. EST gb_T04695 comes from this gene.

[Arabidopsis thaliana]

265308 Seq. No. Contig ID 8613 1.R1011

LIB3159-004-Q1-K1-G4 5'-most EST

BLASTX Method g4309700 NCBI GI BLAST score 170



```
6.0e-12
E value
Match length
                  94
                  43
% identity
                  (AC006266) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  265309
Seq. No.
                  8615 1.R1011
Contig ID
5'-most EST
                  LIB3078-034-Q1-K1-D12
                  265310
Seq. No.
                  8617 1.R1011
Contig ID
5'-most EST
                  LIB3078-034-Q1-K1-D7
                  265311
Seq. No.
                  8618 1.R1011
Contig ID
5'-most EST
                  cyk700052216.f1
Method
                  BLASTX
                  g629858
NCBI GI
BLAST score
                  667
                  6.0e-70
E value
                  129
Match length
% identity
                  100
NCBI Description protein kinase C inhibitor - maize
                  265312
Seq. No.
                  8618 3.R1011
Contig ID
                  fC-zmle700208029a1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q629858
BLAST score
                  142
E value
                  6.0e-09
Match length
                  36
% identity
                  81
NCBI Description protein kinase C inhibitor - maize
                  265313
Seq. No.
                  8620 1.R1011
Contig ID
                  cyk700051966.f1
5'-most EST
Method
                  BLASTX
                  g2943792
NCBI GI
BLAST score
                  1964
                  0.0e + 00
E value
                  479
Match length
                   71
% identity
                  (AB006809) PV72 [Cucurbita sp.]
NCBI Description
                   265314
Seq. No.
                  8624 1.R1011
Contig ID
                  uC-zmflmo17164h05b1
5'-most EST
Seq. No.
                  265315
                  8624 2.R1011
Contig ID
5'-most EST
                  uC-zmroteosinte042h01b1
```

36856

265316

8628 1.R1011

LIB3068-025-Q1-K1-E7

Seq. No.

Contig ID

5'-most EST

BLAST score

E value Match length 1324 1.0e-146

415



```
BLASTN
Method
NCBI GI
                  g902200
                   593
BLAST score
                   0.0e+00
E value
Match length
                   593
                   100
% identity
NCBI Description Z.mays complete chloroplast genome
                   265317
Seq. No.
                   8633 1.R1011
Contig ID
                  LIB84-017-Q1-E1-F11
5'-most EST
                   BLASTX
Method
                   g4371292
NCBI GI
BLAST score
                   511
                   2.0e-51
E value
                   198
Match length
                   50
% identity
                  (AC006260) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   265318
                   8634 1.R1011
Contig ID
                   LIB3279-053-P1-K1-D10
5'-most EST
                   BLASTX
Method
                   g3043612
NCBI GI
BLAST score
                   325
E value
                   1.0e-29
Match length
                   190
                   39
% identity
                  (AB011116) KIAA0544 protein [Homo sapiens]
NCBI Description
                   265319
Seq. No.
                   8634 2.R1011
Contig ID
5'-most EST
                   uC-zmroteosinte069g09b1
                   265320
Seq. No.
                   8634_3.R1011
Contig ID
5'-most EST
                   xyt700347177.hl
Method
                   BLASTX
                   q4581109
NCBI GI
BLAST score
                   262
                   3.0e-22
E value
Match length
                   152
                   39
% identity
NCBI Description
                  (AC005825) unknown protein [Arabidopsis thaliana]
Seq. No.
                   265321
Contig ID
                   8634 4.R1011
5'-most EST
                   LIB3067-018-Q1-K1-A11
                   265322
Seq. No.
Contig ID
                   8635 1.R1011
                   LIB3\overline{1}37-012-Q1-K1-D2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3421384
```



% identity (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase NCBI Description [Arabidopsis thaliana] Seq. No. 265323 8640 1.R1011 Contig ID $uC-z\overline{m}flB73009g02b1$ 5'-most EST BLASTX Method NCBI GI q4586049 1142 BLAST score 1.0e-125 E value 358 Match length 56 % identity (AC007020) hypothetical protein [Arabidopsis thaliana] NCBI Description 265324 Seq. No. 8640 2.R1011 Contig ID $uC-z\overline{m}flmo17221e11b1$ 5'-most EST 265325 Seq. No. 8640 3.R1011 Contig ID uC-zmrob73076b02b1 5'-most EST BLASTX Method q4586049 NCBI GI BLAST score 177 1.0e-12 E value 35 Match length 83 % identity NCBI Description (AC007020) hypothetical protein [Arabidopsis thaliana] 265326 Seq. No. Contig ID 8641 1.R1011 uC-zmf1B73046d09b1 5'-most EST BLASTX Method NCBI GI g2052383 1356 BLAST score 1.0e-150 E value 327 Match length % identity 74 NCBI Description (U66345) calreticulin [Arabidopsis thaliana] Seq. No. 265327 8645 1.R1011 Contig ID LIB3078-034-Q1-K1-A5 5'-most EST Seq. No. 265328 8648 1.R1011 Contig ID LIB3078-034-Q1-K1-A8 5'-most EST Method BLASTX NCBI GI g3779218 BLAST score 416 1.0e-40 E value

106 Match length 74 % identity

NCBI Description (AF030879) protein kinase CPK1 [Solanum tuberosum]

265329 Seq. No.



```
Contig ID
                  8649 1.R1011
                  uC-zmflm017205e08b1
5'-most EST
                  BLASTX
Method
                  q2995953
NCBI GI
BLAST score
                  167
                   2.0e-11
E value
                   49
Match length
% identity
                   67
                   (AF053565) glutaredoxin I [Mesembryanthemum crystallinum]
NCBI Description
                   265330
Seq. No.
                   8649 2.R1011
Contig ID
                   tfd700569261.h2
5'-most EST
                   BLASTX
Method
                   g2995953
NCBI GI
BLAST score
                   274
                   6.0e-24
E value
                   85
Match length
% identity
                   64
                   (AF053565) glutaredoxin I [Mesembryanthemum crystallinum]
NCBI Description
                   265331
Seq. No.
                   8652 1.R1011
Contig ID
5'-most EST
                   LIB3078-033-Q1-K1-H8
                   BLASTX
Method
NCBI GI
                   g3550983
BLAST score
                   527
                   7.0e-54
E value
Match length
                   135
% identity
                   73
                   (AB010690) mutM homologue-2 [Arabidopsis thaliana]
NCBI Description
                   >gi_3820622 (AF099971) putative formamidopyrimidine-DNA
                   glycosylase 2 [Arabidopsis thaliana]
                   265332
Seq. No.
                   8654 1.R1011
Contig ID
                   uC-zmroteosinte030b07b1
5'-most EST
                   BLASTX
Method
                   g2982243
NCBI GI
                   291
BLAST score
                   8.0e-26
E value
                   156
Match length
                   41
% identity
                  (AF051204) hypothetical protein [Picea mariana]
NCBI Description
                   265333
Seq. No.
                   8654 2.R1011
Contig ID
5'-most EST
                   uwc700150821.hl
                   265334
Seq. No.
                   8666 1.R1011
Contig ID
                   LIB3078-033-Q1-K1-F10
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3157943
BLAST score
                   349
```

36859

1.0e-33

164

E value Match length



% identity 46
NCBI Description (AC002131) Contains similarity to BAP31 protein gb_X81816
from Mus musculus. [Arabidopsis thaliana]

Method BLASTX
NCBI GI g2444271
BLAST score 635
E value 3.0e-66
Match length 186
% identity 66

NCBI Description (AF019637) putative amino acid or GABA permease

[Arabidopsis thaliana]

Seq. No. 265336 Contig ID 8670_1.R1011 5'-most EST wty700169301.h1

Method BLASTX
NCBI GI g2459446
BLAST score 901
E value 4.0e-97
Match length 306
% identity 58

NCBI Description (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis

thaliana]

Seq. No. 265337 Contig ID 8670_2.R1011

5'-most EST LIB3180-036-P2-M2-B5

Method BLASTX
NCBI GI g2459446
BLAST score 483
E value 2.0e-48
Match length 155
% identity 59

NCBI Description (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis

thaliana]

 Seq. No.
 265338

 Contig ID
 8670_3.R1011

5'-most EST uC-zmflb73353g09a1

 Seq. No.
 265339

 Contig ID
 8671_1.R1011

 5'-most EST
 wty700164312.h1

Seq. No. 265340 Contig ID 8671_2.R1011

5'-most EST LIB3078-033-Q1-K1-F7

Method BLASTX
NCBI GI g4589961
BLAST score 158
E value 4.0e-10
Match length 197
% identity 28



```
(AC007169) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  265341
                  8673 1.R1011
Contig ID
                  uC-zmflb73079f12b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2244797
BLAST score
                  173
                  4.0e-12
E value
Match length
                  66
                  59
% identity
NCBI Description
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  265342
Contig ID
                  8673 2.R1011
5'-most EST
                  LIB3059-009-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g2244797
BLAST score
                  196
                  5.0e-15
E value
Match length
                  65
% identity
                  57
NCBI Description
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
                  265343
Seq. No.
Contig ID
                  8684 1.R1011
5'-most EST
                  xsy700217670.h1
Method
                  BLASTX
NCBI GI
                  q2969887
                   951
BLAST score
                  1.0e-103
E value
Match length
                  298
                   60
% identity
                  (Y16766) sucrose/H+ symporter [Daucus carota]
NCBI Description
                  >gi 2969889 emb CAA76368 (Y16767) sucrose/H+ symporter
                   [Daucus carota]
Seq. No.
                   265344
                   8688 1.R1011
Contig ID
                  uC-zmflmo17202a03b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3927836
BLAST score
                  245
                   4.0e-20
E value
Match length
                  192
% identity
                   39
NCBI Description
                  (AC005727) unknown protein [Arabidopsis thaliana]
                   265345
                   8689 1.R1011
```

Seq. No. Contig ID rv1700457589.h1 5'-most EST

Seq. No. 265346 8692 1.R1011 Contiq ID uC-zmflB73042c09b1 5'-most EST Method BLASTX

NCBI GI g3915131



BLAST score 408
E value 1.0e-39
Match length 112
% identity 69

NCBI Description THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1)
>gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza sativa] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin h [Oryza sativa] >gi_1930072 (U92541) thioredoxin h [Oryza

sativa]

Seq. No. 265347

Contig ID 8692_3.R1011

5'-most EST LIB3116-026-P1-K2-D4

Seq. No. 265348

Contig ID 8692_5.R1011 5'-most EST wty700170432.h1

Method BLASTX
NCBI GI g3915131
BLAST score 316
E value 3.0e-29
Match length 74
% identity 81

NCBI Description THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1)

>gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza
sativa] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin
h [Oryza sativa] >gi_1930072 (U92541) thioredoxin h [Oryza

sativa]

Seq. No. 265349

Contig ID 8693_1.R1011

5'-most EST uC-zmflb73356c12a2 Method BLASTX

NCBI GI g2739376
BLAST score 1639
E value 0.0e+00
Match length 526
% identity 59

NCBI Description (AC002505) putative permease [Arabidopsis thaliana]

Seq. No. 265350 Contig ID 8693 4.R1011

5'-most EST LIB3180-011-P2-M1-E8

Seq. No. 265351 Contig ID 8697 1.R1011

5'-most EST LIB3078-025-Q1-K1-F11

Method BLASTX
NCBI GI g4240033
BLAST score 320
E value 3.0e-29
Match length 80
% identity 71

NCBI Description (AB018587) ZmGRla [Zea mays]

Seq. No. 265352 Contig ID 8703_1.R1011



```
5'-most EST
                   ceu700434019.h1
Seq. No.
                  265353
                  8704 1.R1011
Contig ID
                  LIB3078-033-Q1-K1-D2
5'-most EST
Seq. No.
                  265354
                  8705 1.R1011
Contig ID
                  tzu700206722.h1
5'-most EST
Method
                  BLASTX
                  q960289
NCBI GI
BLAST score
                   1984
                   0.0e+00
E value
Match length
                   559
% identity
                   69
                  (L34343) anthranilate synthase alpha subunit [Ruta
NCBI Description
                   graveolens]
                   265355
Seq. No.
                   8705 2.R1011
Contiq ID
                   LIB3088-002-Q1-K1-D6
5'-most EST
Method
                   BLASTX
NCBI GI
                   g960289
BLAST score
                   429
                   5.0e-42
E value
                   108
Match length
                   75
% identity
                  (L34343) anthranilate synthase alpha subunit [Ruta
NCBI Description
                   graveolens]
                   265356
Seq. No.
                   8707 1.R1011
Contig ID
5'-most EST
                   wty700171321.h1
                   BLASTX
Method
                   g2668750
NCBI GI
                   587
BLAST score
E value
                   1.0e-60
Match length
                   112
                   100
% identity
                  (AF034949) ribosomal protein L30 [Zea mays]
NCBI Description
                   265357
Seq. No.
Contig ID
                   8707 2.R1011
                   pwr700453378.h1
5'-most EST
Method
                   BLASTX
                   g2668750
NCBI GI
BLAST score
                   582
E value
                   4.0e-60
Match length
                   112
% identity
                  (AF034949) ribosomal protein L30 [Zea mays]
NCBI Description
                   265358
```

Seq. No. 265358 Contig ID 8708_1.R1011

5'-most EST LIB3115-024-P1-K1-G6

Seq. No. 265359

Match length

% identity

268 60

NCBI Description Zea mays HRGP gene, AC1503 line



```
8708 2.R1011
Contig ID
5'-most EST
                  LIB3062-008-Q1-K1-D10
                  265360
Seq. No.
Contig ID
                  8713 1.R1011
                  wen700336680.h1
5'-most EST
                  BLASTX
Method
                  q3212868
NCBI GI
BLAST score
                  339
                  8.0e-63
E value
                  209
Match length
                  59
% identity
                 (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                  265361
Seq. No.
                  8713 4.R1011
Contig ID
5'-most EST
                  cat700019482.rl
Seq. No.
                  265362
                  8715 1.R1011
Contig ID
                  uC-zmflmo17335h04b1
5'-most EST
Method
                  BLASTX
                  q4006882
NCBI GI
BLAST score
                  1237
                  1.0e-136
E value
                  386
Match length
                   60
% identity
                  (Z99707) UDP-glucuronyltransferase-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   265363
Contig ID
                   8715 2.R1011
5'-most EST
                  uC-zmrob73053q10a1
Method
                  BLASTX
NCBI GI
                  g4006882
BLAST score
                   168
                   1.0e-11
E value
Match length
                   44
% identity
                   68
                 (Z99707) UDP-glucuronyltransferase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   265364
Seq. No.
                  8715 3.R1011
Contig ID
                  tzu700202373.h1
5'-most EST
                   265365
Seq. No.
Contig ID
                  8720 1.R1011
                  LIB3060-025-Q1-K1-G5
5'-most EST
                  BLASTN
Method
                  g4007864
NCBI GI
                  59
BLAST score
                   2.0e-24
E value
```



265366 Seq. No. 8724 1.R1011 Contig ID uC-zmflmo17117b07b1 5'-most EST BLASTX Method g2191165 NCBI GI BLAST score 243 2.0e-20 E value 84 Match length 58 % identity (AF007270) A IG002P16.14 gene product [Arabidopsis NCBI Description thaliana] 265367 Seq. No. 8727 1.R1011 Contig ID LIB3067-019-Q1-K1-E12 5'-most EST Method BLASTN g20155 NCBI GI 45 BLAST score 4.0e-16 E value 85 Match length 89 % identity NCBI Description O.sativa random single-copy DNA fragment 12RG214R 265368 Seq. No. 8731 1.R1011 Contig ID LIB3078-032-Q1-K1-G3 5'-most EST BLASTX Method NCBI GI g4539422 BLAST score 472 1.0e-47 E value 108 Match length 78 % identity NCBI Description (AL049171) putative protein [Arabidopsis thaliana] 265369 Seq. No. 8734_1.R1011 Contig ID 5'-most EST dyk700102091.h1 - 265370 Seq. No. 8737 1.R1011 Contig ID LIB3078-032-Q1-K1-F3 5'-most EST Method BLASTX g3805845 NCBI GI 640 BLAST score 7.0e-67 E value 204 Match length % identity 62 NCBI Description (AL031986) putative protein [Arabidopsis thaliana] Seq. No. 265371

8741 1.R1011 Contig ID 5'-most EST xjt700094675.h1

Seq. No. 265372 8742 1.R1011 Contig ID

LIB3078-032-Q1-K1-G11 5'-most EST



Seq. No. 265373

Contig ID 8742_2.R1011

5'-most EST uC-zmflmo17267g12a1

Seq. No. 265374

Contig ID 8742_4.R1011 5'-most EST xjt700093705.h1

Seq. No. 265375

Contig ID 8745_1.R1011 5'-most EST fwa700099042.h1

Seq. No. 265376

Contig ID 8745_2.R1011

5'-most EST LIB3136-060-Q1-K1-C3

Seq. No. 265377

Contig ID 8745 4.R1011

5'-most EST uC-zmflb73266a02b2

Method BLASTX
NCBI GI g4309681
BLAST score 168
E value 8.0e-12
Match length 70

% identity 51

NCBI Description (AC006930) R33423_1 [Homo sapiens]

Seq. No. 265378

Contig ID 8747_1.R1011 5'-most EST dyk700104813.h1

Seq. No. 265379

Contig ID 8754_1.R1011 5'-most EST ntr700074751.h1

Method BLASTX
NCBI GI g2668744
BLAST score 804
E value 7.0e-86
Match length 148

% identity 99

NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]

Seq. No. 265380

Contig ID 8754_2.R1011

5'-most EST LIB148-023-Q1-E1-A4

Method BLASTX
NCBI GI 92668744
BLAST score 791
E value 2.0e-84
Match length 148
% identity 98

NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]

Seq. No. 265381

Contig ID 8754_3.R1011 5'-most EST wyr700239225.h1

Method BLASTX



NCBI GI g2668744
BLAST score 352
E value 4.0e-33
Match length 72
% identity 93

NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]

Seq. No. 265382

Contig ID 8754 4.R1011

5'-most EST LIB3078-032-Q1-K1-D8

Method BLASTX
NCBI GI g2668744
BLAST score 566
E value 2.0e-58
Match length 106
% identity 98

NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]

Seq. No. 265383

Contig ID 8758 1.R1011

5'-most EST LIB3059-060-Q1-K1-C7

Seq. No. 265384

Contig ID 8760 1.R1011

5'-most EST LIB3078-032-Q1-K1-E2

Seq. No. 265385 Contig ID 8767 1.R1011

5'-most EST ymt700221047.h1

Method BLASTX
NCBI GI g3776005
BLAST score 1904
E value 0.0e+00
Match length 428

% identity 87

NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No. 265386

Contig ID 8767_2.R1011

5'-most EST uC-zmflb73280d01b2

Method BLASTX
NCBI GI g3776005
BLAST score 879
E value 1.0e-94
Match length 185
% identity 93

NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No. 265387

Contig ID 8767_5.R1011 5'-most EST zuv700352895.h1

Method BLASTX
NCBI GI g3776005
BLAST score 349
E value 6.0e-33
Match length 80
% identity 88



NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No. 265388

Contig ID 8767 6.R1011

5'-most EST LIB143-056-Q1-E1-C6

Method BLASTX
NCBI GI g3776005
BLAST score 356
E value 1.0e-33
Match length 129
% identity 63

NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No. 265389

Contig ID 8767 7.R1011

5'-most EST uC-zmflmo17131f08a1

Method BLASTX
NCBI GI g3776005
BLAST score 225
E value 6.0e-25
Match length 128
% identity 85

NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No. 265390

Contig ID 8767_8.R1011 5'-most EST rv1700454141.h1

Seq. No. 265391

Contig ID 8772 1.R1011

5'-most EST uC-zmflmo17100h05b1

Seq. No. 265392

Contig ID 8773 1.R1011

5'-most EST LIB3150-092-P1-N1-B3

Method BLASTX
NCBI GI g1346033
BLAST score 1406
E value 1.0e-156
Match length 268
% identity 99

NCBI Description FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS)

(FARNESYL DIPHOSPHATE SYNTHETASE) (DIMETHYLALLYLTRANSFERASE

/ GERANYLTRANSTRANSFERASE >gi_662368 (L39789) farnesyl

pyrophosphate synthetase [Zea mays]

Seq. No. 265393

Contig ID 8773_2.R1011

5'-most EST LIB3067-004-Q1-K1-H10

Method BLASTX
NCBI GI g1346033
BLAST score 926
E value 1.0e-100
Match length 174
% identity 100

NCBI Description FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS)

(FARNESYL DIPHOSPHATE SYNTHETASE) (DIMETHYLALLYLTRANSFERASE



/ GERANYLTRANSTRANSFERASE >gi_662368 (L39789) farnesyl
pyrophosphate synthetase [Zea mays]

Seq. No. 265394 Contig ID 8773 3.R1011

5'-most EST LIB3150-050-Q1-N1-A6

Method BLASTN
NCBI GI g662367
BLAST score 204
E value 1.0e-111
Match length 238
% identity 96

NCBI Description Zea mays farnesyl pyrophosphate synthetase (fps) mRNA,

complete cds

Seq. No. 265395

Contig ID 8774_1.R1011

5'-most EST uC-zmflmo17391a01a1

Method BLASTX
NCBI GI g3763926
BLAST score 377
E value 3.0e-35
Match length 409
% identity 34

NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]

Seq. No. 265396

Contig ID 8774 2.R1011

5'-most EST LIB3088-042-Q1-K1-E6

Seq. No. 265397

Contig ID 8774 4.R1011

5'-most EST LIB3069-031-Q1-K1-A2

Seq. No. 265398
Contig ID 8777_1.R1011
5'-most EST xmt700265457.h1

Method BLASTX NCBI GI g2529668

BLAST score 710 E value 8.0e-75 Match length 242 % identity 56

NCBI Description (AC002535) putative photolyase/blue-light receptor

[Arabidopsis thaliana] >gi_3319288 (AF053366)

photolyase/blue light photoreceptor PHR2 [Arabidopsis

thaliana]

Seq. No. 265399

Contig ID 8785 1.R1011

5'-most EST uC-zmflb73294e08b1

Method BLASTX
NCBI GI g3878494
BLAST score 548
E value 1.0e-59
Match length 321
% identity 43



NCBI Description (Z79602) predicted using Genefinder; Similarity to Yeast hypothetical protein YAE2 (SW:YAE2_YEAST); cDNA EST EMBL:T01631 comes from this gene; cDNA EST EMBL:M88949 comes from this gene [Caenorhabditis elegans]

Seq. No. 265400

Contig ID 8791 1.R1011

5'-most EST LIB3078-032-Q1-K1-A2

Seq. No. 265401

Contig ID 8796 1.R1011

5'-most EST LIB3136-014-Q1-K2-A4

Method BLASTX
NCBI GI g1711355
BLAST score 456
E value 2.0e-45
Match length 159
% identity 58

NCBI Description SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE

>gi_421786_pir__S34678 short-chain alcohol dehydrogenase Norway spruce >qi 395223 emb CAA52213 (X74115) short-chain

alcohol dehydrogenase [Picea abies]

Seq. No. 265402

Contig ID 8799_1.R1011

5'-most EST uC-zmrob73004f02b1

Seq. No. 265403

Contig ID 8802 1.R1011

5'-most EST uC-zmflb73012a06b1

Method BLASTX
NCBI GI g3212861
BLAST score 552
E value 2.0e-56
Match length 174
% identity 64

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 265404

Contig ID 8803_1.R1011 5'-most EST fwa700099573.h1

Method BLASTX
NCBI GI g2495171
BLAST score 1395
E value 1.0e-155
Match length 372
% identity 92

NCBI Description DELTA-AMINOLEVULINIC ACID DEHYDRATASE PRECURSOR

(PORPHOBILINOGEN SYNTHASE) (ALADH)

>gi 1041423 emb CAA63139 (X92402) aminolevulinate

dehydratase [Hordeum vulgare]

Seq. No. 265405

Contig ID 8805_1.R1011

5'-most EST LIB3078-031-Q1-K1-G4

Method BLASTX NCBI GI g2315153



```
BLAST score
                  916
                  3.0e-99
E value
                  234
Match length
% identity
                  72
                  (Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
NCBI Description
                  265406
Seq. No.
                  8807 1.R1011
Contig ID
                  LIB3078-031-Q1-K1-D12
5'-most EST
                  BLASTX
Method
                  g1653954
NCBI GI
                  201
BLAST score
                  1.0e-15
E value
                  105
Match length
                  41
% identity
                  (D90917) hypothetical protein [Synechocystis sp.]
NCBI Description
                  265407
Seq. No.
                   8812 1.R1011
Contig ID
                   pmx700088982.h1
5'-most EST
                   BLASTX
Method
                   g4335773
NCBI GI
                   257
BLAST score
                   1.0e-21
E value
                   77
Match length
                   70
% identity
                  (AC006284) unknown protein [Arabidopsis thaliana]
NCBI Description
                   265408
Seq. No.
                   8812 3.R1011
Contig ID
                   LIB143-052-Q1-E1-B7
5'-most EST
                   BLASTX
Method
                   g1732509
NCBI GI
                   254
BLAST score
                   1.0e-21
E value
                   68
Match length
                   69
% identity
                   (U62741) putative cytoskeletal protein [Arabidopsis
NCBI Description
                   thaliana]
                   265409
Seq. No.
                   8814 1.R1011
Contig ID
                   uC-zmflmo17306a09b1
5'-most EST
Method
                   BLASTX
                   q1705651
NCBI GI
BLAST score
                   451
E value
                   1.0e-44
Match length
                   137
% identity
                   63
                   20 KD NUCLEAR CAP BINDING PROTEIN (NCBP 20 KD SUBUNIT)
NCBI Description
                   (CBP20) >gi_984139_emb_CAA58962_ (X84157) subunit of the
                   dimeric cap binding complex CBC [Homo sapiens]
                   >qi 1582342 prf 2118330A cap-binding protein [Homo
                   sapiens]
```

36871

265410

8814 2.R1011

Seq. No. Contig ID



5'-most EST LIB3059-001-Q1-K2-A5

Method BLASTX
NCBI GI g1705651
BLAST score 170
E value 1.0e-11
Match length 46
% identity 70

NCBI Description 20 KD NUCLEAR CAP BINDING PROTEIN (NCBP 20 KD SUBUNIT)

(CBP20) >gi_984139_emb_CAA58962_(X84157) subunit of the

dimeric cap binding complex CBC [Homo sapiens] >gi_1582342_prf__2118330A cap-binding protein [Homo

sapiens]

Seq. No. 265411 Contig ID 8815 1.R1011

5'-most EST nbm700476017.h1

Method BLASTX
NCBI GI g4204314
BLAST score 224
E value 1.0e-17
Match length 197
% identity 29

NCBI Description (AC003027) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 265412 Contig ID 8816 1.R1011

5'-most EST LIB3136-014-Q1-K2-G1

Method BLASTX
NCBI GI g1361983
BLAST score 2198
E value 0.0e+00
Match length 634
% identity 65

NCBI Description ARP protein - Arabidopsis thaliana >gi 886434 emb CAA89858

(Z49776) ARP protein [Arabidopsis thalīana]

Seq. No. 265414

Contig ID 8826_1.R1011

5'-most EST LIB3078-017-Q1-K1-B2

Method BLASTX
NCBI GI g2795806
BLAST score 880
E value 9.0e-95
Match length 221
% identity 76

NCBI Description (AC003674) unknown protein [Arabidopsis thaliana]

Seq. No. 265415

Contig ID 8829_1.R1011 5'-most EST rvt700551662.h1

Method BLASTX NCBI GI g4587550 BLAST score 250

```
E value
                     1.0e-29
Match length
                     178
 % identity
                     41
 NCBI Description
                     (AC006577) EST gb R64848 comes from this gene. [Arabidopsis
                     thaliana]
 Seq. No.
                     265416
 Contig ID
                     8832 1.R1011
 5'-most EST
                    LIB3078-031-Q1-K1-C5
                     265417
 Seq. No.
 Contig ID
                    8833 1.R1011
 5'-most EST
                    LIB3137-027-Q1-K1-A10
 Method
                    BLASTX
 NCBI GI
                     g3550483
 BLAST score
                     859
 E value
                     3.0e-92
 Match length
                     203
                    83
 % identity
 NCBI Description
                     (AJ224324) cp31BHv [Hordeum vulgare]
 Seq. No.
                     265418
 Contig ID
                     8833 2.R1011
 5'-most EST
                     fwa700099747.h1
                    BLASTX
 Method
 NCBI GI
                    q100903
 BLAST score
                     340
 E value
                     5.0e - 32
 Match length
                    98
                    50
 % identity
 NCBI Description
                    nucleic acid-binding protein - maize >gi 168526 (M74566)
                    nucleic acid-binding protein [Zea mays]
                     265419
 Seq. No.
 Contig ID
                    8843 1.R1011
 5'-most EST
                    LIB3062-057-Q1-K1-B12
 Method
                    BLASTX
 NCBI GI
                    g3023189
 BLAST score
                     727
 E value
                     6.0e-77
 Match length
                    183
 % identity
                     76
                    14-3-3-LIKE PROTEIN C (14-3-3-LIKE PROTEIN B)
 NCBI Description
                    >gi_1848208_emb_CAA72094_ (Y11211) 14-3-3-like protein B
[Nicotiana tabacum] >gi_2689475 (U91724) 14-3-3 isoform c
                     Nicotiana tabacum]
                    265420
 Seq. No.
 Contig ID
                    8843~2.R1011
 5'-most EST
                    uer700578004.h1
 Method
                    BLASTX
 NCBI GI
                    g1168189
 BLAST score
                    322
 E value
                    5.0e-30
 Match length
                    76
 % identity
 NCBI Description
                   14-3-3-LIKE PROTEIN A (VFA-1433A) >qi 1076542 pir S52899
```

```
14-3-3 brain protein homolog - fava bean
>gi_695765_emb_CAA88415 (Z48504) 14-3-3 brain protein
homolog [Vicia faba]
```

Contig ID 8846 1.R1011 -LIB3068-042-Q1-K1-C9 5'-most EST BLASTX Method NCBI GI g556851 BLAST score 174 E value 5.0e-12Match length 101 % identity 33

Seq. No.

265421

NCBI Description (X81994) S2 cDNA [Phalaris coerulescens]

Seq. No. 265422

Contig ID 8847 1.R1011

5'-most EST LIB36-019-Q1-E1-C11

Method BLASTX NCBI GI q3122724 BLAST score 323 E value 1.0e-29 Match length 69 % identity 88

NCBI Description 60S RIBOSOMAL PROTEIN L38 >gi_2289009 (AC002335) ribosomal

protein L38 isolog [Arabidopsis thaliana]

265423 Seq. No. Contig ID 8847 2.R1011 5'-most EST uwc700155974.h1

Method BLASTX NCBI GI g3122724 BLAST score 306 E value 9.0e-28 Match length 69 % identity 87

NCBI Description 60S RIBOSOMAL PROTEIN L38 >gi_2289009 (AC002335) ribosomal

protein L38 isolog [Arabidopsis thaliana]

Seq. No. 265424

Contig ID 8847 3.R1011

5'-most EST LIB3088-029-Q1-K1-E8

Seq. No. 265425

Contig ID 8847 4.R1011 5'-most EST clt700045290.f1

`Seq. No. 265426

Contig ID 8848 1.R1011

5'-most EST LIB3078-031-Q1-K1-B3

Method BLASTX NCBI GI g2244865 BLAST score 161 E value 6.0e-11Match length 84 % identity 42

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

265427 Seq. No. 8850 1.R1011 Contig ID 5'-most EST LIB83-007-Q1-E1-E9

265428 Seq. No.

8850 2.R1011 Contig ID

5'-most EST LIB3078-031-Q1-K1-B5

265429 Seq. No. 8850 3.R1011 Contig ID 5'-most EST uC-zmflb73096c01b1

265430 Seq. No.

Contig ID 8854 1.R1011

5'-most EST uC-zmflb73070g01b1

Method BLASTX NCBI GI g2462748 BLAST score 1746 E value 0.0e+00Match length 364 90 % identity

NCBI Description (AC002292) putative Clathrin Coat Assembly protein

[Arabidopsis thaliana]

265431 Seq. No.

8854_2.R1011 Contig ID

5'-most EST LIB3066-024-Q1-K1-A3

Method BLASTX NCBI GI g2462748 BLAST score 375 E value 6.0e-36 Match length 91 78 % identity

NCBI Description (AC002292) putative Clathrin Coat Assembly protein

[Arabidopsis thaliana]

Seq. No. 265432

Contig ID 8854_3.R1011

57 -most EST uC-zmflmo17179f12b1

Method BLASTX NCBI GI g2462748 BLAST score 428 E value 4.0e-57 Match length 134 % identity 84

NCBI Description (AC002292) putative Clathrin Coat Assembly protein

[Arabidopsis thaliana]

Seq. No. 265433

8854 4.R1011 Contig ID 5'-most EST ymt700219502.h1

Method BLASTX NCBI GI g2462748 BLAST score 443 E value 6.0e-44Match length 101



% identity 82
NCBI Description (AC002292) putative Clathrin Coat Assembly protein
[Arabidopsis thaliana]

 Seq. No.
 265434

 Contig ID
 8855_1.R1011

 5'-most EST
 nbm700469076.h1

 Method
 BLASTX

Method BLASTX
NCBI GI g1723436
BLAST score 1279
E value 1.0e-141
Match length 483
% identity 54

NCBI Description HYPOTHETICAL 119.9 KD PROTEIN C56F8.03 IN CHROMOSOME I

>gi_1204225_emb_CAA93574_ (Z69728) unknown

[Schizosaccharomyces pombe]

 Seq. No.
 265435

 Contig ID
 8858_1.R1011

 5'-most EST
 zuv700352934.h1

 Method
 BLASTX

NCBI GI g3256746
BLAST score 222
E value 6.0e-18
Match length 104
% identity 46

NCBI Description (AP000002) 109aa long hypothetical protein [Pyrococcus

horikoshii]

Seq. No. 265436

Contig ID 8859_1.R1011 5'-most EST ntr700072305.h2

Method BLASTX
NCBI GI g3037045
BLAST score 163
E value 1.0e-10
Match length 194
% identity 27

NCBI Description '(AF052621) hypothetical protein COX4AL [Mus musculus]

Seq. No. 265438 Contig ID 8865_1.R1011

5'-most EST LIB3066-042-Q1-K1-C6

Seq. No. 265439 Contig ID 8865_2.R1011

5'-most EST LIB3068-020-Q1-K1-A3

Seq. No. 265440
Contig ID 8865_3.R1011
5'-most EST xsy700209475.h1

Seq. No. 265441



```
Contig ID
                  8868 1.R1011
                  fwa700101356.hl
5'-most EST
Method
                  BLASTX
                  q2780767
NCBI GI
BLAST score
                  178
                  7.0e-13
E value
Match length
                  63
% identity
                   49
                   (AB010203) ORF9; putative [Leptospira interrogans]
NCBI Description
                  265442
Seq. No.
Contig ID
                  8869 1.R1011
                   gct701178785.h2
5'-most EST
                  BLASTN
Method
NCBI GI
                   g902585
BLAST score
                   41
                   1.0e-13
E value
Match length
                   65
% identity
                   91
NCBI Description Zea mays clone MubG9 ubiquitin gene, complete cds
                   265443
Seq. No.
Contiq ID
                   8871 1.R1011
                   pmx700091974.h1
5'-most EST
Method
                   BLASTX
                   g2654358
NCBI GI
BLAST score
                   575
                   6.0e-59
E value
Match length
                   184
% identity
                   58
                  (Y15522) MNUDC protein [Mus musculus]
NCBI Description
                   >gi_2808636_emb_CAA57201_ (X81443) Sig 92 [Mus musculus]
                   265444
Seq. No.
                   8871 2.R1011
Contig ID
                   uC-zmflb73164b09a1
5'-most EST
                   265445
Seq. No.
                   8871 3.R1011
Contig ID
                   LIB3153-007-Q1-K1-F2
5'-most EST
                   BLASTX
Method
                   g3128168
NCBI GI
                   797
BLAST score
                   3.0e-85
E value
                   187
Match length
                   72
% identity
                  (AC004521) putative carboxyl-terminal peptidase
NCBI Description
                   [Arabidopsis thaliana]
                   265446
Seq. No.
                   8877 1.R1011
Contig ID
                   LIB3078-037-Q1-K1-C7
 5'-most EST
```

8877 2.R1011

uer700579638.h1

Seq. No.

Contig ID

5'-most EST



```
265448
Seq. No.
Contig ID
                   8878 1.R1011
5'-most EST
                   fwa700099949.h1
Method
                   BLASTX
                   g4454459
NCBI GI
BLAST score
                   868
E value
                   3.0e-93
Match length
                   228
                   75
% identity
NCBI Description
                  (AC006234) unknown protein [Arabidopsis thaliana]
                   265449
Seq. No.
Contig ID
                   8878 3.R1011
5'-most EST
                   uer700577417.h1
Seq. No.
                   265450
Contig ID
                   8878 5.R1011
5'-most EST
                   pmx700091462.h1
Method
                  BLASTX
NCBI GI
                   g2665536
BLAST score
                   866
E value
                   3.0e-93
Match length
                   185
                   92
% identity
NCBI Description
                  (AF027808) HCF106 precursor protein [Zea mays]
Seq. No.
                   265451
Contig ID
                   8878 7.R1011
5'-most EST
                   pwr700449848.h2
Method
                   BLASTN
NCBI GI
                   g2665535
BLAST score
                   126
E value
                   2.0e-64
Match length
                   251
                   93
% identity
NCBI Description
                  Zea mays HCF106 precursor protein (Hcf106) mRNA, nuclear
                   gene encoding chloroplast protein, complete cds
Seq. No.
                   265452
Contig ID
                   8879 1.R1011
5'-most EST
                   LIB3060-001-Q1-K2-D11
Seq. No.
                   265453
Contig ID
                   8881 1.R1011
5'-most EST
                  LIB3078-030-Q1-K1-E10
Method
                   BLASTX
NCBI GI
                   g2342683
BLAST score
                   1181
E value
                   1.0e-130
Match length
                   318
% identity
                   67
NCBI Description
                   (AC000106) Contains similarity to Bos beta-mannosidase
                   (gb U46067). [Arabidopsis thaliana]
```

(m) 15 % . . .

Seq. No. 265454
Contig ID 8887_1.R1011
5'-most EST LIB3067-056-Q1-K1-G3



```
Method
                  BLASTX
                  g4567260
NCBĮ GI
BLAST score
                  1325
                  1.0e-147
E value
Match length
                  307
                  80
% identity
NCBI Description
```

(AC006841) putative NADPH dependent mannose 6-phosphate

reductase [Arabidopsis thaliana]

>gi 4582440 gb AAD24825.1 AC007142 3 (AC007142) putative NADPH-dependent mannose-6-phosphate reductase [Arabidopsis

thaliana]

Seq. No. 265455

Contig ID 8888 1.R1011

5'-most EST LIB3060-021-Q1-K1-D12

BLASTX Method g3130064 NCBI GI BLAST score 785 E value 5.0e-84 Match length 156 % identity 99

NCBI Description (AJ006055) glutathione reductase [Zea mays]

Seq. No. 265456 Contig ID 8888 2.R1011

5'-most EST LIB3158-010-Q1-K1-C11

BLASTX Method NCBI GI q3130064 BLAST score 1112 E value 1.0e-122 Match length 266

97 % identity

(AJ006055) glutathione reductase [Zea mays] NCBI Description

Seq. No. 265457

Contig ID 8892 1.R1011

5'-most EST LIB3078-030-Q1-K1-C2

Seq. No. 265458 Contig ID 8901 1.R1011 5'-most EST fwa700099619.h1

Method BLASTX NCBI GI g3915845 BLAST score 290 E value 1.0e-25 Match length 125 % identity 49

NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S9

>gi 3603065 gb AAC35726 (AF041468) ribosomal protein S9

[Guillardia theta]

265459 Seq. No.

8913 1.R1011 Contig ID 5'-most EST pmx700085386.hl

Method BLASTX NCBI GI g3258570 BLAST score 527



sativa]

% identity

```
E value
                    1.0e-53
  Match length
                    157
                    65
  % identity
  NCBI Description
                   (U89959) Unknown protein [Arabidopsis thaliana]
                    265460
  Seq. No.
                    8915 1.R1011
  Contig ID
  5'-most EST
                    uC-zmflmo17066g11b1
  Seq. No.
                    265461
  Contig ID
                    8916 1.R1011
  5'-most EST
                    uC-zmflMo17005a05b1
                    265462
  Seq. No.
  Contig ID
                    8916 2.R1011
5'-most EST
                    LIB3059-011-Q1-K1-D11
                    BLASTX
  Method
                    g4455361
  NCBI GI
                    199
  BLAST score
                    3.0e-15
  E value
  Match length
                    54
                    72
  % identity
  NCBI Description (AL035524) putative protein [Arabidopsis thaliana]
                    265463
  Seq. No.
                    8918_1.R1011
  Contig ID
  5'-most EST
                    nwy700447225.h1
                    BLASTX
  Method
  NCBI GI
                    q4544454
  BLAST score
                     602
  E value
                     3.0e-62
                    141
  Match length
                    82
  % identity
  NCBI Description (AC006592) putative DNAJ protein [Arabidopsis thaliana]
  Seq. No.
                    265464
  Contig ID
                    8919 1.R1011
  5'-most EST
                    pmx700085110.h1
  Method
                    BLASTX
  NCBI GI
                    q4204266
  BLAST score
                     427
  E value
                     6.0e-42
  Match length
                    132
  % identity
                     66
  NCBI Description (AC005223) 52263 [Arabidopsis thaliana]
  Seq. No.
                     265465
  Contig ID
                     8920 1.R1011
  5'-most EST
                     LIB189-013-Q1-E1-A10
  Method
                     BLASTX
  NCBI GI
                     q2081612
  BLAST score
                     1211
  E value
                     1.0e-133
                    330
  Match length
```

36880

NCBI Description (D49714) deltal-pyrroline-5-carboxylate synthetase [Oryza

The state of the s



```
265466
Seq. No.
                  8920 2.R1011
Contig ID
5'-most EST
                  fC-zmfl700612075r1
Seq. No.
                  265467
                  8921 1.R1011
Contig ID
                  LIB3078-029-Q1-K1-H11
5'-most EST
Method
                  BLASTX
NCBI GI
                  g114089
BLAST score
                  367
E value
                  5.0e-35
Match length
                  116
                  65
% identity
                  RAS-RELATED PROTEIN ARA-4 >gi 81633 pir JS0641 GTP-binding
NCBI Description
                  protein ara-4 - Arabidopsis thaliana
                  >gi_217839_dbj_BAA00831_ (D01026) small GTP-binding protein
                  [Arabidopsis thaliana] >gi 3763922 (AC004450) GTP-binding
                  protein [Arabidopsis thaliana]
                  265468
Seq. No.
Contig ID
                  8927 1.R1011
                  ypc700804077.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2827709
BLAST score
                  1255
E value
                  1.0e-138
                  304
Match length
                  78
% identity
NCBI Description
                  (AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.
                  265469
Contig ID
                  8928 1.R1011
                  uC-zmflmo17072a08b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2982445
BLAST score
                   389
                   3.0e-37
E value
Match length
                  122
% identity
                   66
NCBI Description
                  (AL022224) putative protein [Arabidopsis thaliana]
Seq. No.
                   265470
                   8929 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17099a10b1
Method
                  BLASTX
NCBI GI
                   g119355
BLAST score
                   2284
E value
                   0.0e + 00
Match length
                   446
% identity
                   100
NCBI Description
                  ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                   >gi_100869_pir__S16257 phosphopyruvate hydratase (EC
```

36881

[Zea mays]

4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase

NCBI GI

g119355

```
Seq. No.
                   265471
Contig ID
                   8929 2.R1011
5'-most EST
                   LIB3279-012-P1-K1-E8
                   BLASTX
Method
                   g2191135
NCBI GI
BLAST score
                   744
E value
                   1.0e-78
Match length
                   389
% identity
                   39
NCBI Description
                   (AF007269) A IG002N01.14 gene product [Arabidopsis
                   thaliana]
Seq. No.
                   265472
Contig ID
                   8929 3.R1011
5'-most EST
                   pmx700091546.hl
                   BLASTX
Method
NCBI GI
                   g113169
BLAST score
                   503
E value
                   9.0e-51
Match length
                   127
% identity
                   81
NCBI Description ACYL CARRIER PROTEIN II PRECURSOR (ACP II) >gi_166969
                   (M63799) acyl carrier protein II [Hordeum vulgare]
                   >gi_228694_prf__1808324A acyl carrier protein II [Hordeum
                   vulgare]
Seq. No.
                   265473
Contig ID
                   8929 4.R1011
5'-most EST
                   LIB3079-019-Q1-K1-G1
Method
                   BLASTX
NCBI GI
                   q119355
BLAST score
                   242
E value
                   3.0e-20
Match length
                   51
% identity
                   94
NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                   >gi_100869_pir__S16257 phosphopyruvate hydratase (EC
                   4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
                   [Zea mays]
Seq. No.
                   265474
Contig ID
                   8929 5.R1011
5'-most EST
                  LIB189-025-Q1-E1-C12
Method
                  BLASTN
NCBI GI
                  g22272
BLAST score
                  228
E value
                  1.0e-125
Match length
                  315
                  93
% identity
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
Seq. No.
                  265475
Contig ID
                  8929 6.R1011
5'-most EST
                  uC-zmroteosinte019a10b1
Method
                  BLASTX
```



```
BLAST score
                  266
E value
                  8.0e-23
Match length
                  58
% identity
                  93
                  ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                  >gi 100869 pir S16257 phosphopyruvate hydratase (EC
                  4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
                   [Zea mays]
Seq. No.
                  265476
Contig ID
                  8929 8.R1011
                  LIB3117-003-Q1-K1-A6
5'-most EST
Method
                  BLASTX
NCBI GI
                  a119355
BLAST score
                  217
E value
                  2.0e-17
Match length
                  42
                  100
% identity
NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                  >gi_100869_pir__S16257 phosphopyruvate hydratase (EC
                   4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
                   [Zea mays]
Seq. No.
                  265477
                  8929 10.R1011
Contig ID
5'-most EST
                  LIB3180-002-P1-M1-F8
Method
                  BLASTN
NCBI GI
                  q22272
BLAST score
                  95
E value
                  8.0e-46
Match length
                  187
% identity
                  99
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
Seq. No.
                  265478
                  8929 23.R1011
Contig ID
5'-most EST
                  LIB3088-005-Q1-K1-F9
Seq. No.
                  265479
                  8931 1.R1011
Contig ID
5'-most EST
                  LIB3150-048-Q1-N1-C12
Method
                  BLASTX
NCBI GI
                  q485518
BLAST score
                  659
E value
                  6.0e-69
Match length
                  129
                  99
% identity
NCBI Description
                  ubiquitin / ribosomal protein CEP52 - rice
                  >gi 303857 dbj BAA02154 (D12629) ubiquitin/ribosomal
```

polyprotein [Oryza sativa]

265480 Seq. No.

Contig ID 8931 2.R1011

5'-most EST uC-zmflmo17140e03a1

Method BLASTX

36883



g485518 NCBI GI 196 BLAST score 6.0e-15 E value 36 Match length 97 % identity ubiquitin / ribosomal protein CEP52 - rice NCBI Description >gi 303857 dbj BAA02154 (D12629) ubiquitin/ribosomal polyprotein [Oryza sativa] 265481 Seq. No. 8931 3.R1011 Contig ID 5'-most EST gwl700618372.h1 Method BLASTX NCBI GI q485518 BLAST score 659 E value 7.0e-69 129 Match length 99 % identity ubiquitin / ribosomal protein CEP52 - rice NCBI Description >gi 303857 dbj BAA02154 (D12629) ubiquitin/ribosomal polyprotein [Oryza sativa] 265482 Seq. No. 8931 4.R1011 Contig ID 5'-most EST uC-zmroteosinte057a07b1 Method BLASTX g485518 NCBI GI BLAST score 641 E value 5.0e-67 129 Match length % identity 97 ubiquitin / ribosomal protein CEP52 - rice NCBI Description >gi_303857_dbj_BAA02154_ (D12629) ubiquitin/ribosomal polyprotein [Oryza sativa] Seq. No. 265483 Contig ID 8931 5.R1011 5'-most EST LIB84-029-Q1-E1-A2 Method BLASTX NCBI GI q485518 BLAST score 487 E value 3.0e-49Match length 94 % identity 98 ubiquitin / ribosomal protein CEP52 - rice NCBI Description >gi 303857 dbj BAA02154 (D12629) ubiquitin/ribosomal polyprotein [Oryza sativa]

Seq. No. 265484 Contig ID 8938 1.R1011

5'-most EST LIB3078-029-Q1-K1-E7

Method BLASTX
NCBI GI g2493738
BLAST score 208
E value 2.0e-16
Match length 74
% identity 53



NCBI Description ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT (ENDOPEPTIDASE CLP) >gi 1377852 (U55059) ClpP [Yersinia enterocolitica] 265485 Seq. No. 8940 1.R1011 Contig ID LIB84-004-Q1-E1-D12 5'-most EST ${\tt BLASTX}$ Method g2773154 NCBI GI 167 BLAST score 2.0e-11 E value 64 Match length 50 % identity (AF039573) abscisic acid- and stress-inducible protein NCBI Description [Oryza sativa] 265486 Seq. No. 8940 2.R1011 Contig ID LIB3115-021-P1-K1-A6 5'-most EST BLASTX Method NCBI GI g2773154 BLAST score 202 1.0e-15 E value 72 Match length 51 % identity (AF039573) abscisic acid- and stress-inducible protein NCBI Description [Oryza sativa] 265487 Seq. No. 8945 1.R1011 Contig ID 5'-most EST LIB3078-029-Q1-K1-F9 265488 Seq. No. 8946_1.R1011 Contig ID pmx700087784.h1 5'-most EST Method BLASTX NCBI GI g3582333 BLAST score 466 2.0e-46 E value Match length 110 79 % identity NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana] 265489 Seq. No. Contig ID 8948 1.R1011 5'-most EST uC-zmflb73260e01b2 Method BLASTX

NCBI GI q4502395 BLAST score 506

E value 1.0e-50 Match length 364 35 % identity

UNKNOWN >qi 3342519 (AF077301) Bcl-2-interacting protein NCBI Description

beclin [Homo sapiens]

265490 Seq. No. 8949 1.R1011 Contig ID



```
5'-most EST
                   LIB36-012-Q1-E1-H3
Method
                   BLASTX
                   g3355471
NCBI GI
BLAST score
                   694
                   9.0e-73
E value
Match length
                   291
                   45
% identity
                   (AC004218) putative lysophospholipase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   265491
                   8951 1.R1011
Contig ID
                   gct701180107.h1
5'-most EST
                   BLASTX
Method
                   g4539404
NCBI GI
BLAST score
                   268
                   3.0e-23
E value
                   67
Match length
% identity
                   70
                  (AL049524) putative protein [Arabidopsis thaliana]
NCBI Description
                   265492
Seq. No.
                   8956 1.R1011
Contig ID
                   uC-zmroB73017g03b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g626041
BLAST score
                   574
                   4.0e-59
E value
Match length
                   119
                   92
% identity
NCBI Description translation initiation factor eIF-1A - wheat (fragment)
                   265493
Seq. No.
                   8956 2.R1011
Contig ID
                   LIB3150-059-Q1-N1-A9
5'-most EST
                   BLASTX
Method
                   g1352427
NCBI GI
BLAST score
                   383
                   1.0e-54
E value
Match length
                   125
                   92
% identity
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)
NCBI Description
                   (EIF-4C)
                   265494
Seq. No.
                   8956_3.R1011
Contig ID
                   xsy7\overline{0}0209114.h1
                                                                           ج"ز
5'-most EST
                   BLASTX
Method
                   g1352427
NCBI GI
BLAST score
                   529
                   1.0e-53
E value
                   119
Match length
                   85
% identity
NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)
```

Seq. No.

(EIF-4C)

265495



```
8960 1.R1011
Contig ID
                  LIB3159-008-Q1-K1-D1
5'-most EST
                  265496
Seq. No.
                  8962 2.R1011
Contig ID
                  cyk700048239.f1
5'-most EST
                  265497
Seq. No.
                  8964 1.R1011
Contig ID
                  LIB3067-033-Q1-K1-F8
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1916290
                   271
BLAST score
                   4.0e-23
E value
                  125
Match length
% identity
                   47
                  (U89876) ALY [Mus musculus]
NCBI Description
                   265498
Seq. No.
                   8964 3.R1011
Contig ID
                   LIB3079-005-Q1-K1-B8
5'-most EST
                   265499
Seq. No.
                   8970 1.R1011
Contig ID
                   xmt7\overline{0}0257732.h1
5'-most EST
                   BLASTX
Method
                   g125065
NCBI GI
BLAST score
                   657
                   1.0e-68
E value
                   297
Match length
                   53
% identity
                   60 KD JASMONATE-INDUCED PROTEIN >gi 419795_pir__S25092
NCBI Description
                   jasmonate-induced protein - barley >gi_19011_emb_CAA47017_
                   (X66376) jasmonate-induced protein [Hordeum vulgare]
                   265500
Seq. No.
Contig ID
                   8974 1.R1011
                   tzu700201886,h1
5'-most EST
                   BLASTX
Method
                   q3033400
NCBI GI
                   705
BLAST score
E value
                   2.0e-74
                   155
Match length
% identity
                   (AC004238) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   265501
Contig ID
                   8976 2.R1011
                   pmx700083821.h1
5'-most EST
                   265502
```

Method BLASTX NCBI GI g2351374 BLAST score 1454



```
1.0e-162
E value
Match length
                  308
                  91
% identity
                  (U54560) putative 26S proteasome subunit athMOV34
NCBI Description
                  [Arabidopsis thaliana]
                  265503
Seq. No.
                  8981 4.R1011
Contig ID
                  LIB3088-030-Q1-K1-B7
5'-most EST
                  265504
Seq. No.
Contig ID
                  8986 1.R1011
                  LIB83-016-Q1-E1-C4
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2911078
BLAST score
                  911
                  2.0e-98
E value
Match length
                  276
% identity
                  64
                  (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                  265505
Seq. No.
                  8986 3.R1011
Contig ID
                  fwa700098949.h1
5'-most EST
                  BLASTX
Method
                  g2911078
NCBI GI
BLAST score
                  208
E value
                  9.0e-20
                  70
Match length
                  71
% identity
                  (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                  265506
Seq. No.
                  8992 1.R1011
Contig ID
                  vux700156661.h1
5'-most EST
                  265507
Seq. No.
Contig ID
                  8995 1.R1011
                  uC-zmflB73106f11b1
5'-most EST
                  BLASTX
Method
                  g4176420
NCBI GI
BLAST score
                   555
E value
                   5.0e-71
                   251
Match length
                   54
% identity
NCBI Description (AB008097) cytochrome P450 [Arabidopsis thaliana]
                   265508
Seq. No.
                   8997 1.R1011
Contig ID
                  LIB3159-010-Q1-K1-A12
5'-most EST
Method
                  BLASTX
NCBI GI
                   q3702327
```

BLAST score 278 2.0e-24 E value Match length 125

55

% identity

(AC005397) unknown protein [Arabidopsis thaliana] NCBI Description



```
Seq. No.
                  265509
                  8999 1.R1011
Contig ID
5'-most EST
                  ntr700071985.h1
Method
                  BLASTX
NCBI GI
                  q710626
                  175
BLAST score
                  3.0e-12
E value
                  44
Match length
                  68
% identity
NCBI Description
                  (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941
                   (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                  thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis
                  thaliana]
                  265510
Seq. No.
Contig ID
                  8999 2.R1011
5'-most EST
                  uC-zmflmo17035d09b1
                  BLASTX
Method
                  g710626
NCBI GI
BLAST score
                  167
E value
                  4.0e-11
                  37
Match length
                  70
% identity
                   (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941
NCBI Description
                   (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                  thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis
                  thaliana]
                  265511
Seq. No.
                  8999 3.R1011
Contig ID
5'-most EST
                  qmh700030177.f1
Method
                  BLASTX
                  g710626
NCBI GI
BLAST score
                  189
E value
                   9.0e-14
Match length
                  72
% identity
                   58
                   (D30719) ERD15 protein [Arabidopsis thaliana] >gi 3241941
NCBI Description
                   (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                   thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis
```

Seq. No. 265512 Contig ID 8999 4.R1011

5'-most EST dyk700106253.h1

Method BLASTX

NCBI GI g710626

BLAST score 175

E value 4.0e-12

Match length 51

% identity 59

NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941

(AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis thaliana]

thaliana]



```
      Seq. No.
      265513

      Contig ID
      8999_5.R1011

      5'-most EST
      uC-zmflb73016c02b1
```

 Seq. No.
 265514

 Contig ID
 8999_6.R1011

 5'-most EST
 LIB3136-025-Q1-K1-H5

 Method
 BLASTX

Method BLASTX
NCBI GI g710626
BLAST score 177
E value 2.0e-12
Match length 39
% identity 72

NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941 (AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis

thaliana]

Seq. No. 265515 Contig ID 8999_8.R1011

5'-most EST uC-zmflmo17138b05b1

Method BLASTX
NCBI GI g710626
BLAST score 177
E value 3.0e-12
Match length 39
% identity 72

NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941

(AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis

thaliana]

Seq. No. 265516

Contig ID 8999_10.R1011 5'-most EST wty700166650.h1

Method BLASTX
NCBI GI g710626
BLAST score 186
E value 1.0e-13
Match length 64
% identity 58

NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941

(AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis

thaliana]

Seq. No. 265517

Contig ID 9001_1.R1011

5'-most EST uC-zmflb73092d08b2

Method BLASTX
NCBI GI g113497
BLAST score 1406
E value 1.0e-156
Match length 360
% identity 69

NCBI Description ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE)

(ALPHA-D-GALACTOSIDE GALACTOHYDROLASE)



>gi 99880 pir S07472 alpha-galactosidase (EC 3.2.1.22) precursor - guar >gi_18292_emb_CAA32772_ (X14619) alpha-galactosidase preproprotein [Cyamopsis tetragonoloba]

265518 Seq. No. 9001 2.R1011 Contig ID uC-zmflMo17008e12b1 5'-most EST

Method BLASTX q113497 NCBI GI BLAST score 283 4.0e-25 E value 67 Match length % identity 67

ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) NCBI Description

(ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi_99880_pir__S07472 alpha-galactosidase (EC 3.2.1.22)

precursor - quar >gi 18292 emb CAA32772 (X14619)

alpha-galactosidase preproprotein [Cyamopsis tetragonoloba]

265519 Seq. No.

Contig ID 9001 3.R1011

LIB3079-005-Q1-K1-A11 5'-most EST

BLASTX Method NCBI GI g2204226 533 BLAST score 3.0e-54E value 140 Match length % identity

(Y13848) alpha-galactosidase [Hordeum vulgare] NCBI Description

265520 Seq. No.

9001 4.R1011 Contig ID

uC-zmflb73033d04b1 5'-most EST

BLASTX Method g2492782 NCBI GI 381 BLAST score 2.0e-36 E value 202 Match length 43 % identity

ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) NCBI Description

(ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi_504489 (L27992)

alpha-galactosidase [Coffea arabica]

265521 Seq. No.

9004 1.R1011 Contig ID

fC-zmro700449136a1 5'-most EST

BLASTX Method NCBI GI g1657621 1083 BLAST score 0.0e + 00E value 390 Match length % identity

(U72505) G6p [Arabidopsis thaliana] >gi 3068711 (AF049236) NCBI Description

putative acyl-coA dehydrogenase [Arabidopsis thaliana]

265522 Seq. No. 9005_1.R1011 Contig ID



```
uC-zmflmo17043a09b1
5'-most EST
                  BLASTX
Method
                  g2131724
NCBI GI
BLAST score
                  196
                  1.0e-14
E value
Match length
                  96
                   44
% identity
                  hypothetical protein YLL010c - yeast (Saccharomyces
NCBI Description
                  cerevisiae) >gi_1360175_emb_CAA97454_ (Z73115) ORF YLL010c
                   [Saccharomyces cerevisiae] >gi_1495214_emb_CAA62782_
                   (X91488) L1341 protein [Saccharomyces cerevisiae]
                   265523
Seq. No.
                   9005 2.R1011
Contig ID
                   LIB3078-028-Q1-K1-D7
5'-most EST
                   BLASTX
Method
                   q2289786
NCBI GI
                   295
BLAST score
                   3.0e-26
E value
                   110
Match length
                   49
% identity
                  (D88153) HYA22 [Homo sapiens]
NCBI Description
                   265524
Seq. No.
                   9005 3.R1011
Contig ID
                   LIB3061-021-Q1-K1-F1
5'-most EST
                   265525
Seq. No.
Contig ID
                   9005 4.R1011
                   uC-zmflb73337d09a1
5'-most EST
                   BLASTX
Method
                   q3600051
NCBI GI
                   172
BLAST score
                   5.0e-12
E value
                   53
Match length
                   72
 % identity
                  (AF080120) contains similarity to the single-strand binding
NCBI Description
                   proteins family (Pfam: SSB.hmm, score: 24.02) [Arabidopsis
                   thaliana]
                   265526
 Seq. No.
                   9007 1.R1011
 Contig ID
                   LIB3078-028-Q1-K1-E1
 5'-most EST
                   BLASTX
 Method
                   g4468796
 NCBI GI
                   619
 BLAST score
                   1.0e-64
 E value
 Match length
                   144
                   86
 % identity
 NCBI Description (AJ010439) GST6 protein [Zea mays]
```

265527 Seq. No. 9012 1.R1011 Contig ID tzu700203262.h1 5'-most EST BLASTX Method q3650030 NCBI GI

BLAST score

5'-most EST

Method



```
9.0e-18
E value
                  82
Match length
                  54
% identity
                  (AC005396) unknown protein [Arabidopsis thaliana]
NCBI Description
                  265528
Seq. No.
                  9013 1.R1011
Contig ID
                  LIB3136-023-Q1-K1-C3
5'-most EST
                  BLASTX
Method
                  g3068705
NCBI GI
                  549
BLAST score
                  8.0e-56
E value
                  248
Match length
                   48
% identity
                  (AF049236) unknown [Arabidopsis thaliana]
NCBI Description
                   265529
Seq. No.
                   9013 2.R1011
Contig ID
                   uC-zmflb73063f12b1
5'-most EST
                  -265530
Seq. No.
                   9014_1.R1011
Contig ID
                   gw1700612942.h1
5'-most EST
                   BLASTX
Method
                   g3892056
NCBI GI
                   569
BLAST score
                   2.0e-58
E value
Match length
                   126
                   87
% identity
                  (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
NCBI Description
                   265531
Seq. No.
                   9014 2.R1011
Contig ID
                   LIB3061-044-Q1-K1-E3
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3892056
BLAST score
                   573
                   7.0e-59
E value
                   126
Match length
% identity
                  (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
NCBI Description
                   265532
Seq. No.
                   9014 3.R1011
Contig ID
                   LIB3116-012-Q1-K1-F8
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3892056
BLAST score
                   202
E value
                   1.0e-16
Match length
                   50
 % identity
                  (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
NCBI Description
                    265533
Seq. No.
                    9014 4.R1011
 Contig ID
```

36893

uC-zmroteosinte057b10b1

BLASTX

NCBI GI

E value

BLAST score

393

5.0e-41



```
NCBI GI
                  g3892056
BLAST score
                  559
                  3.0e-57
E value
Match length
                  126
                  86
% identity
                  (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
NCBI Description
                  265534
Seq. No.
                  9016 1.R1011
Contig ID
                  uC-zmroteosinte051a10b2
5'-most EST
                  BLASTX
Method
                  g3033384
NCBI GI
BLAST score
                  283
                   9.0e-25
E value
                  86
Match length
                   67
% identity
                  (AC004238) putative CTP synthase [Arabidopsis thaliana]
NCBI Description
                   265535
Seq. No.
                   9017 1.R1011
Contig ID
                   LIB3059-035-Q1-K1-H6
5'-most EST
                   265536
Seq. No.
                   9019 1.R1011
Contig ID
                   LIB3078-028-Q1-K1-B4
5'-most EST
                   265537
Seq. No.
                   9023 1.R1011
Contig ID
                   uC-zmflb73151b06b1
5'-most EST
                   BLASTX
Method
                   g1353193
NCBI GI
                   1089
BLAST score
                   1.0e-119
E value
                   354
Match length
                   60
% identity
                   O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268
NCBI Description
                   O-methyltransferase (EC 2.1.1.-) - maize >gi 404070
                   (L14063) O-methyltransferase [Zea mays]
                   265538
Seq. No.
                   9027 1.R1011
Contig ID
                   uC-zmroteosinte094b07b2
5'-most EST
                   BLASTX
Method
                   g3928166
NCBI GI
                   287
BLAST score
                   3.0e-25
E value
                   284
Match length
                   26
% identity
NCBI Description (AJ010317) Sand [Fugu rubripes]
                   265539
Seq. No.
                   9027 2.R1011
Contig ID
                   pmx700091434.h1
 5'-most EST
                   BLASTX
Method
                   q3355468
```



```
105
  Match length
                     90
  % identity
                     (AC004218) putative ribosomal protein L35 [Arabidopsis
  NCBI Description
                     thaliana]
                     265540
  Seq. No.
                     9027 3.R1011
  Contig ID
                     wyr700242076.hl
  5'-most EST
                     BLASTX
  Method
                     g3355468
  NCBI GI
                     396
  BLAST score
                     4.0e-38
  E value
                     122
  Match length
                     71
  % identity
                     (AC004218) putative ribosomal protein L35 [Arabidopsis
  NCBI Description
                     thaliana]
                     265541
  Seq. No.
                     9027 4.R1011
  Contig ID
                     LIB3118-012-Q1-K1-H8
  5'-most EST
                     BLASTX
  Method
                     g3355468
  NCBI GI
                     453
  BLAST score
                     6.0e-45
™ E value
                     122
  Match length
                     80
  % identity
                     (AC004218) putative ribosomal protein L35 [Arabidopsis
  NCBI Description
                     thaliana]
                     265542
  Seq. No.
                     9027 5.R1011
  Contig ID
                     LIB3059-047-Q1-K1-E1
  5'-most EST
                     BLASTX
  Method
                     q3355468
  NCBI GI
                     202
  BLAST score
                     4.0e-20
  E value
  Match length
                     64
  % identity
                     (AC004218) putative ribosomal protein L35 [Arabidopsis
  NCBI Description
                     thaliana]
  Seq. No.
                     265543
  Contig ID
                     9027 6.R1011
                     xdb700339289.h1
   5'-most EST
                     BLASTN
  Method
  NCBI GI
                     g218177
  BLAST score
                     35
                     4.0e-10
  E value
  Match length
                     73
                     86
   % identity
                     Rice mRNA for ribosomal protein L35 (NH77 gene), partial
  NCBI Description
                      sequence >gi 3106972 dbj D42703_D42703 Rice callus cDNA,
                     NH077
                      265544
   Seq. No.
```

9034 1.R1011

uC-zmflb73049c03b1

Contig ID

5'-most EST



```
265545
Seq. No.
Contig ID
                   9034 2.R1011
                   LIB3078-027-Q1-K1-H10
5'-most EST
                   BLASTX
Method
                   q2315153
NCBI GI
BLAST score
                   890
                   8.0e-96
E value
Match length
                   274
% identity
                   64
                   (Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
NCBI Description
                   265546
Seq. No.
                   9040 1.R1011
Contig ID
5'-most EST
                   fC-zmro700573388a1
Method
                   BLASTX
                   g2446996
NCBI GI
BLAST score
                   1476
                   1.0e-164
E value
Match length
                   282
% identity
                   95
                   (D63953) fatty acid desaturase [Zea mays]
NCBI Description
                   >gi 2447000 dbj BAA22442 (D84409) fatty acid desaturase
                   [Zea mays]
                   265547
Seq. No.
                   9045 1.R1011
Contig ID
5'-most EST
                   LIB3078-027-Q1-K1-G5
                   BLASTX
Method
                   g2493453
NCBI GI
BLAST score
                   323
                   2.0e-29
E value
                   245
Match length
                   38
% identity
                  CALPAIN P94, LARGE (CATALYTIC) SUBUNIT (CALCIUM-ACTIVATED
NCBI Description
                   NEUTRAL PROTEINASE) (CANP) (P94 PROTEIN) (MUSCLE-SPECIFIC
                   CALCIUM-ACTIVATED NEUTRAL PROTEASE 3 LARGE SUBUNIT)
                   >gi_1362714_pir__S57196 calpain (EC 3.4.22.17) p94 heavy
chain - chicken >gi_1552167_dbj_BAA07230_ (D38028) p94
                   [Gallus gallus] >gi 1096148 prf 2111239C
                   calpain:SUBUNIT=large:ISOTYPE=p94 [Gallus gallus]
                   265548
Seq. No.
Contig ID
                   9047 1.R1011
                   hvj700623354.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q453189
BLAST score
                   540
E value
                   5.0e-55
                   109
Match length
                   99
% identity
NCBI Description
                   (X57956) acyl carrier protein [Zea mays]
```

>gi 228957 prf 1814481A acyl carrier protein [Zea mays]

Seq. No.

265554



```
Method
                  BLASTX
                  q453189
NCBI GI
BLAST score
                  573
                  6.0e-59
E value
Match length
                  116
                  99
% identity
                   (X57956) acyl carrier protein [Zea mays]
NCBI Description
                  >qi 228957 prf 1814481A acyl carrier protein [Zea mays]
                  265550
Seq. No.
                  9047 3.R1011
Contig ID
5'-most EST
                  LIB3088-045-Q1-K1-E12
Method
                  BLASTX
                  q453189
NCBI GI
BLAST score
                  192
E value
                  2.0e-14
Match length
                   44
% identity
                   93
                   (X57956) acyl carrier protein [Zea mays]
NCBI Description
                  >gi 228957 prf 1814481A acyl carrier protein [Zea mays]
                   265551
Seq. No.
                   9047 4.R1011
Contig ID
                   uC-zmroteosinte002d07b1
5'-most EST
Method
                   BLASTX
                   q453189
NCBI GI
                   311
BLAST score
E value
                   5.0e-32
Match length
                   81
                   93
% identity
                  (X57956) acyl carrier protein [Zea mays]
NCBI Description
                   >gi 228957 prf 1814481A acyl carrier protein [Zea mays]
Seq. No.
                   265552
                   9051 1.R1011
Contig ID
                   LIB3279-054-P1-K1-B2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2565275
BLAST score
                   676
E value
                   6.0e-71
                   142
Match length
                   84
% identity
                  (AF023611) Dim1p homolog [Homo sapiens]
NCBI Description
                   265553
Seq. No.
Contig ID
                   9053 1.R1011
5'-most EST
                   LIB3078-027-Q1-K1-F5
Method
                   BLASTX
NCBI GI
                   g2459446
                   297
BLAST score
                   7.0e-27
E value
                   143
Match length
% identity
                   48
                   (ACO02332) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                   thaliana]
```



```
9053 2.R1011
Contig ID
                  LIB3150-007-Q1-N1-H4
5'-most EST
                  BLASTX
Method
                  q2459446
NCBI GI
                  371
BLAST score
                  2.0e-35
E value
                  135
Match length
                  56
% identity
                  (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                  thaliana]
                  265555
Seq. No.
                  9054 1.R1011
Contig ID
5'-most EST
                  uC-zmflMo17085g05b1
                  BLASTX
Method
NCBI GI
                  g4235093
                  298
BLAST score
                  9.0e-27
E value
                  149
Match length
                   44
% identity
                  (AF108944) beta-xylosidase [Aspergillus niger]
NCBI Description
                  265556
Seq. No.
                  9054 2.R1011
Contig ID
                  LIB3078-027-Q1-K1-E6
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2760844
                   491
BLAST score
                   2.0e-49
E value
Match length
                  225
                   46
% identity
NCBI Description
                  (AC003105) hypothetical protein [Arabidopsis thaliana]
                   265557
Seq. No.
                   9057_1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17073a09b1
Method
                   BLASTX
NCBI GI
                   q1209756
BLAST score
                   1671
                   0.0e + 00
E value
                   483
Match length
% identity
                   66
                  (U43629) integral membrane protein [Beta vulgaris]
NCBI Description
                   265558
Seq. No.
                   9057 2.R1011
Contig ID
5'-most EST
                   nwy7\overline{0}0446823.h1
Method
                   BLASTX
NCBI GI
                   q1209756
BLAST score
                   178
E value
                   9.0e-13
Match length
                   48
% identity
                   60
                  (U43629) integral membrane protein [Beta vulgaris]
NCBI Description
```

265559

9057 3.R1011

Seq. No.

Contig ID

Match length

% identity

346



```
LIB3115-002-Q1-K1-H4
  5'-most EST
  Method
                     BLASTX
                     q1209756
  NCBI GI
  BLAST score
                     220
                     2.0e-17
  E value
  Match length
                     59
                     66
  % identity
                    (U43629) integral membrane protein [Beta vulgaris]
  NCBI Description
                     265560
  Seq. No.
                     9057_4.R1011
  Contig ID
                     uC-zmroB73070e05b1
  5'-most EST
  Method
                     BLASTX
                     g1871194
  NCBI GI
  BLAST score
                     265
  E value
                     2.0e-22
  Match length
                     165
                     38
  % identity
                     (U90439) DNA binding protein isolog [Arabidopsis thaliana]
  NCBI Description
                     >gi 2335092 (AC002339) putative DNA binding protein
                     [Arabidopsis thaliana]
                     265561
  Seq. No.
                     9057 7.R1011
  Contig ID
  5'-most EST
                     LIB3136-011-Q1-K1-D3
  Seq. No.
                     265562
  Contig ID
                     9057 9.R1011
                     uC-z\overline{m}rob73075c05b1
  5'-most EST
  Seq. No.
                     265563
  Contig ID
                     9057 10.R1011
                     uC-zmflb73139a10b1
  5'-most EST
                     265564
  Seq. No.
  Contig ID
                     9058_1.R1011
5'-most EST
                     uC-zmflmo17324c04a1
  Method
                     BLASTX
  NCBI GI
                     q2493493
  BLAST score
                     831
  E value
                     4.0e-89
  Match length
                     213
  % identity
                     82
  NCBI Description
                     SERINE CARBOXYPEPTIDASE II-1 PRECURSOR (CP-MII.1)
                     >gi 619352 bbs 153538 CP-MII.1=serine carboxypeptidase
                     [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 324
                     265565
  Seq. No.
                     9058 2.R1011
  Contig ID
  5'-most EST
                     fC-zmle700582460f1
  Method
                     BLASTX
  NCBI GI
                     g4263777
  BLAST score
                     1272
  E value
                     1.0e-140
```



NCBI Description (AC006068) putative serine carboxypeptidase II [Arabidopsis thaliana] >gi_4510391_gb_AAD21479.1_ (AC007017) putative

serine carboxypeptidase II [Arabidopsis thaliana]

Seq. No. 265566

Contig ID 9058_3.R1011 5'-most EST cyk700050636.f1

Seq. No. 265567

Contig ID 9058_4.R1011 5'-most EST hvj700622136.h1

Method BLASTX
NCBI GI g2493493
BLAST score 188
E value 4.0e-31
Match length 74
% identity 86

NCBI Description SERINE CARBOXYPEPTIDASE II-1 PRECURSOR (CP-MII.1)

>gi_619352_bbs_153538 CP-MII.1=serine carboxypeptidase

[Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 324

aa]

Seq. No. 265568

Contig ID 9060_1.R1011 5'-most EST uer700578967.h1

Seq. No. 265569

Contig ID 9066 1.R1011

5'-most EST uC-zmflb73088b12b2

Method BLASTX
NCBI GI g3122914
BLAST score 1636
E value 0.0e+00
Match length 537
% identity 58

NCBI Description VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)

>gi_1890130 (U89986) valyl tRNA synthetase [Arabidopsis

thaliana]

Seq. No. 265570

Contig ID 9066_3.R1011 5'-most EST fxb700397419.h1

Seq. No. 265571

Contig ID 9068 1.R1011

5'-most EST uC-zmflb73260d12b2

Method BLASTX
NCBI GI g2244847
BLAST score 172
E value 5.0e-12
Match length 132
% identity 30

NCBI Description (Z97337) hydroxyproline-rich glycoprotein homolog

[Arabidopsis thaliana]

Seq. No. 265572

Contig ID 9069_1.R1011



5'-most EST xsy700211133.h1 BLASTX Method g1778149 NCBI GI BLAST score 1430 1.0e-159 E value 334 Match length 87 % identity (U66404) phosphate/phosphoenolpyruvate translocator NCBI Description precursor [Zea mays] 265573 Seq. No. 9071 1.R1011 Contig ID 5'-most EST LIB3067-028-Q1-K1-C8 BLASTX Method NCBI GI q2632129 BLAST score 590 E value 8.0e-61 Match length 202 % identity 67 NCBI Description (AJ222589) poly(ADP-ribose) polymerase [Zea mays] Seq. No. 265574 9073 1.R1011 Contig ID 5'-most EST pmx700086941.h1 BLASTN Method NCBI GI g3821780 BLAST score 36 E value 3.0e-10 Match length 48 67 % identity NCBI Description Xenopus laevis cDNA clone 27A6-1 Seq. No. 265575 9073 2.R1011 Contig ID 5'-most EST uC-zmflb73172d12b2 265576 Seq. No. Contig ID 9076 1.R1011 5'-most EST hvj700623358.h1 Seq. No. 265577 Contig ID 9078 1.R1011 5'-most EST rvt700551825.h1 Seq. No. 265578 9078 2.R1011 Contig ID 5'-most EST nwy700444023.hl 265579 Seq. No. Contig ID 9078_3.R1011 5'-most EST gct701179005.h1

Seq. No. 265580 Contig ID 9079 1.R1011

5'-most EST LIB3137-062-Q1-K1-A5

Seq. No. 265581



```
9081 1.R1011
Contig ID
                  kem7\overline{0}0612205.h1
5'-most EST
                  265582
Seq. No.
Contig ID
                  9084 1.R1011
                  LIB3068-035-Q1-K1-F1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4103635
                   179
BLAST score
                   6.0e-13
E value
                   124
Match length
                   33
% identity
                  (AF026538) ABA-responsive protein [Hordeum vulgare]
NCBI Description
                   265583
Seq. No.
                   9089 1.R1011
Contig ID
                   uC-zmroB73020d06b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2738750
                   1849
BLAST score
                   0.0e + 00
E value
                   372
Match length
                   95
% identity
NCBI Description (AF016305) ATP sulfurylase [Zea mays]
                   265584
Seq. No.
                   9089 2.R1011
Contig ID
                   LIB3060-021-Q1-K1-H10
5'-most EST
Method
                   BLASTN
                   q2738749
NCBI GI
BLAST score
                   260
                   1.0e-144
E value
                   328
Match length
                   96
% identity
NCBI Description Zea mays ATP sulfurylase mRNA, complete cds
                   265585
Seq. No.
                   9090 1.R1011
Contig ID
                   LIB3066-007-Q1-K1-D12
5'-most EST
                   BLASTX
Method
                   g3334333
NCBI GI
                   471
BLAST score
                   3.0e-47
E value
                   128
Match length
                   70
 % identity
                   SUPEROXIDE DISMUTASE-2 (CU-ZN) >gi 2660798 (AF034832)
NCBI Description
                   cytosolic copper/zinc superoxide dismutase
                    [Mesembryanthemum crystallinum]
                    265586
 Seq. No.
                    9097 1.R1011
 Contig ID
                   ypc700799583.hl
 5'-most EST
                    265587
 Seq. No.
                    9105_1.R1011
 Contig ID
                    LIB3069-051-Q1-K1-C6
 5'-most EST
```

BLASTX

Method

. . Santa



NCBI GI g1938549 BLAST score 196 E value 9.0e-15 Match length 74 % identity 53

NCBI Description (U97016) similar to drosophila Rlc1 gene product

(NID:g563361) and S. cerevisiae mitochondrial 60S ribosomal protein L4 (YML4) (NID:g459259) [Caenorhabditis elegans]

Seq. No. 265588

Contig ID 9106_1.R1011 5'-most EST ymt700224379.h1

Seq. No. Contig ID

9108_1.R1011

265589

5'-most EST uC-zmflmo17122h08b1

Method BLASTX
NCBI GI g1052960
BLAST score 1677
E value 0.0e+00
Match length 349
% identity 90

NCBI Description (U37437) PNIL34 [Ipomoea nil]

 Seq. No.
 265590

 Contig ID
 9108_2.R1011

 5'-most EST
 hvj700623571.h1

Method BLASTX
NCBI GI g4503607
BLAST score 383
E value 3.0e-72
Match length 330
% identity 50

NCBI Description electron transfer flavoprotein, alpha polypeptide

>gi_119636_sp_P13804_ETFA_HUMAN_ELECTRON_TRANSFER FLAVOPROTEIN_ALPHA-SUBUNIT_PRECURSOR_(ALPHA-ETF)

>gi_87351_pir__A31998 electron transfer flavoprotein alpha

chain precursor - human >gi_182251 (J04058) electron

transport flavoprotein [Homo sapiens]

Seq. No. 265591

Contig ID 9108_3.R1011 5'-most EST qmh700028561.f1

Method BLASTX
NCBI GI g1293686
BLAST score 192
E value 7.0e-14
Match length 235
% identity 29

NCBI Description (U53925) Mus musculus transcription factor C1 mRNA,

complete cds. [Mus musculus]

Seq. No. 265592 Contig ID 9108_4.R1011

5'-most EST LIB3066-024-Q1-K1-E1

Method BLASTN NCBI GI g3821780



```
.BLAST score
                   3.0e-10
E value
                   36
Match length
                   100
% identity
                   Xenopus laevis cDNA clone 27A6-1
NCBI Description
Seq. No.
                   265593
                   9108 8.R1011
Contig ID
                   vux700159535.hl
5'-most EST
                   265594
Seq. No.
                   9108 9.R1011
Contig ID
                   uC-zmflb73177g07b1
5'-most EST
                   BLASTX
Method
                   g1293686
NCBI GI
                   172
BLAST score
                   7.0e-12
E value
                   136
Match length
                   35
% identity
                   (U53925) Mus musculus transcription factor C1 mRNA,
NCBI Description
                   complete cds. [Mus musculus]
                   265595
Seq. No.
                   9108 10.R1011
Contig ID
                   LIB3067-005-Q1-K1-H9
5'-most EST
                   265596
Seq. No.
                   9109_1.R1011
Contig ID
                   uC-zmflmo17118b08b1
 5'-most EST
Method
                   BLASTX
                   g3258570
NCBI GI
BLAST score
                   726
                   2.0e-76
 E value
 Match length
                   345
                   45
 % identity
                   (U89959) Unknown protein [Arabidopsis thaliana]
 NCBI Description
                   265597
 Seq. No.
                    9109 2.R1011
 Contig ID
                   tzu700204376.hl
 5'-most EST
                   BLASTX
 Method
                    g3258570
 NCBI GI
                    373
 BLAST score
                    2.0e-35
 E value
                    168
 Match length
                    51
 % identity
                  (U89959) Unknown protein [Arabidopsis thaliana]
 NCBI Description
                    265598
 Seq. No.
                    9110 1.R1011
 Contig ID
                    uC-zmflmo17155a07b1
 5'-most EST
                    BLASTX
 Method
                    g168397
 NCBI GI
                    914
 BLAST score
```

8.0e-99

171

100

E value

Match length

% identity



NCBI Description (L08425) auxin-binding protein [Zea mays]

>gi_264278_bbs_123706 (S53630) auxin-binding protein, ABP

[corn, Peptide, 201 aa] [Zea mays]

Seq. No. 265599

Contig ID 9114_1.R1011 5'-most EST xyt700342718.h1

Method BLASTX
NCBI GI g4337195
BLAST score 1500
E value 1.0e-167
Match length 392
% identity 72

NCBI Description (AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No. 265600

Contig ID 9114 3.R1011

5'-most EST uC-zmflb73074g10a1

Method BLASTX
NCBI GI g4337195
BLAST score 145
E value 5.0e-09
Match length 39

% identity 62

NCBI Description (AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No. 265601

Contig ID 9114_5.R1011

5'-most EST uC-zmflmo17060b12a1

Seq. No. 265602

Contig ID 9115 1.R1011

5'-most EST LIB3153-013-Q1-K1-D5

Method BLASTX
NCBI GI g2827713
BLAST score 1320
E value 1.0e-146
Match length 317

% identity 77

NCBI Description (AL021684) pyridoxal-phosphate-dependent aminotransferase -

like protein [Arabidopsis thaliana]

Seq. No. 265603

Contig ID 9118_1.R1011

5'-most EST LIB83-002-Q1-E1-E12

Method BLASTX
NCBI GI g1084479
BLAST score 651
E value 5.0e-68
Match length 151
% identity 89

NCBI Description H+-transporting ATP synthase (EC 3.6.1.34) delta chain -

maize (fragment) >gi 311237 emb CAA46804 (X66005)

H(+)-transporting ATP synthase [Zea mays]

Seq. No. 265604

Contig ID 9118 2.R1011



```
LIB3116-013-Q1-K1-F12
5'-most EST
Method
                  BLASTX
                  g1084479
NCBI GI
BLAST score
                  708
                  1.0e-74
E value
                  169
Match length
                  86
% identity
                  H+-transporting ATP synthase (EC 3.6.1.34) delta chain -
NCBI Description
                  maize (fragment) >gi_311237_emb_CAA46804_ (X66005)
                  H(+)-transporting ATP synthase [Zea mays]
                   265605
Seq. No.
                   9118 3.R1011
Contig ID
                   LIB3116-002-Q1-K1-F9
5'-most EST
                   BLASTN
Method
                   g311236
NCBI GI
BLAST score
                   139
                   4.0e-72
E value
Match length
                   139
% identity
                   100
                  Z.mays mRNA for ATPase (delta subunit)
NCBI Description
                   265606
Seq. No.
                   9121 1.R1011
Contig ID
                   uwc700153461.hl
5'-most EST
                   265607
Seq. No.
                   9126 1.R1011
Contig ID
5'-most EST
                   cyk700048851.f1
Method
                   BLASTX
                   q3335378
NCBI GI
                   491
BLAST score
                   6.0e-49
E value
                   204
Match length
                   52
% identity
                   (AC003028) Myb-related transcription activator [Arabidopsis
NCBI Description
                   thaliana]
                   265608
Seq. No.
                   9126 2.R1011
Contig ID
                   wyr700240864.hl
5'-most EST
                   BLASTX
Method
                   g3335378
NCBI GI
                   278
BLAST score
                   2.0e-24
E value
                   77
Match length
                   73
% identity
                   (AC003028) Myb-related transcription activator [Arabidopsis
NCBI Description
                   thaliana]
                   265609
Seq. No.
                   9126_3.R1011
Contig ID
                   pmx700082219.hl
 5'-most EST
                   BLASTX
Method
                   q3335378
NCBI GI
```

213

2.0e-16

BLAST score

E value



55 Match length % identity (AC003028) Myb-related transcription activator [Arabidopsis NCBI Description thaliana] 265610 Seq. No. 9126 4.R1011 Contig ID LIB3068-035-Q1-K1-C8 5'-most EST BLASTN Method g2062705 NCBI GI 36 BLAST score 1.0e-10 E value 36 Match length 100 % identity Human butyrophilin (BTF5) mRNA, complete cds NCBI Description 265611 Seq. No. Contig ID 9129 1.R1011 LIB3078-026-Q1-K1-F7 5'-most EST 265612 Seq. No. 9136 1.R1011 Contig ID 5'-most EST pmx700091720.h1 265613 Seq. No. 9136 2.R1011 Contig ID ymt700220742.h1 5'-most EST BLASTX Method NCBI GI q3882239 BLAST score 334 7.0e-31E value 206 Match length % identity 38 (AB018302) KIAA0759 protein [Homo sapiens] NCBI Description 265614 Seq. No. 9140 1.R1011 Contig ID $mwy7\overline{0}0438170.h1$ 5'-most EST BLASTX Method g3775987 NCBI GI 1504 BLAST score 1.0e-170 E value 411 Match length 74 % identity NCBI Description (AJ010457) RNA helicase [Arabidopsis thaliana] 265615 Seq. No. 9145 1.R1011 Contig ID LIB3159-015-Q1-K1-G10 5'-most EST

265616 Seq. No. 9145 2.R1011 Contig ID LIB189-031-Q1-E1-A6 5'-most EST

265617 Seq. No. 9145 3.R1011 Contig ID qmh700030666.f1 5'-most EST



```
BLASTX
Method
NCBI GI.
                   q2842757
                   378
BLAST score
                   6.0e-36
E value
                   172
Match length
                   53
% identity
                   LIGHT-INDUCIBLE PROTEIN CPRF-2 >gi_1806261_emb_CAA41453_
NCBI Description
                   (X58577) DNA-binding protein; bZIP type [Petroselinum
                   265618
Seq. No.
                   9145 4.R1011
Contig ID
                   LIB3116-014-Q1-K1-D10
5'-most EST
                   265619
Seq. No.
                   9145 5.R1011
Contig ID
                   uC-zmf1b73226d01b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2842757
                   363
BLAST score
                   2.0e-34
E value
                   118
Match length
                   63
% identity
                   LIGHT-INDUCIBLE PROTEIN CPRF-2 >gi_1806261_emb_CAA41453_
NCBI Description
                   (X58577) DNA-binding protein; bZIP type [Petroselinum
                   crispum]
                   265620
Seq. No.
Contig ID
                   9150 1.R1011
                   uC\text{-}z\bar{m}flmo17267b12b1
5'-most EST
                   BLASTX
Method
                   q3738329
NCBI GI
                   550
BLAST score
                    5.0e-56
E value
                    149
Match length
                    74
 % identity
NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]
                    265621
 Seq. No.
                    9150 2.R1011
 Contig ID
                    LIB3151-035-Q1-K1-E2
 5'-most EST
                    BLASTX
 Method
                    g3738329
 NCBI GI
                    224
 BLAST score
                    5.0e-18
 E value
                    72
 Match length
                    67
 % identity
 NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]
                    265622
 Seq. No.
                    9152 1.R1011
 Contig ID
                    LIB3059-056-Q1-K1-D4
 5'-most EST
```

 Seq. No.
 265623

 Contig ID
 9156_1.R1011

 5'-most EST
 dyk700106903.h1

 Method
 BLASTX



NCBI GI g2462754 324 BLAST score 2.0e-29 E value Match length 211 % identity 34

(AC002292) Unknown protein [Arabidopsis thaliana] NCBI Description

265624 Seq. No.

9156 2.R1011 Contig ID xjt700093031.hl 5'-most EST

Seq. No. 265625

9157 1.R1011 Contig ID yyf700352418.h1 5'-most EST

Method BLASTX NCBI GI q4454263 196 BLAST score E value 2.0e-14 Match length 231 29 % identity

(Y18046) FGFR1 oncogene partner (FOP) [Homo sapiens] NCBI Description

Seq. No. 265626

9157 3.R1011 Contig ID

uC-zmflmo17160f07b1 5'-most EST

265627 Seq. No. Contig ID 9157 4.R1011 5'-most EST xsy700217512.h1

BLASTX Method q2191168 NCBI GI 223 BLAST score 3.0e-34E value 179 Match length

52 % identity

(AF007270) contains similarity to myosin heavy chain NCBI Description

[Arabidopsis thaliana]

265628 Seq. No. 9157 5.R1011 Contig ID 5'-most EST uC-zmflb73416h10a1

265629 Seq. No.

Contig ID 9157 6.R1011 rv1700456503.h1 5'-most EST

265630 Seq. No. Contig ID 9157 8.R1011

5'-most EST LIB3068-028-Q1-K1-E12

Seq. No. 265631 9157 9.R1011 Contig ID

LIB3062-029-Q1-K1-D4 5'-most EST

BLASTX Method NCBI GI g2191168 BLAST score 171 E value 1.0e-11



```
74
Match length
% identity
                   (AF007270) contains similarity to myosin heavy chain
NCBI Description
                   [Arabidopsis thaliana]
                   265632
Seq. No.
                   9162 1.R1011
Contig ID
                  LIB3078-026-Q1-K1-A11
5'-most EST
                   BLASTX
Method
                   q1749676
NCBI GI
BLAST score
                   290
                   2.0e-40
E value
                   240
Match length
% identity
                   (D89234) similar to Saccharomyces cerevisiae ORF YGR205W,
NCBI Description
                   EMBL Accession Number Z72990 [Schizosaccharomyces pombe]
                   265633
Seq. No.
Contig ID
                   9163 1.R1011
                   LIB3078-026-Q1-K1-A12
5'-most EST
                   BLASTX
Method
                   g3777602
NCBI GI
BLAST score
                   625
                   3.0e-65
E value
                   128
Match length
                   93
% identity
                  (AF095709) 50S ribosomal protein L10 [Oryza sativa]
NCBI Description
                   265634
Seq. No.
                   9166 1.R1011
Contig ID
                   LIB189-023-Q1-E1-B1
5'-most EST
                   BLASTX
Method
                   g1362192
NCBI GI
BLAST score
                   249
                   5.0e-21
E value
                   59
Match length
                   76
% identity
NCBI Description ferredoxin--thioredoxin reductase (EC 1.18.-.-) variable
                   chain - maize
                   265635
Seq. No.
                   9167 1.R1011
Contig ID
                   wen700331819.h1
 5'-most EST
                   BLASTX
Method
                   g2073375
 NCBI GI
                   1681
 BLAST score
                   0.0e+00
 E value
                   346
 Match length
                   91
 % identity
                   (D85317) farnesyl pyrophosphate synthase [Oryza sativa]
 NCBI Description
```

>gi_4063829_dbj_BAA36276_ (AB021747) farnesyl diphosphate

synthase [Oryza sativa]

265636 Seq. No. 9167_2.R1011 Contig ID

uC-zmroteosinte067e12b1 5'-most EST

BLASTX Method



NCBI GI g2773154
BLAST score 150
E value 2.0e-09
Match length 34
% identity 85

NCBI Description (AF039573) abscisic acid- and stress-inducible protein

[Oryza sativa]

Seq. No. 265637

Contig ID 9167 3.R1011

5'-most EST LIB3068-057-Q1-K1-B9

Seq. No. 265638

Contig ID 9167_5.R1011

5'-most EST LIB3136-051-Q1-K1-B7

Method BLASTN
NCBI GI g2773153
BLAST score 84
E value 2.0e-39
Match length 196
% identity 86

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

Seq. No. 265639

Contig ID 9167 6.R1011

5'-most EST uC-zmflb73412e02a1

Method BLASTX
NCBI GI g2073375
BLAST score 354
E value 1.0e-33
Match length 80
% identity 88

NCBI Description (D85317) farnesyl pyrophosphate synthase [Oryza sativa]

>gi_4063829_dbj_BAA36276_ (AB021747) farnesyl diphosphate

synthase [Oryza sativa]

Seq. No. 265640

Contig ID 9167_7.R1011 5'-most EST nwy700444866.h1

Seq. No. 265641

Contig ID 9174_1.R1011

5'-most EST uC-zmroteosinte084g05b1

Method BLASTX
NCBI GI g2244772
BLAST score 1448
E value 1.0e-161
Match length 385
% identity 72

NCBI Description (Z97335) transport protein [Arabidopsis thaliana]

Seq. No. 265642

Contig ID 9184_1.R1011

5'-most EST LIB3078-025-Q1-K1-G4

Seq. No. 265643



```
Contig ID
                   9186 1.R1011
                   LIB3181-009-P1-K2-H2
5'-most EST
                   BLASTX
Method
                   q1705463
NCBI GI
BLAST score
                   875
                   2.0e-94
E value
Match length
                   214
% identity
                   77
                   BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi_2129547_pir__S71201
NCBI Description
                   biotin sythase - Arabidopsis thaliana >gi_1045316 (U24147)
                   biotin sythase [Arabidopsis thaliana] >gi_1403662 (U31806)
                   BIO2 protein [Arabidopsis thaliana] >gi_1769457 (L34413)
                   biotin synthase [Arabidopsis thaliana] >gi_2288983
                   (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana]
                   >gi 1589016_prf 2209438A biotin synthase [Arabidopsis
                   thaliana]
                   265644
Seq. No.
                   9192 1.R1011
Contig ID
                   uC-zmflb73084e02b2
5'-most EST
                   BLASTX
Method
                   g1651904
NCBI GI
BLAST score
                   198
                   1.0e-14
E value
                   157
Match length
                   32
% identity
                   (D90901) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                   265645
                   9197 1.R1011
Contig ID
                   LIB3067-045-Q1-K1-D11
5'-most EST
                   BLASTX
Method
                   g4105190
NCBI GI
                   522
BLAST score
                   1.0e-52
E value
                   246
Match length
                    46
% identity
                   (AF044127) peroxisomal short-chain alcohol dehydrogenase
NCBI Description
                    [Homo sapiens]
                    265646
Seq. No.
                    9197 3.R1011
Contig ID
                   LIB3180-005-P2-M1-C10
5'-most EST
                   BLASTX
Method
                    g3877595
NCBI GI
                    283
BLAST score
                    3.0e-25
E value
Match length
                    114
                    54
% identity
                   (Z79696) predicted using Genefinder; Similarity to Human
NCBI Description
                    HEP27 protein (TR:G1079566); cDNA EST yk281b1.5 comes from this gene; cDNA EST yk281b1.3 comes from this gene
```

[Caenorhabditis elegans] >gi_3879853_emb_CAB04734_ (Zpredicted using Genefinder; Similarity to Human HEP27

protein (TR:G1079566); cDNA EST yk281b1.5 comes from this

gene; cDNA EST yk281b1.3 comes from this gene

[Caenorhabditis elegans]



```
265647
Seq. No.
                  9202 1.R1011
Contig ID
                  LIB3060-011-Q1-K1-D12
5'-most EST
                  BLASTX
Method
                  q3913633
NCBI GI
                  339
BLAST score
                  2.0e-31
E value
                  161
Match length
                  47
% identity
NCBI Description HYPOTHETICAL PROTEIN F8A5.25 >gi_2462742 (AC002292) Unknown
                  protein [Arabidopsis thaliana]
                  265648
Seq. No.
                  9202 2.R1011
Contig ID
                  pmx700088818.hl
5'-most EST
                   265649
Seq. No.
Contig ID
                   9203 1.R1011
                  LIB3078-025-Q1-K1-E11
5'-most EST
                   BLASTX
Method
                   q3643090
NCBI GI
                   844
BLAST score
                   1.0e-90
E value
                   257
Match length
                   62
% identity
                  (AF075582) protein phosphatase-2C; PP2C [Mesembryanthemum
NCBI Description
                   crystallinum]
                   265650
Seq. No.
                   9204 1.R1011
Contig ID
                   LIB189-020-Q1-E1-H5
5'-most EST
                   BLASTX
Method
                   q3643085
NCBI GI
BLAST score
                   951
                   1.0e-108
E value
Match length
                   327
% identity
                   (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum
NCBI Description
                   crystallinum]
                   265651
Seq. No.
                   9208 1.R1011
Contig ID
                   gct701178645.hl
5'-most EST
                   265652
Seq. No.
                   9210 1.R1011
 Contig ID
                   xsy700217516.h1
 5'-most EST
                   265653
 Seq. No.
                   9210 2.R1011
 Contig ID
                   ymt700223942.h1
 5'-most EST
```

265654

9210 3.R1011

qmh700025987.fl

Seq. No.

Contig ID

5'-most EST



```
Seq. No.
                   265655
                   9211 1.R1011
Contig ID
                   ymt700224174.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3915189
BLAST score
                   511
                   1.0e-51
E value
Match length
                   142
                   65
% identity
                   UBIQUITIN-CONJUGATING ENZYME X (UBIQUITIN-PROTEIN LIGASE)
NCBI Description
                   (UBIQUITIN CARRIER PROTEIN)
Seq. No.
                   265656
                   9211 2.R1011
Contig ID
                   qw17\overline{0}0616395.h1
5'-most EST
Seq. No.
                   265657
                   9214 1.R1011
Contig ID
                   uC-zmroteosinte120d09b2
5'-most EST
                   BLASTX
Method
                   q2224911
NCBI GI
                   690
BLAST score
                   1.0e-121
E value
Match length
                   467
                   56
% identity
                   (U93048) somatic embryogenesis receptor-like kinase [Daucus
NCBI Description
                   carota]
Seq. No.
                   265658
                   9216 1.R1011
Contig ID
                   LIB3066-029-Q1-K1-F2
5'-most EST
                   BLASTX
Method
                   g127297
NCBI GI
BLAST score
                   219
                   3.0e-17
E value
                   200
Match length
                   33
% identity
                   MPV17 PROTEIN >gi 346714_pir__S29031 mpv17 protein - mouse
NCBI Description
                   >gi_199790 (M36411) Mpv17 [Mus musculus]
                   265659
Seq. No.
                   9220 1.R1011
Contig ID
                   pwr700451542.hl
 5'-most EST
                   265660
Seq. No.
                   9221 1.R1011
Contig ID
                   LIB3068-010-Q1-K1-H4
 5'-most EST
                   BLASTX
Method
                   g1653619
NCBI GI
BLAST score
                   218
                   3.0e-17
E value
                   156
Match length
                    37
 % identity
                   (D90915) spermidine/putrescine-binding periplasmic protein
```

265661 Seq. No.

NCBI Description

[Synechocystis sp.]



Contig ID 9221_2.R1011 5'-most EST LIB83-010-Q1-E1-H6 Method BLASTN NCBI GI 93821780

BLAST score 36 E value 8.0e-11 Match length 48 % identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 265662

Contig ID 9228_1.R1011

5'-most EST LIB3180-038-P2-M2-D6

Method BLASTX
NCBI GI g266346
BLAST score 1202
E value 1.0e-132
Match length 289
% identity 81

NCBI Description KETOL-ACID REDUCTOISOMERASE PRECURSOR (ACETOHYDROXY-ACID

REDUCTOISOMERASE) (ALPHA-KETO-BETA-HYDROXYLACIL REDUCTOISOMERASE) >gi_81509_pir__S17180 ketol-acid reductoisomerase (EC 1.1.1.86) precursor - spinach

>gi 21234 emb CAA40356 (X57073) ketol-acid

reductoisomerase [Spinacia oleracea]

Seq. No. 265663

Contig ID 9228 2.R1011 5'-most EST wyr700240841.h1

Method BLASTX
NCBI GI g480450
BLAST score 1377
E value 1.0e-153
Match length 309
% identity 86

NCBI Description ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis

thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid

reductoisomerase [Arabidopsis thaliana]

Seq. No. 265664

Contig ID 9230 1.R1011

5'-most EST LIB3078-024-Q1-K1-G8

Seq. No. 265665 Contig ID 9234 1

Contig ID 9234_1.R1011 5'-most EST qmh700029957.f1

Seq. No. 265666

Contig ID 9234 2.R1011

5'-most EST uC-zmromo17091d02a1

Seq. No. 265667

Contig ID 9241 1.R1011

5'-most EST LIB3061-051-Q1-K1-H4

Method BLASTX NCBI GI g4538913

BLAST score 371



E value 5.0e-35 Match length 169 % identity 51

NCBI Description (ALO49482) putative protein [Arabidopsis thaliana]

Seq. No. 265668

Contig ID 9241_3.R1011

5'-most EST uC-zmflm017093h08b1

Method BLASTX
NCBI GI 94538913
BLAST score 166
E value 1.0e-11
Match length 55

% identity 60 NCBI Description (ALO49482) putative protein [Arabidopsis thaliana]

Seq. No. 265669

Contig ID 9241 5.R1011 5'-most EST xjt700093116.h1

Seq. No. 265670

Contig ID 9242 1.R1011

5'-most EST uC-zmflb73140h02b1

Method BLASTX
NCBI GI g3122638
BLAST score 1696
E value 0.0e+00
Match length 478
% identity 69

NCBI Description PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1

>gi_1076381_pir__S49820 PRL1 protein - Arabidopsis thaliana

>gi_577733_emb_CAA58031_ (X82824) PRL1 [Arabidopsis
thaliana] >gi_577735_emb_CAA58032_ (X82825) PRL1

[Arabidopsis thaliana] >gi_2244947_emb CAB10369.1 (Z97339)

PRL1 protein - Arabidopsis thaliana

Seq. No. 265671 Contig ID 9243_1.R1011

5'-most EST LIB143-002-Q1-E1-C4

Seq. No. 265672 Contig ID 9243 2.R1011

5'-most EST LIB3088-043-Q1-K1-B5

 Seq. No.
 265673

 Contig ID
 9243_5.R1011

 5'-most EST
 hbs701183592.h1

Seq. No. 265674 Contig ID 9244_1.R1011

5'-most EST LIB3078-024-Q1-K1-E8

Method BLASTX
NCBI GI g10874
BLAST score 240
E value 8.0e-20
Match length 226
% identity 31

36916



```
NCBI Description (X02974) pot. w(+) polypeptide [Drosophila melanogaster]
                  265675
Seq. No.
                  9245 1.R1011
Contig ID
                  fwa700100559.hl
5'-most EST
                  265676
Seq. No.
                  9247 1.R1011
Contig ID
                  uer700582736.h1
5'-most EST
                  265677
Seq. No.
                  9248 1.R1011
Contig ID
                  LIB3070-008-Q1-N1-E12
5'-most EST
                   265678
Seq. No.
                   9250 1.R1011
Contig ID
                  xsy700209818.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4510348
BLAST score
                   303
                   2.0e-27
E value
                   124
Match length
                   50
% identity
                  (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                   265679
Seq. No.
                   9252 1.R1011
Contig ID
                   LIB3136-008-Q1-K1-B1
5'-most EST
                   BLASTX
Method
                   q266578
NCBI GI
                   241
BLAST score
                   5.0e-20
E value
                   56
Match length
                   77
 % identity
                   METALLOTHIONEIN-LIKE PROTEIN 1 >gi 100898 pir S17560
NCBI Description
                   metallothionein-like protein - maize >gi_236730_bbs_57629
                   (S57628) metallothionein homologue [Zea mays, Peptide, 76
                   aa] [Zea mays] >gi_559536_emb_CAA57676_ (X82186)
                   metallothionein- like protein [Zea mays]
                   >gi 228095_prf__1717215A metallothionein-like protein [Zea
                   mays]
                   265680
 Seq. No.
                   9252 2.R1011
 Contig ID
                   LIB84-014-Q1-E1-G2
 5'-most EST
                   BLASTX
 Method
                   g266578
 NCBI GI
                   241
 BLAST score
                    4.0e-20
 E value
 Match length
                    56
                    77
 % identity
 NCBI Description METALLOTHIONEIN-LIKE PROTEIN 1 >gi_100898_pir__S17560
                   metallothionein-like protein - maize >gi_236730_bbs_57629
                    (S57628) metallothionein homologue [Zea mays, Peptide, 76
                    aa] [Zea mays] >gi_559536_emb_CAA57676 (X82186)
                    metallothionein- like protein [Zea mays]
```

>gi_228095_prf__1717215A metallothionein-like protein [Zea



mays]

265681 Seq. No. 9252 3.R1011 Contig ID LIB3116-010-Q1-K1-C9 5'-most EST BLASTN Method g236729 NCBI GI 347 BLAST score 0.0e + 00E value 458 Match length 94 % identity NCBI Description metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt] 265682 Seq. No. 9252_4.R1011 Contig ID wyr700240503.hl 5'-most EST BLASTN Method g559535 NCBI GI 142 BLAST score 9.0e-74 E value 475 Match length 93 % identity Z.mays mRNA for metallothionein NCBI Description 265683 Seq. No. 9254 1.R1011 Contig ID LIB3150-066-P2-K1-F8 5'-most EST 265684 Seq. No. 9261_1.R1011 Contig ID LIB84-028-Q1-E1-G10 5'-most EST BLASTX Method g2695931 NCBI GI 574 BLAST score 5.0e-59 E value 177 Match length % identity 71 (AJ222779) hypothetical protein [Hordeum vulgare] NCBI Description 265685 Seq. No. 9268 1.R1011 Contig ID uC-zmflmo17242a11b1 5'-most EST BLASTX Method g584825 NCBI GI 669 BLAST score 6.0e-70 E value Match length 149 % identity 81 B2 PROTEIN >gi 322726 pir_ S32124 B2 protein - carrot NCBI Description >qi 297889 emb CAA51078 (X72385) B2 protein [Daucus carota] 265686 Seq. No. 9268 2.R1011 Contig ID wty700173088.hl 5'-most EST

36918

BLASTX

g584825

Method NCBI GI



```
499
BLAST score
                  4.0e-50
E value
                  117
Match length
                  81
% identity
                  B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot
NCBI Description
                  >gi 297889_emb_CAA51078_ (X72385) B2 protein [Daucus
                  carota]
                   265687
Seq. No.
                   9268 3.R1011
Contig ID
                  uC-zmflmo17240a03a1
5'-most EST
                   BLASTX
Method
                   g584825
NCBI GI
                   238
BLAST score
                   6.0e-20
E value
                   55
Match length
                   80
% identity
                   B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot
NCBI Description
                   >gi 297889_emb_CAA51078_ (X72385) B2 protein [Daucus
                   carota]
                   265688
Seq. No.
                   9268 4.R1011
Contig ID
                   LIB36-002-Q1-E1-A11
5'-most EST
                   BLASTX
Method
                   g584825
NCBI GI
                   615
BLAST score
                   8.0e-64
E value
                   152
Match length
                   74
% identity
                   B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot
NCBI Description
                   >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus
                   carota]
                   265689
Seq. No.
                   9268_5.R1011
Contig ID
5'-most EST
                   uC-zmflb73225b02a1
                   265690
Seq. No.
                   9268 6.R1011
Contig ID
 5'-most EST
                   uC-zmflb73017b01b1
                   BLASTX
Method
                   g584825
NCBI GI
                   336
 BLAST score
                    2.0e-31
 E value
                   74
Match length
                    80
 % identity
                   B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot
 NCBI Description
                    >qi 297889 emb CAA51078 (X72385) B2 protein [Daucus
                    carota]
                    265691
 Seq. No.
                    9269 1.R1011
 Contig ID
                    xsy700214514.h1
 5'-most EST
```

36919

BLASTX

330

g1652297

Method

NCBI GI BLAST score



```
4.0e-30
E value
                   261
Match length
                   36
% identity
NCBI Description (D90904) hypothetical protein [Synechocystis sp.]
                   265692
Seq. No.
                   9273 1.R1011
Contiq ID
                   vux700158019.h1
5'-most EST
                   BLASTX
Method
                   q4544419
NCBI GI
                   468
BLAST score
                   2.0e-46
E value
                   144
Match length
                   65
% identity
                   (AC006955) unknown protein [Arabidopsis thaliana]
NCBI Description
                   265693
Seq. No.
                   9275 2.R1011
Contig ID
                   uC-z\overline{m}flm017214f10b1
5'-most EST
                   BLASTX
Method
                   g4490737
NCBI GI
                   594
BLAST score
                   4.0e-61
E value
                   289
Match length
                   50
% identity
                   (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   265694
                   9275 4.R1011
Contig ID
                   uC-zmflm017209e07b1
5'-most EST
                   BLASTX
Method
                   g4490737
NCBI GI
BLAST score
                   222
                   7.0e-18
E value
                   74
Match length
                   57
% identity
                   (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
                   265695
Seq. No.
                   9275 5.R1011
Contig ID
                   uC-zmflmo17152a11a1
5'-most EST
                   BLASTX
Method
                   q4490737
NCBI GI
                   202
BLAST score
                    1.0e-15
E value
                    51
Match length
                    73
 % identity
                   (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
                    265696
Seq. No.
                    9277 1.R1011
 Contig ID
                    LIB3078-024-Q1-K1-B12
 5'-most EST
Method
                    BLASTX
                    g3264828
 NCBI GI
 BLAST score
                    209
```

36920

2.0e-16

111

E value Match length



% identity (AF072404) cotton fiber expressed protein 1 [Gossypium NCBI Description hirsutum] 265697 Seq. No. 9280 1.R1011 Contig ID wty700168868.h1 5'-most EST BLASTX Method g4240207 NCBI GI 191 BLAST score 4.0e-14 E value Match length 154 29 % identity (AB020666) KIAA0859 protein [Homo sapiens] NCBI Description 265698 Seq. No. 9282 1.R1011 Contig ID LIB3078-024-Q1-K1-B9 5'-most EST 265699 Seq. No. 9287 1.R1011 Contig ID wyr700239494.hl 5'-most EST BLASTX Method g4335719 NCBI GI 194 BLAST score 3.0e-14E value 99 Match length 44 % identity (AC006248) putative RING-H2 finger protein RHG1a NCBI Description [Arabidopsis thaliana] 265700 Seq. No. 9287 2.R1011 Contig ID LIB3069-054-Q1-K1-F1 5'-most EST 265701 Seq. No. 9290 1.R1011 Contig ID LIB3078-024-Q1-K1-B11 5'-most EST 265702 Seq. No. 9293 1.R1011 Contig ID 5'-most EST LIB3078-023-Q1-K1-H7 265703 Seq. No. 9295 1.R1011 Contig ID LIB3078-024-Q1-K1-A1 5'-most EST Seq. No. 265704 9299 1.R1011 Contig ID LIB3059-021-Q1-K1-D9 5'-most EST Method BLASTX q464981 NCBI GI BLAST score 768 8.0e-82 E value Match length 148

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN

94

% identity



LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

265705 Seq. No. Contig ID 9299 3.R1011 5'-most EST LIB3157-019-Q1-K1-E7

Seq. No. 265706

9300 1.R1011 Contig ID 5'-most EST uC-zmflb73038f04b1

Method BLASTX NCBI GI g2500380 BLAST score 508 2.0e-51 E value Match length 105 % identity 88

60S RIBOSOMAL PROTEIN L44 >gi 2119128 pir JC4923 ribosomal NCBI Description protein RL44 - upland cotton >gi_1553129 (U64677) ribosomal

protein L44 isoform a [Gossypium hirsutum] >gi 1553131 (U64678) ribosomal protein L44 isoform b [Gossypium

hirsutum]

Seq. No. 265707

Contig ID 9305 1.R1011

5'-most EST uC-zmflB73045g07b1

Method BLASTX NCBI GI a2497281 BLAST score 426 E value 7.0e-42 Match length 164

% identity 49

TRANSLATION INITIATION FACTOR IF-2 NCBI Description

>gi_1651769_dbj_BAA16696_ (D90900) initiation factor IF-2

[Synechocystis sp.]

265708 Seq. No.

9305 2.R1011 Contig ID 5'-most EST ceu700421777.h1

Method BLASTX q2497281 NCBI GI BLAST score 167 1.0e-11 E value Match length 50 % identity 60

NCBI Description TRANSLATION INITIATION FACTOR IF-2

>qi 1651769 dbj BAA16696 (D90900) initiation factor IF-2

[Synechocystis sp.]

Seq. No. 265709

Contig ID 9309 1.R1011

5'-most EST LIB3078-023-Q1-K1-G2

Method BLASTX NCBI GI q2760606 BLAST score 765 2.0e-81 E value Match length 166 % identity 87

36922



```
(AB001568) phospholipid hydroperoxide glutathione
NCBI Description
                  peroxidase-like protein [Arabidopsis thaliana] >gi_3004869
                  (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis
                  thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500)
                  phospholipid hydroperoxide glutathione peroxidase
                  [Arabidopsis thaliana]
                  265710
Seq. No.
                  9309 2.R1011
Contig ID
                  hbs701182639.hl
5'-most EST
                  BLASTX
Method
                  g4138608
NCBI GI
BLAST score
                  179
                  1.0e-12
E value
                  41
Match length
                  90
% identity
                  (AJ010455) glutathione peroxidase [Triticum aestivum]
NCBI Description
Seq. No.
                   265711
                   9309 3.R1011
Contig ID
                   uwc700150715.hl
5'-most EST
                  BLASTX
Method
                   g1362150
NCBI GI
BLAST score
                   211
                   1.0e-16
E value
                   59
Match length
                   75
% identity
                   hypothetical protein (clone AFN3) - wild oat (fragment)
NCBI Description
                   >gi 726478 (U20000) putative ORF1 [Avena fatua]
                   265712
Seq. No.
                   9310 1.R1011
Contig ID
                   LIB3078-023-Q1-K1-G3
5'-most EST
                   BLASTX
Method
                   g2065019
NCBI GI
                   544
BLAST score
                   2.0e-55
E value
Match length
                   239
% identity
                   45
                   (Y09823) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   265713
Seq. No.
                   9310 2.R1011
Contig ID
                   uC-zmflb73338h11a1
5'-most EST
                   265714
Seq. No.
                   9310 3.R1011
 Contig ID
 5'-most EST
                   fwa700101319.hl
                   265715
 Seq. No.
                   9321 1.R1011
 Contig ID
                   LIB3078-023-Q1-K1-E4
 5'-most EST
```

 Seq. No.
 265716

 Contig ID
 9324 1.R1011

 5'-most EST
 nbm700473576.h1

4.2



```
265717
Seq. No.
                   9325 1.R1011
Contig ID
                   uC-zmroteosinte037c11b1
5'-most EST
Method
                   BLASTX
                   g1524359
NCBI GI
BLAST score
                   270
                   3.0e-23
E value
Match length
                   172
                   37
% identity
NCBI Description (X98090) GTPase [Synechocystis PCC6803]
                   265718
Seq. No.
                   9331 1.R1011
Contig ID
                   xsy700211065.h1
5'-most EST
                   BLASTX
Method
                   g462195
NCBI GI
BLAST score
                   546
                   1.0e-55
E value
Match length
                   115
                   90
% identity
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                   >gi_100682_pir__S21636 GOS2 protein - rice
                   >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                   >gi^{-}37899\overline{50} (\overline{A}F094774) translation initiation factor [Oryza
                   satīva]
                   265719
Seq. No.
Contig ID
                   9331 2.R1011
                   uC-zmflb73173f02b1
5'-most EST
                   265720
Seq. No.
                   9331 5.R1011
Contia ID
                   xmt7\overline{0}0258230.h1
5'-most EST
                   265721
Seq. No.
                   9347 1.R1011
Contig ID
                   LIB3078-023-Q1-K1-D1
5'-most EST
                    265722
Seq. No.
                    9348 1.R1011
Contig ID
                    ypc700800645.hl
5'-most EST
                    BLASTX
Method
                    g1173104
NCBI GI
                    704
BLAST score
                    4.0e-74
E value
                    221
Match length
                    54
% identity
                   RIBONUCLEASE 2 PRECURSOR >gi_289210 (M98336) ribonuclease
NCBI Description
                    [Arabidopsis thaliana] >gi 2642160 (AC003000) ribonuclease,
                    RNS2 [Arabidopsis thaliana]
                    265723
 Seq. No.
                    9348_3.R1011
Contig ID
```

LIB36-022-Q1-E1-G6 5'-most EST

BLASTX Method q1173104 NCBI GI 181 BLAST score

NCBI Description



```
1.0e-27
E value
                   93
Match length
                   60
% identity
                  RIBONUCLEASE 2 PRECURSOR >gi 289210 (M98336) ribonuclease
NCBI Description
                   [Arabidopsis thaliana] >gi 2\overline{6}42160 (AC003000) ribonuclease,
                   RNS2 [Arabidopsis thaliana]
                   265724
Seq. No.
                   9349 1.R1011
Contig ID
                   LIB3078-023-Q1-K1-B7
5'-most EST
                   BLASTX
Method
                   g2183249
NCBI GI
                   358
BLAST score
                   6.0e-34
E value
                   84
Match length
                   80
% identity
                   (AF002211) glutathione-S-transferase [Triticum aestivum]
NCBI Description
                   >gi 4185800 (AF109714) glutathione S-transferase [Triticum
                   aestivum]
                   265725
Seq. No.
                   9354 1.R1011
Contig ID
                   LIB3078-023-Q1-K1-C11
5'-most EST
                   BLASTX
Method
                   q4417288
NCBI GI
BLAST score
                   661
                   4.0e-69
E value
                   168
Match length
                   80
% identity
                   (AC007019) unknown protein [Arabidopsis thaliana]
NCBI Description
                   265726
Seq. No.
                   9357 1.R1011
Contig ID
5'-most EST
                   xmt700257619.h1
                   265727
Seq. No.
Contig ID
                   9359 1.R1011
                   LIB3078-023-Q1-K1-C7
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3861153
BLAST score
                   306
E value
                   1.0e-27
Match length
                   105
                   56
% identity
                   (AJ235272) CYANELLE 50S RIBOSOMAL PROTEIN L20 (rplT)
NCBI Description
                   [Rickettsia prowazekii]
                   265728
Seq. No.
                   9359 2.R1011
Contig ID
                   LIB3079-059-Q1-K1-A11
5'-most EST
                   BLASTX
Method
                   g3861153
NCBI GI
                   209
BLAST score
                   4.0e-16
E value
                   65
Match length
                   62
% identity
```

(AJ235272) CYANELLE 50S RIBOSOMAL PROTEIN L20 (rplT)

BLAST score

E value

163 2.0e-86



[Rickettsia prowazekii]

```
265729
Seq. No.
                   9363 1.R1011
Contig ID
                   uC-z\overline{m}flb73221c11b1
5'-most EST
                   BLASTX
Method
                   q629844
NCBI GI
BLAST score
                   353
                   4.0e-33
E value
Match length
                   113
% identity
                   65
                   heat shock protein hsp70-5 - maize (fragment)
NCBI Description
                   >gi_498775_emb_CAA55184_ (X78415) heat shock protein 70 kDa
                   [Zea mays]
                   265730
Seq. No.
Contig ID
                   9363 3.R1011
5'-most EST
                   dyk700106071.hl
Method
                   BLASTN
                   q498772
NCBI GI
BLAST score
                   263
                   1.0e-146
E value
Match length
                   348
% identity
                   95
                   Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein
NCBI Description
                   265731
Seq. No.
Contig ID
                   9366 1.R1011
                   LIB3068-048-Q1-K1-D11
5'-most EST
                   BLASTN
Method
                   q551482
NCBI GI
                   470
BLAST score
                   0.0e+00
E value
                   667
Match length
                   96
% identity
                   Zea mays ABA- and ripening-inducible-like protein mRNA,
NCBI Description
                   complete cds
                   265732
Seq. No.
                   9366 2.R1011
Contig ID
                   pwr700450215.hl
5'-most EST
                   BLASTN
Method
                   g2773153
NCBI GI
BLAST score
                   202
                   1.0e-109
E value
                   278
Match length
                   93
% identity
                   Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                    (Asr1) mRNA, complete cds
                   265733
Seq. No.
                   9366 3.R1011
Contig ID
5'-most EST
                   wyr700242849.hl
                   BLASTN
Method
                   g551482
NCBI GI
```



```
285
Match length
% identity
                  Zea mays ABA- and ripening-inducible-like protein mRNA,
NCBI Description
                  complete cds
                   265734
Seq. No.
                   9366 5.R1011
Contig ID
                   gct7\overline{0}1173880.h1
5'-most EST
                   BLASTN
Method
                   g551482
NCBI GI
                   215
BLAST score
                   1.0e-117
E value
                   280
Match length
                   95
% identity
                   Zea mays ABA- and ripening-inducible-like protein mRNA,
NCBI Description
                   complete cds
                   265735
Seq. No.
                   9366 6.R1011
Contig ID
                   LIB3078-047-Q1-K1-E4
5'-most EST
                   BLASTX
Method
                   g2773154
NCBI GI
                   188
BLAST score
                   8.0e-14
E value
                   88
Match length
                   44
% identity
                   (AF039573) abscisic acid- and stress-inducible protein
NCBI Description
                   [Oryza sativa]
                   265736
Seq. No.
                   9366 7.R1011
Contig ID
                   LIB3068-061-Q1-K1-C6
5'-most EST
Method
                   BLASTN
                   q551482
NCBI GI
                   120
BLAST score
E value
                   7.0e-61
Match length
                   170
                   98
% identity
                   Zea mays ABA- and ripening-inducible-like protein mRNA,
NCBI Description
                   complete cds
                   265737
Seq. No.
                   9366 8.R1011
Contig ID
                   zla700379694.h1
5'-most EST
                   265738
Seq. No.
Contig ID
                   9366 9.R1011
                   arm700460788.hl
5'-most EST
                   BLASTN
Method
                   g551482
NCBI GI
                   176
BLAST score
                    3.0e - 94
E value
                    346
Match length
                    92
 % identity
                   Zea mays ABA- and ripening-inducible-like protein mRNA,
NCBI Description
```

complete cds



265739 Seq. No. 9370 1.R1011 Contig ID xsy700207602.hl 5'-most EST BLASTX Method NCBI GI q3122234 BLAST score 1130 1.0e-124 E value Match length 272 % identity 82 EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT NCBI Description (EIF-2-BETA) (P38) >gi 2306768 (U87163) eIF-2 beta subunit [Triticum aestivum] 265740 Seq. No. 9372 1.R1011 Contig ID 5'-most EST LIB3078-023-Q1-K1-A12 Method BLASTX NCBI GI q4467098 523 BLAST score 3.0e-53 E value 152 Match length % identity 68 (AL035538) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 265741 9374 1.R1011 Contig ID 5'-most EST LIB143-022-Q1-E1-B8 Method BLASTX g3204108 NCBI GI BLAST score 731 E value 2.0e-77 Match length 181 % identity 77 (AJ006764) putative deoxycytidylate deaminase [Cicer NCBI Description arietinum] 265742 Seq. No. 9374 2.R1011 Contig ID 5'-most EST $wty7\overline{0}0166330.h1$ BLASTX Method NCBI GI g3204108 BLAST score 375 E value 5.0e-36 Match length 89 % identity NCBI Description (AJ006764) putative deoxycytidylate deaminase [Cicer arietinum] 265743 Seq. No. 9374 3.R1011 Contig ID 5'-most EST wty700171206.h1 Method BLASTX

Method BLASTX
NCBI GI g3204108
BLAST score 209
E value 8.0e-17
Match length 45
% identity 87



NCBI Description (AJ006764) putative deoxycytidylate deaminase [Cicer arietinum]

Seq. No. 265744 Contig ID 9379_1.R1011

5'-most EST uC-zmflb73011h07b1

Method BLASTX
NCBI GI g2262105
BLAST score 673
E value 2.0e-99
Match length 373

% identity 48

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 265745

Contig ID 9382_1.R1011

5'-most EST LIB189-019-Q1-E1-E10

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 2.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 265746

Contig ID 9382_2.R1011

5'-most EST LIB3116-006-Q1-K1-A8

Seq. No. 265747

Contig ID 9385 1.R1011

5'-most EST LIB3078-023-Q1-K1-A10

Method BLASTX
NCBI GI g2827663
BLAST score 193
E value 1.0e-14
Match length 136
% identity 12

NCBI Description (AL021637) membrane-associated salt-inducible-like protein

[Arabidopsis thaliana]

Seq. No. 265748 Contig ID 9401 1.R1011

5'-most EST LIB3088-007-Q1-K1-E5

Method BLASTX
NCBI GI g3953459
BLAST score 180
E value 2.0e-23
Match length 93
% identity 60

NCBI Description (AC002328) F20N2.4 [Arabidopsis thaliana]

Seq. No. 265750

36929



```
9403 1.R1011
Contig ID
                  LIB3066-003-Q1-K1-B11
5'-most EST
                  BLASTX
Method
                  q4103324
NCBI GI
                   763
BLAST score
                   5.0e-81
E value
                   161
Match length
                   87
% identity
                   (AF022716) GDP-mannose pyrophosphorylase [Solanum
NCBI Description
                   tuberosum]
Seq. No.
                   265751
                   9403 2.R1011
Contig ID
                   LIB3061-001-Q1-K2-G8
5'-most EST
                   BLASTX
Method
                   g2642159
NCBI GI
                   1189
BLAST score
                   1.0e-131
E value
                   264
Match length
% identity
                   (AC003000) putative mannose-1-phosphate guanyltransferase
NCBI Description
                   [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose
                   pyrophosphorylase [Arabidopsis thaliana] >gi_4151925
                   (AF108660) CYT1 protein [Arabidopsis thaliana]
                   265752
Seq. No.
                   9403 3.R1011
Contig ID
                   LIB3078-022-Q1-K1-E3
5'-most EST
Method
                   BLASTX
                   g4103324
NCBI GI
                   253
BLAST score
                   1.0e-21
E value
                   49
Match length
                   96
% identity
                   (AF022716) GDP-mannose pyrophosphorylase [Solanum
NCBI Description
                   tuberosum]
                   265753
 Seq. No.
                   9404 1.R1011
 Contig ID
                   LIB148-009-Q1-E1-F7
 5'-most EST
                   BLASTX
 Method
                   g3122858
 NCBI GI
                   1744
 BLAST score
                    0.0e + 00
 E value
                    466
 Match length
                    73
 % identity
                   D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR
 NCBI Description
                    >gi_2189964_dbj_BAA20405_ (AB003280) Phosphoglycerate
```

dehydrogenase [Arabidopsis thaliana]

>gi 2804258 dbj BAA24440 (AB010407) phosphoglycerate

dehydrogenase [Arabidopsis thaliana]

265754 Seq. No. 9404 3.R1011 Contig ID

uC-zmroteosinte019d04b1 5'-most EST

BLASTX Method g3122858 NCBI GI



BLAST score 340 1.0e-31 E value 89 Match length 76 % identity

D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR NCBI Description

>gi_2189964_dbj_BAA20405_ (AB003280) Phosphoglycerate

dehydrogenase [Arabidopsis thaliana]

>gi_2804258_dbj_BAA24440_ (AB010407) phosphoglycerate

dehydrogenase [Arabidopsis thaliana]

265755 Seq. No. 9404 6.R1011 Contig ID uwc700151208.hl 5'-most EST

265756 Seq. No. 9410 1.R1011 Contig ID $rv17\overline{0}0456739.h1$ 5'-most EST

BLASTX Method g4586038 NCBI GI BLAST score 659 5.0e-69 E value 159 Match length

76 % identity (AC007109) putative heat shock protein [Arabidopsis NCBI Description

thaliana]

265757 Seq. No.

9410_2.R1011 Contig ID

LIB3078-022-Q1-K1-C4 5'-most EST

BLASTX Method q2842490 NCBI GI 222 BLAST score 5.0e-18 E value 59 Match length

69 % identity

NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]

265758 Seq. No.

9411 1.R1011 Contig ID

LIB3279-055-P1-K1-F10 5'-most EST

265759 Seq. No.

9412_1.R1011 Contig ID

LIB3069-034-Q1-K1-F6 5'-most EST

BLASTN Method g4138731 NCBI GI 1417 BLAST score 0.0e + 00E value 1421 Match length 100 % identity

NCBI Description Zea mays mRNA for proline-rich protein

265760 Seq. No.

9412 2.R1011 Contig ID

LIB3078-052-Q1-K1-H12 5'-most EST

BLASTN Method g4138731 NCBI GI

5'-most EST

```
BLAST score
                   357
                   0.0e + 00
E value
                   541
Match length
                   31
% identity
NCBI Description Zea mays mRNA for proline-rich protein
                   265761
Seq. No.
                   9415 1.R1011
Contig ID
                   uC-zmflmo17202c11b1
5'-most EST
                   BLASTX
Method
                   g4105798
NCBI GI
                   979
BLAST score
                   1.0e-106
E value
Match length
                   263
                   59
% identity
                  (AF049930) PGP237-11 [Petunia x hybrida]
NCBI Description
                   265762
Seq. No.
                   9415 2.R1011
Contig ID
                   uC-zmflmo17160h07b1
5'-most EST
                   265763
Seq. No.
                   9415_3.R1011
Contig ID
                   uC-zmflmo17065g04b1
5'-most EST
                   265764
Seq. No.
                   9415 4.R1011
Contig ID
                   uC-z\overline{m}flb73051f09a2
5'-most EST
                   265765
Seq. No.
                   9415 6.R1011
Contig ID
                   LIB3180-021-P2-M1-C12
5'-most EST
                   BLASTX
Method
                   g4105798
NCBI GI
                   274
BLAST score
                   5.0e-24
E value
Match length
                   76
% identity
                   57
                   (AF049930) PGP237-11 [Petunia x hybrida]
NCBI Description
                   265766
Seq. No.
                   9416 1.R1011
Contig ID
                   uC-zmflMo17007f12b1
5'-most EST
                   BLASTX
Method
                   q4587518
NCBI GI
                   1680
BLAST score
E value
                   0.0e + 00
Match length
                   409
                   79
% identity
                   (AC007060) Strong similarity to F19I3.8 gi_3033381 putative
NCBI Description
                   UDP-galactose-4-epimerase from Arabidopsis thaliana BAC
                   gb AC004238 and is a member of PF_01370 the NAD dependent
                   epimerase/dehydratase family. EST gb_AA59
                   265767
Seq. No.
                   9424 1.R1011
Contig ID
```

36932

LIB3078-022-Q1-K1-B10

Method

BLASTX



```
265768
Seq. No.
                  9425 1.R1011
Contig ID
                  LIB3079-056-Q1-K1-D1
5'-most EST
Method
                  BLASTX
                  g4204372
NCBI GI
                  345
BLAST score
E value
                  3.0e-32
Match length
                  111
% identity
                  68
NCBI Description (U62748) acidic ribosomal protein P2a-2 [Zea mays]
Seq. No.
                  265769
                  9425 2.R1011
Contig ID
                  LIB3068-012-Q1-K1-F3
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1173073
BLAST score
                  358
E value
                  1.0e-33
Match length
                  112
% identity
                  69
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P2 >gi_1076787_pir__S54179
                  acidic ribosomal protein 60S - maize
                  >gi_2130117_pir__S65781 acidic ribosomal protein P2 - maize
                  >gi 790508 emb CAA60251 (X86553) 60S acidic ribosomal
                  protein [Zea mays]
Seq. No.
                  265770
                  9425 3.R1011
Contig ID
5'-most EST
                  LIB3059-046-Q1-K1-B10
Method
                  BLASTX
NCBI GI
                  g4204372
BLAST score
                  361
E value
                  4.0e-34
Match length
                  112
                  70
% identity
NCBI Description (U62748) acidic ribosomal protein P2a-2 [Zea mays]
                  265771
Seq. No.
Contig ID
                  9425 4.R1011
5'-most EST
                  LIB143-032-Q1-E1-B8
Method
                  BLASTX
NCBI GI
                  g1173073
BLAST score
                  350
                  5.0e-33
E value
Match length
                  113
% identity
                  69
                  60S ACIDIC RIBOSOMAL PROTEIN P2 >gi 1076787 pir S54179
NCBI Description
                  acidic ribosomal protein 60S - maize
                  >gi 2130117 pir S65781 acidic ribosomal protein P2 - maize
                  >gi_790508_emb_CAA60251_ (X86553) 60S acidic ribosomal
                  protein [Zea mays]
                  265772
Seq. No.
Contig ID
                  9425 5.R1011
5'-most EST
                  pmx700086942.h1
```

```
q4204372
NCBI GI
                   358
BLAST score
E value
                   1.0e-33
Match length
                   112
                   69
% identity
                  (U62748) acidic ribosomal protein P2a-2 [Zea mays]
NCBI Description
                   265773
Seq. No.
                   9425 6.R1011
Contig ID
5'-most EST
                   xdb7\overline{0}0341544.h1
                   BLASTN
Method
NCBI GI
                   g4204375
BLAST score
                   167
                   5.0e-89
E value
Match length
                   307
                   98
% identity
NCBI Description
                  Zea mays acidic ribosomal protein P2a-4 (rpp2a-4) mRNA,
                  partial cds
Seq. No.
                   265774
                   9425 7.R1011
Contig ID
                   ypc700802718.h1
5'-most EST
Method
                   BLASTN
NCBI GI
                   g899609
BLAST score
                   166
                   2.0e-88
E value
Match length
                   261
                   94
% identity
                  Zea mays acidic ribosomal protein P2 (RPA-2A1) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   265775
Contig ID
                   9425 10.R1011
5'-most EST
                   dyk700104103.h1
Method
                   BLASTN
                   g4204373
NCBI GI
BLAST score
                   230
E value
                   1.0e-126
                   359
Match length
                   92
% identity
                  Zea mays acidic ribosomal protein P2a-3 (rpp2a-3) mRNA,
NCBI Description
                   partial cds
Seq. No.
                   265776
Contig ID
                   9425 14.R1011
5'-most EST
                   cjh700193704.h1
Method
                   BLASTX
NCBI GI
                   g899610
BLAST score
                   286
                   7.0e-26
E value
Match length
                   70
% identity
                   83
NCBI Description
                  (U29383) acidic ribosomal protein P2 [Zea mays]
```

36934

265777

9440 1.R1011

LIB3060-035-Q1-K1-E8

Seq. No. Contig ID

5'-most EST



265778 Seq. No. 9446 1.R1011 Contig ID 5'-most EST LIB3078-022-Q1-K1-A6 Method BLASTX g2286121 NCBI GI 499 BLAST score 3.0e-50 E value Match length 125 74 % identity NCBI Description (U88068) sec14 like protein [Oryza sativa] Seq. No. 265779 9446 2.R1011 Contig ID uC-zmf1b73184h11a1 5'-most EST BLASTX Method NCBI GI g2286121 BLAST score 627 E value 2.0e-65 Match length 186 66 % identity NCBI Description (U88068) sec14 like protein [Oryza sativa] 265780 Seq. No. 9446 3.R1011 Contig ID 5'-most EST uer700580134.h1 265781 Seq. No. 9448 1.R1011 Contig ID 5'-most EST LIB3078-020-Q1-K1-H1 Seq. No. 265782 Contig ID 9449 1.R1011 5'-most EST uer700578783.h1 Method BLASTX NCBI GI q4584358 778 BLAST score E value 9.0e-83 Match length 212 % identity 77 NCBI Description (AC006420) unknown protein [Arabidopsis thaliana] Seq. No. 265783 Contig ID 9449 2.R1011 5'-most EST LIB3066-006-Q1-K1-G1 Method BLASTX q4584358 NCBI GI BLAST score 342 4.0e-32 E value Match length 89 % identity 80

Seq. No. 265784

NCBI Description

Contig ID 9450_1.R1011

5'-most EST uC-zmflb73202d01b1

36935

(AC006420) unknown protein [Arabidopsis thaliana]



```
265785
Seq. No.
                  9452 1.R1011
Contig ID
                  LIB3116-026-P1-K2-A2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4584429
BLAST score
                  299
                  5.0e-27
E value
                  78
Match length
                  69
% identity
NCBI Description (AJ237751) aquaglyceroporin [Nicotiana tabacum]
                  265786
Seq. No.
                  9455 1.R1011
Contig ID
                  LIB3078-020-Q1-K1-H7
5'-most EST
Method
                  BLASTX
                  q4406384
NCBI GI
BLAST score
                  224
                  4.0e-18
E value
Match length
                  66
% identity
NCBI Description (AF112303) serine acetyltransferase [Arabidopsis thaliana]
Seq. No.
                  265787
                  9456 1.R1011
Contig ID
                  rv1700457354.h1
5'-most EST
Method
                  BLASTX
                  q4585987
NCBI GI
BLAST score
                  308
                  2.0e-36
E value
Match length
                  131
% identity
                  65
NCBI Description (AC005287) Similar to nucleolar protein [Arabidopsis
                  thaliana]
Seq. No.
                  265788
Contig ID
                  9466 1.R1011
5'-most EST
                  LIB3062-059-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  g2281107
BLAST score
                  197
                  1.0e-14
E value
                  97
Match length
                  37
% identity
NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]
                  265789
Seq. No.
                  9470 1.R1011
Contig ID
                  LIB143-013-Q1-E1-F11
5'-most EST
Method
                  BLASTX
                  q1174783
NCBI GI
BLAST score
                  1276
E value
                  1.0e-149
Match length
                  346
                  79
% identity
                 TRYPTOPHAN SYNTHASE ALPHA CHAIN PRECURSOR
NCBI Description
```

>gi_1362207_pir__S56665 tryptophan synthase (EC 4.2.1.20)
alpha chain - maize >gi 440171 emb CAA54131 (X76713)



tryptophan synthase, alpha subunit [Zea mays]

```
265790
Seq. No.
                   9470 2.R1011
Contig ID
5'-most EST
                   tfd700576604.h1
                   BLASTX
Method
                   g3878801
NCBI GI
                   156
BLAST score
                   4.0e-10
E value
                   61
Match length
                   48
% identity
                   (Z48795) weak similarity with honeybee ATP synthase A chain
NCBI Description
                   (Swiss Prot accession number Q00275) [Caenorhabditis
                   elegans]
                   265791
Seq. No.
                   9470 5.R1011
Contig ID
                   uC-zmflb73107b11a2
5'-most EST
                   265792
Seq. No.
                   9470 6.R1011
Contig ID
                   ymt7\overline{0}0219594.h1
5'-most EST
                   265793
Seq. No.
                   9470 11.R1011
Contig ID
                   LIB3<del>1</del>37-008-Q1-K1-D4
5'-most EST
                   BLASTN
Method
NCBI GI
                   g440170
                   144
BLAST score
                   3.0e-75
E value
                   282
Match length
                   97
% identity
                   Z.mays (C6000237) trpA gene
NCBI Description
                   265794
Seq. No.
                   9472_1.R1011
Contig ID
5'-most EST
                   xmt700264220.h1
Method
                   BLASTX
                   q2388578
NCBI GI
                    429
BLAST score
                    3.0e-42
E value
                    141
Match length
                    61
% identity
                    (AC000098) Similar to Mycobacterium RlpF (gb_Z84395). ESTs
NCBI Description
                    gb_T75785,gb_R30580,gb_T04698 come from this gene.
                    [Arabidopsis thaliana]
                    265795
Seq. No.
Contig ID
                    9473 1.R1011
                    LIB189-008-Q1-E1-G8
 5'-most EST
                    265796
 Seq. No.
                    9473 2.R1011
 Contig ID
                    LIB84-026-Q1-E1-A7
 5'-most EST
```

36937

265797

9476 1.R1011

Seq. No. Contig ID



pmx700085387.h1 5'-most EST BLASTX Method g913141 NCBI GI BLAST score 1048 1.0e-114 E value Match length 321 64 % identity ARK3 product/receptor-like serine/threonine protein kinase NCBI Description ARK3 [Arabidopsis thaliana, Columbia, Peptide, 851 aa] 265798 Seq. No. 9477 1.R1011 Contig ID LIB3066-034-Q1-K1-C9 5'-most EST BLASTX Method q3047082 NCBI GI 755 BLAST score 8.0e-80 E value 370 Match length 65 % identity (AF058914) similar to Vigna radiata pectinacetylesterase NCBI Description precursor (GB:X99348) [Arabidopsis thaliana] 265799 Seq. No. 9477 2.R1011 Contig ID uwc $7\overline{0}0152928.h1$ 5'-most EST BLASTX Method q3482930 NCBI GI BLAST score 483 1.0e-54 E value Match length 172 59 % identity (AC003970) Similar to pectinacetylesterase [Arabidopsis NCBI Description thaliana] 265800 Seq. No. 9480 1.R1011 Contig ID uC-zmf1b73241b02b25'-most EST Seq. No. 265801 9481 1.R1011 Contig ID LIB3078-020-Q1-K1-E8 5'-most EST BLASTX Method g1575752 NCBI GI 251 BLAST score 2.0e-21 E value 91 Match length 47 % identity (U70672) glutathione S-transferase [Arabidopsis thaliana] NCBI Description 265802 Seq. No. 9482 1.R1011 Contig ID LIB3078-020-Q1-K1-F1 5'-most EST BLASTX Method g4539333 NCBI GI 530 BLAST score

8.0e-54

194

E value

Match length



% identity 54

NCBI Description (AL035539) putative amino acid transport protein

[Arabidopsis thaliana]

Seq. No. 265803

Contig ID 9491_1.R1011

5'-most EST LIB3078-020-Q1-K1-D11

Seq. No. 265804

Contig ID 9502 1.R1011

5'-most EST LIB143-050-Q1-E1-E12

Method BLASTX
NCBI GI g3157910
BLAST score 1908
E value 0.0e+00
Match length 425
% identity 89

NCBI Description (AF003551) lysine-ketoglutarate reductase/saccharopine

dehydrogenase bifunctional enzyme [Zea mays]

Seq. No. 265805

Contig ID 9502 2.R1011

5'-most EST wyr700239496.h1

Method BLASTX
NCBI GI g4099847
RLAST score 360

BLAST score 360 E value 4.0e-34 Match length 106 % identity 63

NCBI Description (U90523) saccharopine dehydrogenase [Arabidopsis thaliana]

Seq. No. 265806

Contig ID 9505 1.R1011

5'-most EST LIB189-007-Q1-E1-A3

Method BLASTX
NCBI GI g400890
BLAST score 327
E value 3.0e-30
Match length 72
% identity 44

NCBI Description PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR

>gi_282837_pir__S26953 photosystem II 22K protein precursor
- spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of
PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864)
photosystem II 22 kda polypeptide [spinach, Peptide, 274

aa] [Spinacia oleracea]

Seq. No. 265807

Contig ID 9505 2.R1011

5'-most EST LIB84-026-Q1-E1-D12

Method BLASTX
NCBI GI g1304215
BLAST score 370
E value 3.0e-35
Match length 83
% identity 42

NCBI Description (D84392) precursor of rice 22 kDa protein of photosystem II



(PSII-S) [Oryza sativa]

```
265808
Seq. No.
                   9505 3.R1011
Contig ID
                   uC-z\overline{m}flmo17141e07a1
5'-most EST
                   BLASTX
Method
                   g1304215
NCBI GI
BLAST score
                   352
                   1.0e-37
E value
Match length
                   146
                   48
% identity
                   (D84392) precursor of rice 22 kDa protein of photosystem II
NCBI Description
                    (PSII-S) [Oryza sativa]
                   265809
Seq. No.
                   9506 1.R1011
Contig ID
                   LIB3078-020-Q1-K1-C1
5'-most EST
Seq. No.
                   265810
                    9509 1.R1011
Contig ID
                    ceu700423412.h1
5'-most EST
                    265811
Seq. No.
                    9516 1.R1011
Contig ID
                    LIB3066-028-Q1-K1-F5
5'-most EST
                    BLASTX
Method
                    g113377
NCBI GI
                    1884
BLAST score
                    0.0e + 00
E value
Match length
                    378
                    95
% identity
                    ALCOHOL DEHYDROGENASE 2 >gi_82671_pir__A23084 alcohol dehydrogenase (EC 1.1.1.1) \overline{2} - maize
NCBI Description
                    >gi_22137_emb_CAA26001_ (X01965) Adh2-N (aa 1-379) [Zea
                    mays]
                    265812
Seq. No.
                    9527 1.R1011
Contig ID
                    LIB3078-019-Q1-K1-F4
 5'-most EST
                    BLASTX
Method
                    g1483177
NCBI GI
                    339
 BLAST score
                    2.0e-31
 E value
                    165
 Match length
                    44
 % identity
                    (D86598) antifreeze-like protein (af70) [Picea abies]
 NCBI Description
                    265813
 Seq. No.
                    9529 1.R1011
 Contig ID
                    LIB3078-019-Q1-K1-F7
 5'-most EST
                    BLASTX
 Method
                    q1653655
 NCBI GI
                     316
 BLAST score
                     1.0e-28
 E value
 Match length
                     173
 % identity
 NCBI Description (D90915) ATP-dependent Clp protease proteolytic subunit
```



[Synechocystis sp.]

```
265814
Seq. No.
                  9534 1.R1011
Contig ID
                  ntr700074216.hl
5'-most EST
                  265815
Seq. No.
Contig ID
                   9539 1.R1011
                  uC-zmflmo17211c02a1
5'-most EST
                  BLASTX
Method
                   g416681
NCBI GI
                   148
BLAST score
                   4.0e-09
E value
                   71
Match length
                   38
% identity
                  ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_280404_pir__S26198 H+-transporting ATP synthase (EC
                   3.6.1.34) delta chain precursor, chloroplast - common
                   tobacco >gi_19787_emb_CAA45153_ (X63607) chloroplast ATP
                   synthase (delta subunit) [Nicotiana tabacum]
                   265816
Seq. No.
                   9541 1.R1011
Contig ID
                   LIB189-025-Q1-E1-D7
5'-most EST
                   BLASTX
Method
                   q4490292
NCBI GI
                   827
BLAST score
                   1.0e-88
E value
Match length
                   218
% identity
                   73
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
                   265817
Seq. No.
                   9541 2.R1011
Contig ID
                   uC-zmflb73379c05a1
 5'-most EST
                   BLASTX
Method
                   g4490292
NCBI GI
                   233
 BLAST score
                   3.0e-19
 E value
                   67
 Match length
                   61
 % identity
                   (AL035678) putative protein [Arabidopsis thaliana]
 NCBI Description
                   265818
 Seq. No.
                   9542 1.R1011
 Contig ID
                   LIB3078-019-Q1-K1-E2
 5'-most EST
                   BLASTX
 Method
                   g2495209
 NCBI GI
                   360
 BLAST score
                   8.0e-34
 E value
                   103
 Match length
                    61
 % identity
                   HYPOTHETICAL 12.9 KD PROTEIN SLR1417
 NCBI Description
                   >gi_1651819_dbj_BAA16746_ (D90900) hypothetical protein
```

Seq. No. 265819

[Synechocystis sp.]



9542 2.R1011 Contig ID

LIB3068-008-Q1-K1-F11 5'-most EST

BLASTX Method g1723388 NCBI GI BLAST score 186 E value 1.0e-13 42 Match length 74 % identity

HYPOTHETICAL 12.4 KD PROTEIN IN APCF-RPS4 INTERGENIC REGION NCBI Description

(ORF114) >gi 2147501 pir S73138 hypothetical protein 114 -Porphyra purpurea chloroplast >gi 1276683 (U38804) ORF114

[Porphyra purpurea]

265820 Seq. No.

Contig ID 9544 1.R1011

5'-most EST uC-zmflmo17127q08b1

Method BLASTX NCBI GI q4490733 BLAST score 182 7.0e-13 E value Match length 181 22 % identity

NCBI Description (AL035709) putative protein [Arabidopsis thaliana]

Seq. No. 265821 Contig ID 9544 2.R1011

5'-most EST uC-zmflb73100e09b1

Seq. No. 265822

Contig ID 9554 1.R1011

5'-most EST uC-zmflmo17241g12b1

Method BLASTX NCBI GI g3953471 BLAST score 1025 E value 1.0e-111 Match length 308

% identity 63

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No. 265823

Contig ID 9554 2.R1011

5'-most EST uC-zmroteosinte007c05b1

Method BLASTX q3953471 NCBI GI BLAST score 312 E value 2.0e-28 Match length 152 64 % identity

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No. 265824

9554 3.R1011 Contig ID

uC-zmf1b73031h07b1 5'-most EST

Method BLASTX NCBI GI g3953471 BLAST score 503 E value 1.0e-50

Match length 135 % identity 65 NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana] Seq. No. 265825 9557 1.R1011 Contig ID LIB3078-019-Q1-K1-C9 5'-most EST Method BLASTX a2501011 NCBI GI BLAST score 299 7.0e-27 E value Match length 200 % identity 41 ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS) NCBI Description >gi 1652625 dbj BAA17545 (D90907) isoleucyl-tRNA synthetase [Synechocystis sp.] Seq. No. 265826 9559 1.R1011 Contig ID xsy700217146.hl 5'-most EST Method BLASTX NCBI GI g1778093 728 BLAST score 1.0e-112 E value Match length 422 % identity 51 NCBI Description (U64902) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris] Seq. No. 265827 Contig ID 9563 1.R1011 5'-most EST LIB3061-027-Q1-K1-C6 Seq. No. 265828 Contig ID 9565 2.R1011 5'-most EST LIB3137-008-Q1-K1-B8 Method BLASTX NCBI GI g4186184 BLAST score 244 E value 1.0e-20 Match length 132 % identity 40 NCBI Description (AF111168) unknown [Homo sapiens] 265829 Seq. No. Contig ID 9565 3.R1011 5'-most EST LIB3137-017-Q1-K1-B12 Method BLASTX q4186184 NCBI GI BLAST score 238 E value 7.0e-20 Match length 118 % identity 46

Seq. No. 265830

NCBI Description

36943

(AF111168) unknown [Homo sapiens]



```
9572 1.R1011
Contig ID
5'-most EST
                  uer700577701.hl
Seq. No.
                  265831
                  9585 1.R1011
Contig ID
5'-most EST
                  xdb700339956.h1
                  BLASTX
Method
NCBI GI
                  g2494041
BLAST score
                  223
E value
                  6.0e-18
Match length
                  85
% identity
                  49
NCBI Description
                  DIAMINOPIMELATE EPIMERASE >qi 1653875 dbj BAA18785
                  (D90917) diaminopimelate epimerase [Synechocystis sp.]
Seq. No.
                  265832
Contig ID
                  9585 2.R1011
5'-most EST
                  qmh700028724.f1
Method
                  BLASTX
NCBI GI
                  g2494041
BLAST score
                  587
                  3.0e-68
E value
Match length
                  221
% identity
                  62
                  DIAMINOPIMELATE EPIMERASE >gi 1653875 dbj BAA18785
NCBI Description
                  (D90917) diaminopimelate epimerase [Synechocystis sp.]
Seq. No.
                  265833
                  9586 1.R1011
Contig ID
5'-most EST
                  uC-zmroteosinte120g07b1
Method
                  BLASTX
NCBI GI
                  q4586049
BLAST score
                  936
E value
                  1.0e-111
Match length
                  306
% identity
NCBI Description (AC007020) hypothetical protein [Arabidopsis thaliana]
                  265834
Seq. No.
                  9586 2.R1011
Contig ID
5'-most EST
                  uC-zmflb73112h01a1
Seq. No.
                  265835
Contig ID
                  9587 1.R1011
5'-most EST
                  LIB3078-001-Q1-K1-C2
Seq. No.
                  265836
                  9590 1.R1011
Contig ID
5'-most EST
                  wyr700240996.hl
Method
                  BLASTX
NCBI GI
                  g2492741
BLAST score
                  169
E value
                  1.0e-11
Match length
                  89
% identity
                  43
                  ESTRADIOL 17 BETA-DEHYDROGENASE 4 (17-BETA-HSD 4)
NCBI Description
```

(17-BETA-HYDROXYSTEROID DEHYDROGENASE 4) (HSD IV)



>gi_1881831_bbs_179863 (S83279) 17 beta-hydroxysteroid
dehydrogenase type IV, HSD IV=peroxisome
proliferator-inducible [rats, F344, liver, Peptide, 735 aa]
[Rattus sp.]

Seq. No. 265837

Contig ID 9591_1.R1011

5'-most EST LIB3180-001-P1-M1-H4

Method BLASTX

NCBI GI 94454032

BLAST score 835

E value 2.0e-89

E value 2.0e-Match length 246 % identity 64

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 265838

Contig ID 9591_3.R1011

5'-most EST LIB3157-004-Q1-K1-F5

Method BLASTX
NCBI GI 94454032
BLAST score 176
E value 9.0e-13
Match length 48
% identity 73

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 265839

Contig ID 9591_4.R1011 5'-most EST nwy700447128.h1

Method BLASTX
NCBI GI 94454032
BLAST score 322
E value 7.0e-30
Match length 107
% identity 56

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 265840

Contig ID 9591_5.R1011 5'-most EST dyk700103184.h1

Method BLASTX
NCBI GI g4454032
BLAST score 221
E value 4.0e-18
Match length 59
% identity 64

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 265841

Contig ID 9593_1.R1011

5'-most EST LIB3059-022-Q1-K1-H1

Method BLASTX
NCBI GI g421941
BLAST score 768
E value 1.0e-81
Match length 189



% identity
NCBI Description

GTP-binding protein, ras-related - common tobacco
>gi_296878_emb_CAA50609_ (X71609) ras-related GTP-binding
protein [Nicotiana tabacum]

Seq. No.

265842
Contig ID
9593_2.R1011
5'-most EST

UC-zmflmo17040f03a1

Seq. No.

265843

Contig ID 9593_4.R1011 5'-most EST uC-zmflmo17103a12b1

 Seq. No.
 265844

 Contig ID
 9595_1.R1011

 5'-most EST
 LIB3078-001-Q1-K1-D5

265845

Contig ID 9596_1.R1011
5'-most EST uC-zmflb73012b04b1
Method BLASTX
NCBI GI g3402282
BLAST score 177
E value 5.0e-12
Match length 110
% identity 37

Seq. No.

% identity 37 NCBI Description (AJ000997) proline-rich protein [Solanum tuberosum]

 Seq. No.
 265846

 Contig ID
 9606_1.R1011

 5'-most EST
 fwa700101189.h1

 Method
 BLASTX

 NCBI GI
 g2499535

 BLAST score
 1164

 E value
 1.0e-128

BLAST score 1164 E value 1.0e-128 Match length 282 % identity 79 NCBI Description 2-080GLUI

NCBI Description 2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi_595681 (U13238) 2-oxoglutarate/malate translocator [Spinacia

oleracea]

Seq. No. 265847 Contig ID 9607_1.R1011 5'-most EST wyr700237382.h1

Method BLASTX
NCBI GI g3786001
BLAST score 643
E value 4.0e-67
Match length 171
% identity 68

NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

 Seq. No.
 265848

 Contig ID
 9609_1.R1011

 5'-most EST
 uwc700150214.h1

Method BLASTX NCBI GI g4585977

```
493
BLAST score
                  6.0e-49
E value
                  178
Match length
% identity
                  53
NCBI Description
                  (AC005287) Unknown protein [Arabidopsis thaliana]
                  265849
Seq. No.
                  9609 2.R1011
Contig ID
5'-most EST
                  uC-zmroteosinte048e08b1
                  BLASTX
Method
                  g3367576
NCBI GI
BLAST score
                  333
E value
                  2.0e-30
Match length
                  103
                  55
% identity
NCBI Description (AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]
                  265850
Seq. No.
Contig ID
                  9609 3.R1011
5'-most EST
                  tfd700572581.h1
                  265851
Seq. No.
Contig ID
                  9609 4.R1011
5'-most EST
                  yyf700348318.h1
                  265852
Seq. No.
                  9609 5.R1011
Contig ID
5'-most EST
                  tzu700204493.hl
                  265853
Seq. No.
                  9614 1.R1011
Contig ID
5'-most EST
                  LIB3159-006-Q1-K1-A2
Method
                  BLASTX
NCBI GI
                  q2244904
BLAST score
                  328
E value
                  1.0e-29
Match length
                  436
                  19
% identity
                  (Z97339) similar to hypothetical protein C02F5.7 - Caenorha
NCBI Description
                  [Arabidopsis thaliana]
                  265854
Seq. No.
                  9622 1.R1011
Contig ID
                  uC-zmflmo170114f07b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q113742
BLAST score
                  668
                  1.0e-69
E value
Match length
                  419
                  37
% identity
NCBI Description
                  AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE)
                  >gi 147142 (M15273) peptidase N [Escherichia coli]
                  >gi 147144 (M15676) aminopeptidase N [Escherichia coli]
```

36947

coli]

>gi_1787163 (AE000195) aminopeptidase N [Escherichia coli]
>gi_4062498_dbj_BAA35684_ (D90731) Aminopeptidase n (EC
3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia



265855 Seq. No. 9622 2.R1011 Contig ID uC-zmflMo17014c02b1 5'-most EST BLASTX Method a113742 NCBI GI 1190 BLAST score 1.0e-131 E value 380 Match length % identity AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE) NCBI Description >gi 147142 (M15273) peptidase N [Escherichia coli] >gi_147144 (M15676) aminopeptidase N [Escherichia coli] >gi 1787163 (AE000195) aminopeptidase N [Escherichia coli] >gi_4062498_dbj_BAA35684_ (D90731) Aminopeptidase n (EC 3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia coli] 265856 Seq. No. 9622 3.R1011 Contig ID uC-zmflmo170112b07b1 5'-most EST BLASTX Method g67529 NCBI GI 262 BLAST score 2.0e-22 E value 125 Match length 51 % identity membrane alanyl aminopeptidase (EC 3.4.11.2) - Escherichia NCBI Description 265857 Seq. No. Contig ID 9632 1.R1011 LIB3078-002-Q1-K1-D4 5'-most EST 265858 Seq. No. 9635 1.R1011 Contig ID LIB3078-002-Q1-K1-E3 5'-most EST 265859 Seq. No. 9638 1.R1011 Contig ID uC-zmrob73064f09a1 5'-most EST 265860 Seq. No. 9642 1.R1011 Contig ID LIB3062-016-Q1-K1-D9 5'-most EST BLASTX Method g3925703 NCBI GI 747 BLAST score 4.0e-79 E value Match length 241 62 % identity (X95905) 14-3-3 protein [Lycopersicon esculentum]

265861 Seq. No. 9644 1.R1011 Contig ID pwr700453340.hl 5'-most EST BLASTX

NCBI Description

Method



NCBI GI q4506489 BLAST score 523 E value 3.0e-53Match length 180 % identity 55

replication factor C (activator 1) 3 (38kD) NCBI Description

> >gi 3915601 sp P40938 AC13 HUMAN ACTIVATOR 1 38 KD SUBUNIT (REPLICATION FACTOR C 38 KD SUBUNIT) (A1 38 KD SUBUNIT)

(RF-C 38 KD SUBUNIT) (RFC38) >gi 1498259 (L07541) replication factor C, 38-kDa subunit [Homo sapiens]

265862 Seq. No.

Contig ID 9645 1.R1011 5'-most EST xjt700096278.h1

Method BLASTX NCBI GI g3947448 375 BLAST score 8.0e-36 E value Match length 153

50 % identity

(AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA NCBI Description

EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this

gene; cDNA EST yk499g5.5 comes from this gene

[Caenorhabdi... >gi_3947543_emb_CAA88952_ (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5

comes from this gene [Caenorhabditi

Seq. No. 265863

Contig ID 9647 1.R1011

5'-most EST LIB3078-002-Q1-K1-G5

Method BLASTX NCBI GI q2924507 BLAST score 571 1.0e-58 E value Match length 169 % identity

(AL022023) cyclophilin - like protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 265864

Contia ID 9649 1.R1011 5'-most EST fwa700097412.h1

Seq. No. 265865

Contig ID 9655 1.R1011 ymt700224709.h1 5'-most EST

Method BLASTX q4220488 NCBI GI 209 BLAST score E value 6.0e-16 Match length 126 % identity 43

NCBI Description (AC006069) unknown protein, 5' partial [Arabidopsis

thaliana]



Seq. No.

Contig ID

265866

9655 2.R1011

```
LIB3062-050-Q1-K1-A1
5'-most EST
                  265867
Seq. No.
                  9660 1.R1011
Contig ID
                  tfd700572772.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3184559
                  279
BLAST score
                  2.0e-24
E value
                  96
Match length
                  56
% identity
                  (AF052290) putative c-type cytochrome biogenesis protein
NCBI Description
                  [Synechococcus PCC7002]
                  265868
Seq. No.
Contig ID
                  9663 1.R1011
5'-most EST
                  wty700166013.hl
                  BLASTX
Method
NCBI GI
                  g4115538
BLAST score
                  488
E value
                  4.0e-71
Match length
                  357
% identity
                  45
                  (AB012116) UDP-glycose:flavonoid glycosyltransferase [Vigna
NCBI Description
                  mungo]
                  265869
Seq. No.
                  9674 1.R1011
Contig ID
5'-most EST
                  rvt700549321.h1
Method
                  BLASTX
NCBI GI
                  g2392771
BLAST score
                  1015
E value
                  1.0e-110
Match length
                  388
% identity
                  55
                  (AC002534) putative kinesin-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  265870
Seq. No.
                  9676 1.R1011
Contig ID
                  LIB3066-015-Q1-K1-F11
5'-most EST
Method
                  BLASTX
                  g1651865
NCBI GI
BLAST score
                  197
                  9.0e-15
E value
Match length
                  99
% identity
                  (D90900) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                  265871
Contig ID
                  9679 1.R1011
                  ymt700220548.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4191791
```



BLAST score 286 E value 4.0e-28 Match length 93 % identity 69

NCBI Description (AC005917) putative sf21 {Helianthus annuus} protein

[Arabidopsis thaliana]

Seq. No. 265872

Contig ID 9679 2.R1011

5'-most EST LIB3088-010-Q1-K1-B9

Seq. No. 265873

Contig ID 9679_3.R1011 5'-most EST tfd700572942.h1

Method BLASTX
NCBI GI g3367537
BLAST score 286
E value 6.0e-25
Match length 154
% identity 44

NCBI Description (AC004392) Contains similarity to ANK repeat region of

Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi_485107 from Caenorhabditis elegans cosmid gb_U00049. This gene is continued from unannotated gene on BAC F19K23 gb_AC000375.

[Arabid

Seq. No. 265874

Contig ID 9688_1.R1011 5'-most EST fwa700100716.h1

Method BLASTX
NCBI GI g231610
BLAST score 1195
E value 1.0e-131
Match length 317

% identity 73

NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR

>gi_67880_pir__PWNTG H+-transporting ATP synthase (EC
3.6.1.34) gamma chain precursor, chloroplast - common
tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

Seq. No. 265875

Contig ID 9688 2.R1011

5'-most EST LIB3066-013-Q1-K1-B10

Method BLASTX
NCBI GI g231610
BLAST score 467
E value 2.0e-47
Match length 178
% identity 58

NCBI Description ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR

>gi_67880_pir__PWNTG H+-transporting ATP synthase (EC
3.6.1.34) gamma chain precursor, chloroplast - common
tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase

(gamma subunit) [Nicotiana tabacum]

Seq. No. 265876



```
9693 1.R1011
Contig ID
                  xjt700094260.h1
5'-most EST
                  265877
Seq. No.
                  9693 2.R1011
Contig ID
                  LIB3062-014-Q1-K1-E3
5'-most EST
                  265878
Seq. No.
                  9696 1.R1011
Contig ID
                  clt700043435.fl
5'-most EST
                  BLASTX
Method
                  q3777600
NCBI GI
BLAST score
                  703
                   3.0e-74
E value
                   158
Match length
% identity
NCBI Description (AF095708) 50S ribosomal protein L5 [Oryza sativa]
Seq. No.
                   265879
                   9697 1.R1011
Contig ID
                   LIB3136-029-Q1-K1-A10
5'-most EST
                   BLASTX
Method
                   g3337366
NCBI GI
BLAST score
                   793
                   2.0e-84
E value
                   460
Match length
% identity
                  (AC004481) unknown protein [Arabidopsis thaliana]
NCBI Description
                   265880
Seq. No.
                   9704 1.R1011
Contig ID
                   fC-zmle700444419a1
5'-most EST
                   BLASTX
Method
                   q4583544
NCBI GI
                   328
BLAST score
                   4.0e-30
E value
                   207
Match length
                   33
% identity
                   (Z95637) acyl-CoA:1-acylglycerol-3-phosphate
NCBI Description
                   acyltransferase [Brassica napus]
                   265881
Seq. No.
                   9721 1.R1011
Contig ID
                   tfd700574081.hl
 5'-most EST
                   265882
 Seq. No.
                   9726 1.R1011
 Contig ID
 5'-most EST
                   LIB3078-009-Q1-K1-C12
                   265883
 Seq. No.
                   9727 1.R1011
 Contig ID
                   xsy700210632.hl
 5'-most EST
                   BLASTX
 Method
                   g1353352
 NCBI GI
                   1223
 BLAST score
                    1.0e-135
 E value
```

36952

361

Match length



```
% identity
                  (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
                   265884
Seq. No.
                   9727 2.R1011
Contig ID
                  hvj700624223.h1
5'-most EST
                   BLASTX
Method
                   g1353352
NCBI GI
                   486
BLAST score
                   6.0e-49
E value
                   133
Match length
                   73
% identity
                  (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                   reinhardtii]
                   265885
Seq. No.
                   9727 5.R1011
Contig ID
                   uC-z\overline{m}flb73151d11a2
5'-most EST
                   BLASTX
Method
                   q1353352
NCBI GI
                   191
BLAST score
                   2.0e-14
E value
                   53
Match length
                   70
% identity
                   (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                   reinhardtii]
                   265886
Seq. No.
                   9727 6.R1011
Contig ID
                   fwa700099203.h1
5'-most EST
                   BLASTX
Method
                   g1353352
NCBI GI
                   372
BLAST score
                   1.0e-35
E value
                   113
Match length
                   72
% identity
                   (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                   reinhardtii]
                   265887
Seq. No.
                    9729 1.R1011
Contig ID
                   LIB3078-009-Q1-K1-D9
 5'-most EST
                   BLASTX
Method
                    q2464852
NCBI GI
BLAST score
                    243
                    3.0e-20
E value
                    142
Match length
                    42
 % identity
                   (Z99707) putative protein [Arabidopsis thaliana]
 NCBI Description
                    265888
 Seq. No.
                    9734 1.R1011
 Contig ID
                    fdz701161125.h1
 5'-most EST
                    265889
 Seq. No.
```

36953

9736 1.R1011

Contig ID



5'-most EST LIB3069-034-01-K1-A11 Method BLASTX NCBI GI q1076531 BLAST score 1063 E value 1.0e-116 Match length 248 % identity 78 hypothetical protein, pollen allergen homolog - garden pea NCBI Description >gi_2129891_pir__S65056 pollen allergen homolog precursor (clone PPA1) - garden pea >gi 732905 emb CAA59470 (X85187) homology with pollen allergens [Pisum sativum] 265890 Seq. No. Contig ID 9736 3.R1011 cjh700197394.h1

5'-most EST BLASTX Method NCBI GI q1076531 BLAST score 364 E value 8.0e-35

75 Match length 87 % identity

NCBI Description hypothetical protein, pollen allergen homolog - garden pea >gi 2129891 pir S65056 pollen allergen homolog precursor (clone PPA1) - garden pea >gi 732905 emb CAA59470 (X85187)

homology with pollen allergens [Pisum sativum]

Seq. No. 265891

9738 1.R1011 Contig ID 5'-most EST pmx700086669.h1

Method BLASTX NCBI GI g1321941 BLAST score 1336 E value 1.0e-148 Match length 448

% identity

NCBI Description (Z48564) dihydrolipoamide dehydrogenase [Synechocystis

PCC6803]

Seq. No. 265892

Contig ID 9738 3.R1011 rvt700549482.h1 5'-most EST

Seq. No. 265893

Contig ID 9748 1.R1011

5'-most EST LIB3078-011-Q1-K1-F3

Method BLASTX q4580990 NCBI GI BLAST score 311 2.0e-28 E value Match length 138 % identity 46

NCBI Description (AF120335) putative transposase [Arabidopsis thaliana]

265894 Seq. No. Contig ID 9749 1.R1011

5'-most EST LIB3279-052-P1-K1-D11

Method BLASTX

NCBI GI q2146745 BLAST score 1444 E value 1.0e-169 Match length 332 % identity NCBI Description protein kinase (EC 2.7.1.-) - Arabidopsis thaliana >gi 642132_dbj_BAA08215_ (D45354) protein kinase [Arabidopsis thaliana] 265895 Seq. No. 9757 1.R1011 Contig ID 5'-most EST uC-zmflb73071a07b3 Method BLASTX NCBI GI g3334144 BLAST score 930 E value 1.0e-122 Match length 237 % identity 92 NCBI Description G1/S-SPECIFIC CYCLIN C-TYPE >gi 1695698 dbj BAA13181 (D86925) C-type cyclin [Oryza sativa] 265896 Seq. No. Contig ID 9768 1.R1011 LIB3180-031-P2-M2-C2 5'-most EST Method BLASTX NCBI GI g3763918 BLAST score 575 E value 4.0e-59 Match length 177 % identity 66 NCBI Description (AC004450) putative isopropylmalate dehydratase [Arabidopsis thaliana] Seq. No. 265897 Contig ID 9775 1.R1011 5'-most EST uC-zmflmo17151b12b1 Method BLASTX NCBI GI q1845195 BLAST score 195 2.0e-14 E value Match length 83 % identity 53 NCBI Description (Y08297) HMGc1 [Zea mays] Seq. No. 265898 Contig ID 9775 3.R1011 5'-most EST LIB3136-012-Q1-K1-D11 265899 Seq. No.

Seq. No. 265899 Contig ID 9787_1.R1011 5'-most EST LIB3060-014-Q1-K1-E3

Method BLASTX

 NCBI GI
 g2688839

 BLAST score
 1152

 E value
 1.0e-126

 Match length
 337

 % identity
 65

NCBI Description (AF003347) ATP phosphoribosyltransferase [Thlaspi

Seq. No. 265900

Contig ID 9788_1.R1011 5'-most EST kem700611143.h1

qoesingense]

Method BLASTX
NCBI GI g4586056
BLAST score 206
E value 2.0e-15
Match length 242
% identity 28

NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]

Seq. No. 265901

Contig ID 9788 2.R1011

5'-most EST uC-zmflmo17204e08a1

Seq. No. 265902

Contig ID 9789_1.R1011

5'-most EST uC-zmflB73004f10b1

Method BLASTX
NCBI GI g4531444
BLAST score 1722
E value 0.0e+00
Match length 447
% identity 71

NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No. 265903

Contig ID 9796_1.R1011

5'-most EST LIB3060-035-Q1-K1-D4

Method BLASTX
NCBI GI g3335333
BLAST score 551
E value 2.0e-56
Match length 156
% identity 72

NCBI Description (AC004512) Similar to chloroplast membrane-associated 30KD

protein precursor (IM30) gb_M73744 from Pisum sativum. ESTs gb_N37557, gb_W43887 and gb_AA042479 come from this

gene. [Arabidopsis thaliana]

Seq. No. 265904

Contig ID 9809_1.R1011

5'-most EST LIB3067-056-Q1-K1-D2

Method BLASTX
NCBI GI g2811029
BLAST score 598
E value 9.0e-62
Match length 175
% identity 64

NCBI Description ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT)

(ACETYLORNITHINE TRANSAMINASE) (AOTA)

>gi_1944511_emb_CAA69936_ (Y08680) acetylornithine

aminotransferase [Alnus glutinosa]





```
Seq. No.
                  265905
                  9810 1.R1011
Contig ID
                  rv1700455835.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2911059
BLAST score
                  1722
                  0.0e+00
E value
Match length
                  434
                  78
% identity
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
                  265906
Seq. No.
                  9823 1.R1011
Contig ID
5'-most EST
                  LIB3078-017-Q1-K1-F2
                  265907
Seq. No.
Contig ID
                  9824 1.R1011
5'-most EST
                  LIB3061-034-Q1-K1-C6
                  265908
Seq. No.
Contig ID
                  9826 1.R1011
                  LIB3078-017-Q1-K1-G3
5'-most EST
                  265909
Seq. No.
Contig ID
                  9826 2.R1011
5'-most EST
                  uC-zmrob73004g12b1
                  265910
Seq. No.
Contig ID
                  9826 3.R1011
5'-most EST
                  LIB189-033-01-E1-B12
                  265911
Seq. No.
Contig ID
                  9827 1.R1011
5'-most EST
                  LIB3078-017-Q1-K1-G7
Seq. No.
                  265912
Contig ID
                  9828 1.R1011
5'-most EST
                  uC-zmflmo17077h06b1
                  BLASTX
Method
                  g4335724
NCBI GI
BLAST score
                  192
E value
                  2.0e-18
Match length
                  179
% identity
                  35
NCBI Description (AC006248) putative RING-H2 finger protein [Arabidopsis
                  thalianal
Seq. No.
                  265913
Contig ID
                  9830 1.R1011
5'-most EST
                  LIB3150-054-Q1-N1-D1
Method
                  BLASTX
NCBI GI
                  g549986
BLAST score
                  212
E value
                  7.0e-17
```

Match length % identity 80 NCBI Description (U13149) possible apospory-associated protein [Pennisetum



ciliare]

Seq. No. 265914

Contig ID 9831_1.R1011

5'-most EST uC-zmflmo17215b02b1

Method BLASTX
NCBI GI g1176658
BLAST score 611
E value 6.0e-63
Match length 259
% identity 49

NCBI Description HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II

>gi 726363 (U23168) No definition line found

[Caenorhabditis elegans]

Seq. No. 265915

Contig ID 9832_1.R1011

5'-most EST uC-zmflMo17092c11b1

Method BLASTX
NCBI GI g3913633
BLAST score 528
E value 1.0e-53
Match length 158

% identity 66

NCBI Description HYPOTHETICAL PROTEIN F8A5.25 >gi 2462742 (AC002292) Unknown

protein [Arabidopsis thaliana]

Seq. No. 265916

Contig ID 9835 1.R1011

5'-most EST LIB3079-031-Q1-K1-F6

Seq. No. 265917

Contig ID 9835_2.R1011

5'-most EST LIB189-019-Q1-E1-E5

Seq. No. 265918

Contig ID 9835 3.R1011

5'-most EST LIB3079-054-Q1-K1-B5

Seq. No. 265919
Contig ID 9836_1.R1011
5'-most EST yyf700347423.h1

Seq. No. 265920

Contig ID 9838 1.R1011

5'-most EST LIB3068-045-Q1-K1-D5

Seq. No. 265921

Contig ID 9844_1.R1011

5'-most EST LIB3159-007-Q1-K1-A7

Seq. No. 265922
Contig ID 9844_2.R1011
5'-most EST tfd700571247.h1

Seq. No. 265923

Contig ID 9845_1.R1011



```
LIB189-014-Q1-E1-A5
5'-most EST
                  BLASTN
Method
                  g3821780
NCBI GI
                  37
BLAST score
                  4.0e-11
E value
                  49
Match length
                  67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  265924
Seq. No.
                  9845 2.R1011
Contig ID
                  xsy700208925.hl
5'-most EST
                  265925
Seq. No.
                  9847 1.R1011
Contig ID
                  LIB3078-018-Q1-K1-H4
5'-most EST
                  BLASTX
Method
                   g2181190
NCBI GI
BLAST score
                   259
                   4.0e-22
E value
                   160
Match length
                   39
% identity
NCBI Description (Y12531) serine/threonine kinase [Brassica oleracea]
                   265926
Seq. No.
                   9850 1.R1011
Contig ID
                   LIB3078-019-Q1-K1-A8
5'-most EST
                   265927
Seq. No.
Contig ID
                   9853 1.R1011
                   LIB3078-019-Q1-K1-C11
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2088650
BLAST score
                   401
                   8.0e-39
E value
Match length
                   119
                   71
 % identity
                   (AF002109) peroxisomal ATP/ADP carrier protein isolog
NCBI Description
                   [Arabidopsis thaliana]
                   265928
 Seq. No.
                   9855 1.R1011
 Contig ID
                   LIB3069-031-Q1-K1-B5
 5'-most EST
                   BLASTX
 Method
 NCBI GI
                   q4104056
                   1402
 BLAST score
                   1.0e-156
 E value
                   309
 Match length
                   78
 % identity
 NCBI Description (AF031194) S276 [Triticum aestivum]
                   265929
 Seq. No.
                   9855 4.R1011
 Contig ID
                   nbm700475101.h1
 5'-most EST
                   BLASTX
 Method
```

g4104056

270

NCBI GI

BLAST score

5'-most EST

Method



```
E value
                  2.0e-23
Match length
                  64
                  81
% identity
                  (AF031194) S276 [Triticum aestivum]
NCBI Description
                  265930
Seq. No.
                  9860 1.R1011
Contig ID
                  ymt700221577.h2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4522012
BLAST score
                  596
                  1.0e-61
E value
                  223
Match length
% identity
                  54
NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]
                  265931
Seq. No.
Contig ID
                  9862 1.R1011
                  LIB3078-020-Q1-K1-A4
5'-most EST
Method
                  BLASTX
NCBI GI
                  q402753
BLAST score
                  1364
                  1.0e-151
E value
Match length
                  299
                  87
% identity
NCBI Description (X71439) translation elongation factor EF-G [Glycine max]
Seq. No.
                  265932
Contig ID
                  9868 1.R1011
                  uC-zmromo17080a10a1
5'-most EST
                  265933
Seq. No.
                  9870 1.R1011
Contig ID
5'-most EST
                  ceu700422567.h1
                  BLASTX
Method
NCBI GI
                  g2463412
BLAST score
                  205
                   9.0e-16
E value
Match length
                  138
% identity
NCBI Description (Y12319) spinocerebellar ataxia type 3 [Rattus norvegicus]
                   265934
Seq. No.
                   9875 1.R1011
Contig ID
5'-most EST
                  LIB3068-058-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  g4512708
BLAST score
                  365
                  2.0e-34
E value
Match length
                  100
% identity
NCBI Description (AC006569) putative glutaredoxin [Arabidopsis thaliana]
Seq. No.
                  265935
Contig ID
                  9878 1.R1011
```

36960

LIB143-056-Q1-E1-E5

BLASTX

E value

6.0e-22



```
q3402751
 NCBI GI
 BLAST score
                    565
                    2.0e-84
 E value
                    265
 Match length
  % identity
                    64
 NCBI Description (AL031187) putative protein [Arabidopsis thaliana]
                    265936
 Seq. No.
                    9878 2.R1011
 Contig ID
                    LIB3061-051-Q1-K1-C1
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    g3402751
 BLAST score
                    337
 E value
                    3.0e-31
                    125
 Match length
  % identity
                    58
 NCBI Description (AL031187) putative protein [Arabidopsis thaliana]
 Seq. No.
                    265937
 Contig ID
                    9885 1.R1011
  5'-most EST
                    LIB3078-022-Q1-K1-D12
 Method
                    BLASTX
 NCBI GI
                    g2191172
 BLAST score
                    184
                    1.0e-13
 E value
· Match length
                    44
                    75
  % identity
 NCBI Description (AF007270) contains similarity to GATA-type zinc fingers
                    (PS:PS00344) [Arabidopsis thaliana]
 Seq. No.
                    265938
                    9894 1.R1011
  Contig ID
  5'-most EST
                    mwy700438513.h1
  Seq. No.
                    265939
  Contig ID
                    9894 2.R1011
  5'-most EST
                    LIB3157-017-Q1-K1-B8
                    265940
  Seq. No.
                    9902 1.R1011
  Contig ID
  5'-most EST
                    ymt700219256.h1
                    BLASTX
  Method
  NCBI GI
                    q4584342
  BLAST score
                    968
  E value
                    1.0e-105
                    377
  Match length
  % identity
  NCBI Description (AC007127) putative ubiquitin protein [Arabidopsis
                    thaliana]
                    265941
  Seq. No.
                    9902 2.R1011
  Contig ID
  5'-most EST
                    LIB3061-025-Q1-K1-G5
                    BLASTX
  Method
                    g4584342
  NCBI GI
  BLAST score
                    256
```



132 Match length % identity (AC007127) putative ubiquitin protein [Arabidopsis NCBI Description thaliana]

265942 Seq. No. 9902 3.R1011

Contig ID LIB3069-008-Q1-K1-F12 5'-most EST

45

BLASTX Method q4584342 NCBI GI 203 BLAST score 1.0e-15 E value 112 Match length

% identity (AC007127) putative ubiquitin protein [Arabidopsis NCBI Description

thaliana]

265943 Seq. No. Contig ID

9904 1.R1011

LIB3078-023-Q1-K1-F9 5'-most EST

Method BLASTX g2462832 NCBI GI 252 BLAST score 1.0e-21 E value 89 Match length

56 % identity

(AF000657) similar to Bacillus CotA [Arabidopsis thaliana] NCBI Description

265944 Seq. No.

9913 1.R1011 Contig ID ymt700222949.h1 5'-most EST

BLASTX Method q4249382 NCBI GI 2023 BLAST score 0.0e + 00E value 512 Match length 73 % identity

(AC005966) Strong similarity to gi_3337350 F13P17.3 NCBI Description

putative permease from Arabidopsis thaliana BAC

gb_AC004481. [Arabidopsis thaliana]

265945 Seq. No. 9915 1.R1011 Contig ID wty700168233.hl 5'-most EST

265946 Seq. No. 9915 2.R1011 Contig ID

uC-zmflmo17127g12b1 5'-most EST

265947 Seq. No.

9915 4.R1011 Contig ID gct701169351.h1 5'-most EST

265948 Seq. No. 9916 1.R1011 Contig ID wty700166009.hl 5'-most EST

BLASTX Method



NCBI GI g2494075
BLAST score 384
E value 4.0e-37
Match length 76
% identity 99

NCBI Description NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE

(NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE

DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE

(NADP+)) (TRIOSEPHOSPHATE DEHYDROGENASE)

>gi_1084478_pir__S43833 glyceraldehyde-3-phosphate

dehydrogenase (NADP+) (EC 1.2.1.9) - maize

>gi 474408 emb CAA53075 (X75326)

glyceraldehyde-3-phosphate dehydrogenase (GAPN) [Zea mays]

Seq. No. 265949

Contig ID 9917_1.R1011 5'-most EST ceu700428023.h1

Seq. No. 265950

Contig ID 9919_1.R1011 5'-most EST qmh700030604.f1

Seq. No. 265951

Contig ID 9919 2.R1011

5'-most EST uC-zmflb73279b12a2

Seq. No. 265952

Contig ID 9926 1.R1011

5'-most EST uC-zmflmo17046g01b1

Method BLASTX
NCBI GI g3549679
BLAST score 270
E value 2.0e-23
Match length 107

% identity 49

NCBI Description (AL031394) putative protein [Arabidopsis thaliana]

Seq. No. 265953

Contig ID 9927 1.R1011

5'-most EST LIB3062-022-Q1-K1-F4

Seq. No. 265954

Contig ID 9943_1.R1011

5'-most EST LIB3078-027-Q1-K1-C7

Seq. No. 265955

Contig ID 9955_1.R1011 5'-most EST fdz701163003.h1

Seq. No. 265956

Contig ID 9956_1.R1011

5'-most EST LIB3078-029-Q1-K1-A12

Seq. No. 265957

Contig ID 9959_1.R1011

5'-most EST LIB3078-029-Q1-K1-B4

Method BLASTN



```
q342643
NCBI GI
BLAST score
                  278
                  1.0e-155
E value
                  330
Match length
                  96
% identity
                  Maize mitochondrion with chloroplast insert containing
NCBI Description
                  rRNAs
                  265958
Seq. No.
                  9960 1.R1011
Contig ID
                  LIB3078-029-Q1-K1-C11
5'-most EST
                  BLASTN
Method
NCBI GI
                   q170779
                   76
BLAST score
                   1.0e-34
E value
                   128
Match length
                   90
% identity
                   T.aestivum ubiquitin activating enzyme E1 (UBA1) gene,
NCBI Description
                   complete cds
                   265959
Seq. No.
Contig ID
                   9962 1.R1011
                   uC-zmflMo17019g11b1
5'-most EST
Method
                   BLASTX
                   q404028
NCBI GI
                   1210
BLAST score
                   1.0e-133
E value
                   309
Match length
                   75
% identity
                   (M96569) oleoyl-acyl carrier protein thioesterase
NCBI Description
                   [Carthamus tinctorius] >gi_445624_prf__1909371A oleoyl acyl
                   carrier protein thioesterase [Carthamus tinctorius]
                   265960
Seq. No.
                   9962 2.R1011
Contig ID
                   uC-zmflmo17072c08b1
5'-most EST
                   BLASTX
Method
                   g1076361
NCBI GI
BLAST score
                   674
                   9.0e-71
E value
                   162
Match length
                   79
 % identity
                   oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) -
NCBI Description
                   Arabidopsis thaliana >gi_2129660_pir__S69197
                   oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14)
                   (clone TE 1-7) - Arabidopsis thaliana
                   >gi 804946_emb_CAA85389_ (Z36912) acyl-(acyl carrier
                   protein) thioesterase [Arabidopsis thaliana]
                   265961
 Seq. No.
                   9971 1.R1011
 Contig ID
                   uC-zmflb73154g03a1
 5'-most EST
                   BLASTX
 Method
                   q4204315
 NCBI GI
                   189
 BLAST score
```

36964

4.0e-14

55

E value

Match length



% identity 62 NCBI Description (AC003027) Unknown protein [Arabidopsis thaliana] Seq. No. 265962

Contig ID 9976 1.R1011 5'-most EST LIB3136-002-P1-K1-E1

Method BLASTX
NCBI GI g3395431
BLAST score 349
E value 2.0e-32
Match length 273
% identity 35

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 265963

Contig ID 9976_2.R1011

5'-most EST LIB3078-030-Q1-K1-E7

Seq. No. 265964

Contig ID 9976_3.R1011

5'-most EST LIB3180-038-P2-M2-H2

Seq. No. 265965

Contig ID 9995_1.R1011 5'-most EST hbs701182520.h1

Seq. No. 265966 Contig ID 9999_1.R1011

5'-most EST LIB3158-016-Q1-K1-E1

Seq. No. 265967

Contig ID 10002_1.R1011 5'-most EST cyk700051264.f1

Method BLASTX
NCBI GI g3258575
BLAST score 1363
E value 1.0e-151
Match length 502
% identity 59

% identity 59
NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 265968

Contig ID 10002_2.R1011

5'-most EST LIB3067-029-Q1-K1-A1

Method BLASTX
NCBI GI g3258575
BLAST score 268
E value 2.0e-23
Match length 96
% identity 62

NCBI Description (U89959) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 265969

Contig ID 10004_1.R1011 5'-most EST xjt700095839.h1

Seq. No. 265970



```
10010 1.R1011
Contig ID
                   xsy70\overline{0}210222.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3256035
BLAST .score
                   1377
                   1.0e-152
E value
                   436
Match length
% identity
                   59
                   (Y14274) putative serine/threonine protein kinase [Sorghum
NCBI Description
                   bicolor]
                   265971
Seq. No.
Contig ID
                   10010 4.R1011
                   LIB3158-003-Q1-K1-G10
5'-most EST
                   BLASTX
Method
                   q3256035
NCBI GI
BLAST score
                   263
E value
                   5.0e-23
Match length
                   109
% identity
                   (Y14274) putative serine/threonine protein kinase [Sorghum
NCBI Description
                   bicolor]
                   265972
Seq. No.
                   10015 1.R1011
Contig ID
                   LIB3078-032-Q1-K1-G9
5'-most EST
                   BLASTX
Method-
                   q283004
NCBI GI
BLAST score
                   296
                   1.0e-26
E value
                   139
Match length
                   50
% identity
                   DNA-binding protein Gt-2 - rice >gi_20249 emb CAA48328
NCBI Description
                   (X68261) gt-2 [Oryza sativa]
                   265973
Seq. No.
                   10017 1.R1011
Contig ID
                   uC-zmflb73017g03b1
5'-most EST
Seq. No.
                   265974
Contig ID
                   10028 1.R1011
                   LIB3061-007-Q1-K1-B10
5'-most EST
                   BLASTX
Method
                   q3269293
NCBI GI
BLAST score
                   188
                   1.0e-13
E value
                   165
Match length
                   36
% identity
                   (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 265975

Contig ID 10028_2.R1011 5'-most EST xyt700345436.h1

Seq. No. 265976

Contig ID 10028_3.R1011 5'-most EST uC-zmflb73055g11b1



Seq. No.

265977

```
10031_1.R1011
Contig ID
                   uC-zmroteosinte014g05b1
5'-most EST
                   BLASTX
Method
                   g2501492
NCBI GI
BLAST score
                   264
                   9.0e-23
E value
                   126
Match length
                   43
% identity
                   FLAVONOL 3-O-GLUCOSYLTRANSFERASE 2 (UDP-GLUCOSE FLAVONOID
NCBI Description
                   3-O-GLUCOSYLTRANSFERASE 2) >gi_542018_pir__S41954
                   UTP-glucose glucosyltransferase - cassava (fragment)
                   >gi_453255_emb_CAA54611_ (X77461) UTP-glucose
                   glucosyltransferase [Manihot esculenta]
                   265978
Seq. No.
                   10034 1.R1011
Contig ID
                   LIB36-018-Q1-E1-G5
5'-most EST
                   265979
Seq. No.
                   10035 1.R1011
Contig ID
                   \texttt{tzu70}\overline{\texttt{0}}\texttt{204848.h1}
5'-most EST
                   BLASTX
Method
                   g1865677
NCBI GI
                   1038
BLAST score
                   1.0e-113
E value
Match length
                   257
                   80
% identity
                   (Y08568) trehalose-6-phosphate synthase [Arabidopsis
NCBI Description
                   thaliana]
                   265980
Seq. No.
                   10035 2.R1011
Contig ID
                   LIB3078-034-Q1-K1-B6
5'-most EST
                   BLASTX
Method
                   q4583546
NCBI GI
BLAST score
                    632
E value
                    9.0e-66
                    186
Match length
                    69
% identity
NCBI Description (AJ010819) GrpE protein [Arabidopsis thaliana]
                    265981
Seq. No.
                    10035 3.R1011
Contig ID
                    fC-zmf1700350230f2
5'-most EST
Method
                    BLASTX
NCBI GI
                    g1865677
BLAST score
                    270
                    3.0e-28
E value
                    90
Match length
                    77
% identity
                   (Y08568) trehalose-6-phosphate synthase [Arabidopsis
NCBI Description
                    thaliana]
```

36967

265982

10036 1.R1011

Seq. No. Contig ID



```
5'-most EST
                  LIB3078-034-Q1-K1-D9
                  265983
Seq. No.
Contig ID
                  10049 1.R1011
                  LIB3078-035-Q1-K1-C10
5'-most EST
                  265984
Seq. No.
Contig ID
                  10054 1.R1011
                  LIB3078-036-Q1-K1-A9
5'-most EST
                  BLASTX
Method
                  q2660670
NCBI GI
BLAST score
                  426
E value
                  3.0e-42
                  106
Match length
                  75
% identity
                  (AC002342) putative Cu2+-transporting ATPase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  265985
                  10065 1.R1011
Contig ID
                  uC-zmroteosinte029e09b1
5'-most EST
                  265986
Seq. No.
                  10074 1.R1011
Contig ID
                  LIB3088-049-Q1-K1-D7
5'-most EST
                  265987
Seq. No.
                  10079 1.R1011
Contig ID
5'-most EST
                  LIB3150-048-Q1-N1-H1
Method
                  BLASTX
                   q3269288
NCBI GI
                   792
BLAST score
                   2.0e-84
E value
                   203
Match length
% identity
                   74
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
                   265988
Seq. No.
Contig ID
                   10079 2.R1011
                   uC-zmrob73022d07a1
5'-most EST
                   BLASTX
Method
                   g3269288
NCBI GI
BLAST score
                   306
                   5.0e-30
E value
Match length
                   87
                   78
% identity
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                   265989
Seq. No.
                   10079 3.R1011
Contig ID
5'-most EST
                   wyr700244131.hl
                   BLASTX
Method
                   g2564066
NCBI GI
                   412
BLAST score
                   2.0e-40
E value
```

36968

99

79

Match length

% identity



```
NCBI Description (D45900) LEDI-3 protein [Lithospermum erythrorhizon]
                   265990
Seq. No.
                   10085 1.R1011
Contig ID
                   LIB3078-038-Q1-K1-D3
5'-most EST
                   265991
Seq. No.
                   10092 1.R1011
Contig ID
                   pwr700451428.h1
5'-most EST
                   BLASTX
Method
                   g729480
NCBI GI
BLAST score
                   1773
                   0.0e+00
E value
Match length
                   365
% identity
                   90
                   FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR (FNR)
NCBI Description
                   >gi_435647_dbj_BAA04232 (D17410) ferredoxin-NADP+
reductase [Oryza sativa] >gi_902936_dbj_BAA07479_ (D38445)
                   root ferredoxin-NADP+ reductase [Oryza sativa]
                   >gi 1096932 prf 2113196A ferredoxin-NADP oxidoreductase
                   [Oryza sativa]
Seq. No.
                   265992
                   10092 2.R1011
Contig ID
                   uC-zmflb73033a11b1
5'-most EST
Method
                   BLASTX
                   q3913653
NCBI GI
BLAST score
                   361
                   5.0e-50
E value
Match length
                   126
                   84
% identity
                   FERREDOXIN--NADP REDUCTASE, EMBRYO ISOZYME PRECURSOR (FNR)
NCBI Description
                   >qi 1778686 dbj BAA13417 (D87547) precursor
                   ferredoxin-NADP+ oxidoreductase [Oryza sativa]
                   265993
Seq. No.
                   10095 1.R1011
Contig ID
5'-most EST
                   fdz701163506.hl
                   BLASTX
Method
NCBI GI
                   q2832632
                   710
BLAST score
                   5.0e-75
E value
Match length
                   223
                   67
% identity
                  (AL021711) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   265994
Contig ID
                   10098 1.R1011
5'-most EST
                   uwc700150735.h1
Method
                   BLASTX
```

Method BLASTX
NCBI GI g135535
BLAST score 2277
E value 0.0e+00
Match length 530
% identity 86

NCBI Description T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)

(CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide



Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_ (D11351) t-complex polypeptide 1 homologue [Arabidopsis thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT alpha/TCP-1 [Arabidopsis thaliana]

Seq. No. 265995

Contig ID 10098_2.R1011 5'-most EST xjt700094854.h1

Method BLASTX
NCBI GI g135535
BLAST score 572
E value 5.0e-59
Match length 129
% identity 89

NCBI Description T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)

(CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_(D11351) t-complex polypeptide 1 homologue [Arabidopsis

thaliana] >qi 2326265 dbj BAA21772 (D11352) CCT

alpha/TCP-1 [Arabidopsis thaliana]

Seq. No. 265996

Contig ID 10098_4.R1011

5'-most EST uC-zmflb73261c02b3 Method BLASTX

Method BLASTX
NCBI GI g135535
BLAST score 359
E value 5.0e-34
Match length 84
% identity 87

NCBI Description T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)

(CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_ (D11351) t-complex polypeptide 1 homologue [Arabidopsis

thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT

alpha/TCP-1 [Arabidopsis thaliana]

Seq. No. 265997

Contig ID 10098_5.R1011 5'-most EST uC-zmflb73317b04b1

Method BLASTX
NCBI GI g135535
BLAST score 202
E value 1.0e-15
Match length 53
% identity 81

NCBI Description T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)

(CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_ (D11351) t-complex polypeptide 1 homologue [Arabidopsis

thaliana] >gi 2326265_dbj_BAA21772_ (D11352) CCT

alpha/TCP-1 [Arabidopsis thaliana]

Seq. No. 265998

Contig ID 10101_1.R1011

5'-most EST LIB3115-006-Q1-K1-F4

Method BLASTX



NCBI GI g119286 243 BLAST score 2.0e-20 E value Match length 105 % identity 52

LOW MOLECULAR MASS EARLY LIGHT-INDUCIBLE PROTEIN PRECURSOR NCBI Description

(ELIP) (CLONE HV90) >gi 100630_pir__S07474 early

light-induced protein, low molecular weight, precursor (clone HV90) - barley chloroplast >gi_19033_emb_CAA33727_ (X15692) precursor peptide (AA -38 to 134) [Hordeum

vulgare]

265999 Seq. No.

Contig ID 10101 2.R1011 fC-zmse700612508r1 5'-most EST

BLASTN Method g19032 NCBI GI BLAST score 64 2.0e-27 E value Match length 176 85

Barley mRNA for chloroplast low molecular mass early NCBI Description

light-inducible protein (ELIP) (clone HV90)

266000 Seq. No.

% identity

10102 1.R1011 Contig ID

LIB3180-015-P2-M1-B7 5'-most EST

Method BLASTX g2499932 NCBI GI 651 BLAST score 5.0e-68 E value 151 Match length 89 % identity

ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_726305 NCBI Description

(U22442) adenine phosphoribosyltransferase form 1 [Triticum

aestivum]

266001 Seq. No.

10102 2.R1011 Contig ID

5'-most EST LIB3068-059-Q1-K1-H7

BLASTX Method g2499932 NCBI GI BLAST score 799 3.0e-85E value 177 Match length 88 % identity

ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi 726305 NCBI Description

(U22442) adenine phosphoribosyltransferase form 1 [Triticum

aestivum]

266002 Seq. No.

Contig ID 10102 5.R1011 5'-most EST vmt700219454.h1

266003 Seq. No.

10104 1.R1011 Contig ID

LIB3066-014-Q1-K1-A12 5'-most EST



```
Method
                  BLASTX
                  q3386567
NCBI GI
BLAST score
                  528
                  1.0e-53
E value
                  112
Match length
                   92
% identity
                   (AF079589) 1-aminocyclopropane-1-carboxylate oxidase
NCBI Description
                   [Sorghum bicolor]
                   266004
Seq. No.
                   10114 1.R1011
Contig ID
                   LIB3078-040-Q1-K1-A9
5'-most EST
                   266005
Seq. No.
Contig ID
                   10122 1.R1011
5'-most EST
                   wty700171791.hl
                   BLASTX
Method
                   q2440029
NCBI GI
                   428
BLAST score
                   4.0e-42
E value
                   87
Match length
                   92
% identity
                   (Y14851) DAL1 protein [Arabidopsis thaliana]
NCBI Description
                   >gi 2440031_emb_CAA75115_ (Y14850) DAL1 protein
                   [Arabidopsis thaliana]
                   266006
Seq. No.
Contig ID
                   10123 1.R1011
                   LIB3078-040-Q1-K1-E10
5'-most EST
                   266007
Seq. No.
                   10124 1.R1011
Contig ID
                   uC-zmflmo17c03b1
5'-most EST
                   BLASTX
Method
                   g2392025
NCBI GI
                   1261
BLAST score
                   1.0e-139
E value
Match length
                   264
% identity
                   87
                  (D88420) stromal ascorbate peroxidase [Cucurbita sp.]
NCBI Description
                   266008
Seq. No.
                   10135 1.R1011
Contig ID
                   cyk700052021.f1
5'-most EST
                   BLASTX
Method
                   g4262147
NCBI GI
BLAST score
                   161
E value
                   1.0e-10
Match length
                   68
% identity
                   49
                   (AC005275) putative homolog of transport inhibitor response
NCBI Description
                   1 [Arabidopsis thaliana]
                   266009
Seq. No.
```

Seq. No. 266009 Contig ID 10135_2.R1011

5'-most EST uC-zmroteosinte034e07b1

Method BLASTX



NCBI GI q2352492 1316 BLAST score 1.0e-145 E value Match length 451 59 % identity

(AF005047) transport inhibitor response 1 [Arabidopsis NCBI Description thaliana] >gi 2352494 (AF005048) transport inhibitor

response 1 [Arabidopsis thaliana]

266010 Seq. No.

10135 3.R1011 Contig ID $uC-zm\overline{f}lb73158h04a1$ 5'-most EST

266011 Seq. No.

10135 5.R1011 Contig ID

LIB3078-045-Q1-K1-A9 5'-most EST

BLASTX Method NCBI GI q2352492 BLAST score 162 1.0e-11 E value Match length 47 68 % identity

(AF005047) transport inhibitor response 1 [Arabidopsis NCBI Description

thaliana] >gi_2352494 (AF005048) transport inhibitor

response 1 [Arabidopsis thaliana]

266012 Seq. No.

Contig ID 10146 1.R1011

LIB3078-045-Q1-K1-E2 5'-most EST

BLASTX Method q1332579 NCBI GI 319 BLAST score 1.0e-41 E value 107 Match length

9 % identity

(X98063) polyubiquitin [Pinus sylvestris] NCBI Description

266013 Seq. No.

10148 1.R1011 Contig ID

LIB3060-024-Q1-K1-F3 5'-most EST

BLASTX Method NCBI GI g1346771 BLAST score 2183 0.0e+00E value 462 Match length 87 % identity

PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP) NCBI Description

>gi_1086117_pir__S52988 phosphoenolpyruvate carboxykinase

(PCK1) - Urochloa panicoides >gi_607752 (U09241)

phosphoenolpyruvate carboxykinase [Urochloa panicoides]

266014 Seq. No.

Contig ID 10148 2.R1011

LIB143-049-Q1-E1-D10 5'-most EST

BLASTX Method NCBI GI g1346771 BLAST score 429



E value 3.0e-42 91 Match length % identity 89 PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP) NCBI Description >gi_1086117_pir__S52988 phosphoenolpyruvate carboxykinase (PCK1) - Urochloa panicoides >gi 607752 (U09241) phosphoenolpyruvate carboxykinase [Urochloa panicoides] 266015 Seq. No. 10148 4.R1011 Contig ID hvj700620909.h1 5'-most EST Method BLASTX NCBI GI g2827717 BLAST score 180 E value 6.0e-29 Match length 114 % identity 77 (AL021684) phosphoenolpyruvate carboxykinase (ATP) - like NCBI Description protein [Arabidopsis thaliana] 266016 Seq. No. 10149 1.R1011 Contig ID 5'-most EST uC-zmflmo17090h04a1 Method BLASTX NCBI GI g3668115 BLAST score 176 1.0e-12 E value Match length 48 % identity . 71 (Y15069) cinnamoyl-CoA reductase [Zea mays] NCBI Description 266017 Seq. No. 10149 2.R1011 Contig ID hbs701184123.h1 5'-most EST BLASTX Method g3668115 NCBI GI 176 BLAST score 2.0e-12 E value Match length 48 71 % identity (Y15069) cinnamoyl-CoA reductase [Zea mays] NCBI Description 266018 Seq. No. 10150 1.R1011 Contig ID 5'-most EST LIB3066-056-Q1-K1-B3 BLASTX Method NCBI GI g2443751 BLAST score 2071 E value 0.0e + 00Match length 464 85 % identity (AF020303) fumarase [Arabidopsis thaliana] >gi 2529676 NCBI Description (AC002535) putative fumarase [Arabidopsis thaliana]

Seq. No. 266019

Contig ID 10151 1.R1011

5'-most EST LIB3078-045-Q1-K1-G2



Method BLASTN
NCBI GI g2062705
BLAST score 35
E value 8.0e-10
Match length 35
% identity 100

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 266020

Contig ID 10151 2.R1011

5'-most EST LIB3180-062-P2-M1-D5

Seq. No. 266021

Contig ID 10152_1.R1011 5'-most EST vux700161284.h1

Seq. No. 266022

Contig ID 10153_1.R1011

5'-most EST uC-zmflb73245c09b2

Method BLASTX
NCBI GI g2618723
BLAST score 412
E value 8.0e-40
Match length 130
% identity 64

NCBI Description (U49073) IAA17 [Arabidopsis thaliana] >gi_2921756

(AF040631) IAA17/AXR3 protein [Arabidopsis thaliana] >gi_4389514_gb_AAB70451_ (AC000104) Identical to

Arabidopsis gb_AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs

gb_H36782 and gb_F14074 come from this gene. [Arabidopsis

thaliana]

Seq. No. 266023

Contig ID 10163_1.R1011 5'-most EST cjh700195534.h1

Method BLASTX NCBI GI g3372233

NCBI GI g3372233 BLAST score 385 E value 3.0e-37 Match length 85

% identity 85

NCBI Description (AF019248) RNA polymerase I, II and III 24.3 kDa subunit

[Arabidopsis thaliana]

Seq. No. 266024

Contig ID 10168 1.R1011

5'-most EST LIB3078-046-Q1-K1-D11

Seq. No. 266025

Contig ID 10169_1.R1011 5'-most EST wty700167040.h1

Method BLASTX
NCBI GI g3212610
BLAST score 573
E value 1.0e-58
Match length 236
% identity 50



Chain A, Sulfite Oxidase From Chicken Liver NCBI Description >gi 3212611 pdb 1SOX_B Chain B, Sulfite Oxidase From Chicken Liver 266026 Seq. No. 10172 1.R1011 Contig ID

LIB3078-046-Q1-K1-E10 5'-most EST BLASTX Method g4567305 NCBI GI BLAST score 172 4.0e-12 E value 107 Match length 38 % identity

(AC005956) hypothetical protein [Arabidopsis thaliana] NCBI Description

266027 Seq. No. Contig ID 10173 1.R1011

uC-zmflmo17330d10b1 5'-most EST

Method BLASTX a4049401 NCBI GI 774 BLAST score 8.0e-82 E value 235 Match length

% identity (AJ131580) glutathione transferase AtGST 10 [Arabidopsis NCBI Description

thaliana]

266028 Seq. No.

Contig ID 10173 2.R1011

5'-most EST LIB3117-013-Q1-K1-F11

63

BLASTX Method NCBI GI g4049401 BLAST score 380 1.0e-36 E value 132 Match length 58 % identity

(AJ131580) glutathione transferase AtGST 10 [Arabidopsis NCBI Description

thaliana]

266029 Seq. No.

10178 1.R1011 Contig ID

uC-zmflmo17180d04b1 5'-most EST

BLASTX Method g3980384 NCBI GI 173 BLAST score 7.0e-12 E value 253 Match length 35 % identity

NCBI Description (AC004561) hypothetical protein [Arabidopsis thaliana]

266030 Seq. No.

10178 2.R1011 Contig ID pmx700091724.hl 5'-most EST

Method BLASTX g3980384 NCBI GI BLAST score 162 6.0e-11 E value



Match length 51 % identity 55

NCBI Description (AC004561) hypothetical protein [Arabidopsis thaliana]

Seq. No. 266031

Contig ID 10181_1.R1011

5'-most EST uC-zmflmo17100b10b1

Method BLASTX
NCBI GI 94249418
BLAST score 235
E value 3.0e-19
Match length 107
% identity 41

NCBI Description (AC006072) putative zinc-finger protein (C-x8-C-x5-C-x3-H

type domains), 5' partial [Arabidopsis thaliana]

Seq. No. 266032

Contig ID 10189 1.R1011

5'-most EST uC-zmflmo17301b01b1

Seq. No. 266033

Contig ID 10193_1.R1011 5'-most EST ymt700219750.h1

Method BLASTX
NCBI GI g2708750
BLAST score 699
E value 3.0e-75
Match length 288
% identity 51

NCBI Description (AC003952) putative physical impedence protein [Arabidopsis

thaliana]

Seq. No. 266034

Contig ID 10199 1.R1011 5'-most EST ceu700422623.h1

Seq. No. 266035

Contig ID 10199_2.R1011 5'-most EST gct701176465.h1

Seq. No. 266036

Contig ID 10204_1.R1011 5'-most EST uC-zmrob73057g04a1

Method BLASTX
NCBI GI 94539383
BLAST score 197
E value 4.0e-15
Match length 71
% identity 45

NCBI Description (AL035526) putative protein (fragment) [Arabidopsis

thaliana]

Seq. No. 266037

Contig ID 10208_1.R1011

5'-most EST LIB3078-048-Q1-K1-B11

Method BLASTX NCBI GI g4490317



BLAST score 397 E value 4.0e-38 Match length 194 % identity 42

NCBI Description (AL035678) putative protein [Arabidopsis thaliana]

Seq. No. 266038

Contig ID 10208 2.R1011

5'-most EST LIB3156-013-Q1-K1-B11

Seq. No. 266039

Contig ID 10210 1.R1011 5'-most EST xjt700095219.h1

Method BLASTX
NCBI GI g1916290
BLAST score 303
E value 4.0e-27
Match length 169
% identity 42

NCBI Description (U89876) ALY [Mus musculus]

Seq. No. 266040

Contig ID 10210 2.R1011

5'-most EST LIB3136-017-Q1-K1-C8

Method BLASTX
NCBI GI g1916290
BLAST score 217
E value 2.0e-17
Match length 138
% identity 39

NCBI Description (U89876) ALY [Mus musculus]

Seq. No. 266041

Contig ID 10216 1.R1011

5'-most EST LIB3078-048-Q1-K1-D9

Method BLASTX
NCBI GI g129646
BLAST score 201
E value 4.0e-15
Match length 144
% identity 36

NCBI Description 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE)

(ETHYLENE-FORMING ENZYME) (EFE) (RIPENING-RELATED PROTEIN PAVOE3) >gi_99498_pir__S11879 ethylene-forming enzyme - avocado >gi_166945 (M32692) ripening-related protein

(pAVOe3) [Persea americana]

Seq. No. 266042

Contig ID 10216_2.R1011 5'-most EST xsy700209137.h1

Seq. No. 266043

Contig ID 10216_3.R1011 5'-most EST pmx700083259.h1

Seq. No. 266044

Contig ID 10217_1.R1011



uC-zmflmo17394e02a1 5'-most EST BLASTX Method q4454469 NCBI GI BLAST score 165 2.0e-11 E value 43 Match length 67 % identity (AC006234) unknown protein [Arabidopsis thaliana] NCBI Description 266045 Seq. No. 10218 1.R1011 Contig ID uC-zmflMo17015f01b1 5'-most EST BLASTX Method g1732028 NCBI GI BLAST score 288 1.0e-25 E value Match length 165 35 % identity (AC000101) unknown [Myxococcus xanthus] NCBI Description 266046 Seq. No. 10219 1.R1011 Contig ID LIB3078-048-Q1-K1-E3 5'-most EST BLASTX Method g3063464 NCBI GI BLAST score 212 4.0e-17 E value Match length 59 68 % identity (AC003981) F22013.26 [Arabidopsis thaliana] NCBI Description 266047 Seq. No. 10224 1.R1011 Contig ID 5'-most EST uC-zmflb73276h07b1 266048 Seq. No. Contig ID 10226 1.R1011 LIB3078-049-Q1-K1-B1 5'-most EST 266049 Seq. No. Contig ID 10231 1.R1011 5'-most EST LIB3137-027-Q1-K1-D12 Method BLASTX g2088647 NCBI GI BLAST score 1609 E value 1.0e-180 Match length 567 % identity 55 (AF002109) hypothetical protein [Arabidopsis thaliana] NCBI Description >gi_3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana] 266050 Seq. No.

Contig ID 10231_2.R1011 5'-most EST ypc700800510.h1

Method BLASTX NCBI GI g2088647



BLAST score 346 E value 4.0e-60 Match length 208 % identity 59

NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana] >qi 3158394 (AF036340) LRR-containing F-box protein

[Arabidopsis thaliana]

Seq. No. 266051

Contig ID 10232 1.R1011 5'-most EST pmx700090729.h1

Seq. No. 266052

Contig ID 10240 1.R1011

5'-most EST LIB3078-050-Q1-K1-G7

Seq. No. 266053

Contig ID 10245_1.R1011 5'-most EST uC-zmflb73325c06a1

Seq. No. 266054

Contig ID 10247_1.R1011

5'-most EST uC-zmroB73017e09b1

Method BLASTX
NCBI GI g131770
BLAST score 341
E value 1.0e-31
Match length 175

% identity 58

NCBI Description 40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)

(VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3D024

ribosomal protein S9.e - slime mold (Dictyostelium discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein

[Dictyostelium discoideum]

Seq. No. 266055

Contig ID 10247_2.R1011 5'-most EST xjt700093003.h1

Method BLASTX
NCBI GI g1351017
BLAST score 205
E value 7.0e-16
Match length 47
% identity 81

NCBI Description 40S RIBOSOMAL PROTEIN S9 (S4) >gi_629697_pir__S45375

ribosomal protein S4 - common tobacco (fragment)

>gi_443960_emb_CAA78463_ (Z14085) RIBOSOMAL PROTEIN S4

[Nicotiana tabacum]

Seq. No. 266056

Contig ID 10252_1.R1011

5'-most EST LIB3078-051-Q1-K1-G4

Method BLASTX
NCBI GI g2131531
BLAST score 214
E value 1.0e-16
Match length 238



```
% identity
                  hypothetical protein YDR496c - yeast (Saccharomyces
NCBI Description
                  cerevisiae) >gi_927766 (U33057) Ydr496cp; CAI: 0.25
                  [Saccharomyces cerevisiae]
                  266057
Seq. No.
                  10253 1.R1011
Contig ID
                  clt700044807.f1
5'-most EST
                  BLASTX
Method
                  g2062168
NCBI GI
                  274
BLAST score
                  4.0e-24
E value
                  82
Match length
                   60
% identity
                  (ACO01645) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  266058
Seq. No.
                  10256 1.R1011
Contig ID
                  LIB3078-051-Q1-K1-H8
5'-most EST
                  BLASTX
Method
                   g1041815
NCBI GI
BLAST score
                   208
                   1.0e-16
E value
                   54
Match length
                   61
% identity
                  (U16721) lipid transfer protein [Oryza sativa]
NCBI Description
                   266059
Seq. No.
                   10262 1.R1011
Contig ID
                   LIB3078-052-Q1-K1-C9
5'-most EST
                   BLASTX
Method
                   g2880051
NCBI GI
                   216
BLAST score
                   3.0e-17
E value
                   67
Match length
                   72
% identity
NCBI Description
                  (AC002340) putative protein kinase [Arabidopsis thaliana]
                   266060
Seq. No.
                   10263 1.R1011
Contig ID
                   ceu700432294.h1
5'-most EST
                   266061
Seq. No.
                   10263 2.R1011
Contig ID
                   LIB3067-040-Q1-K1-E1
5'-most EST
                   266062
Seq. No.
Contig ID
                   10271 1.R1011
5'-most EST
                   pmx700091358.hl
                   BLASTX
Method
                   q641905
NCBI GI
BLAST score
                   746
E value
                   3.0e-79
Match length
                   216
```

NCBI Description (U19267) cysteine proteinase [Zinnia elegans]

69

% identity



Seq. No. 266063

Contig ID 10282 1.R1011

5'-most EST LIB3078-054-Q1-K1-A3

Method BLASTX
NCBI GI g2924507
BLAST score 288
E value 1.0e-25
Match length 67
% identity 75

NCBI Description (AL022023) cyclophilin - like protein [Arabidopsis

thaliana]

Seq. No. 266064

Contig ID 10283 1.R1011

5'-most EST LIB3078-054-Q1-K1-B1

Method BLASTX
NCBI GI g4454458
BLAST score 228
E value 1.0e-18
Match length 87
% identity 53

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 266065

Contig ID 10286_1.R1011 5'-most EST cyk700048826.f1

Method BLASTX
NCBI GI g2702370
BLAST score 300
E value 2.0e-26
Match length 124
% identity 51

NCBI Description (AF038604) contains similarity to Drosophila ovarian tumor

locus protein (GB:X13693) [Caenorhabditis elegans]

Seq. No. 266066

Contig ID 10286_3.R1011

5'-most EST LIB3136-011-Q1-K1-A2

Seq. No. 266067

Contig ID 10286_4.R1011 5'-most EST xjt700094169.h1

Seq. No. 266068

Contig ID 10287_1.R1011

5'-most EST LIB3078-054-Q1-K1-E3

Method BLASTX
NCBI GI g2246625
BLAST score 1314
E value 0.0e+00
Match length 440
% identity 75

NCBI Description (AF004947) protein kinase [Oryza sativa]

Seq. No. 266069

Contig ID 10289_1.R1011

5'-most EST LIB3078-054-Q1-K1-G10

NCBI Description

```
BLASTX
Method
NCBI GI
                  q2832625
                  261
BLAST score
                  1.0e-22
E value
                   84
Match length
                   55
% identity
NCBI Description (AL021711) putative protein [Arabidopsis thaliana]
                   266070
Seq. No.
                   10292 1.R1011
Contig ID
                   LIB3078-054-Q1-K1-H6
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2388578
                   354
BLAST score
                   2.0e-33
E value
                   79
Match length
                   80
% identity
                   (AC000098) Similar to Mycobacterium RlpF (gb Z84395). ESTs
NCBI Description
                   gb T75785, gb R30580, gb T04698 come from this gene.
                   [Arabidopsis thaliana]
                   266071
Seq. No.
Contig ID
                   10294 1.R1011
5'-most EST
                   LIB36-008-Q1-E1-A6
Method
                   BLASTX
                   g3258575
NCBI GI
                   592
BLAST score
                   3.0e-64
E value
                   200
Match length
% identity
                   66
                   (U89959) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   266072
Seq. No.
Contig ID
                   10299 1.R1011
                   wyr700241044.h1
5'-most EST
                   266073
Seq. No.
                   10302 1.R1011
Contig ID
                   uC-zmflmo17067a04b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1871184
                   168
BLAST score
                   1.0e-11
E value
Match length
                   86
                   38
% identity
                  (U90439) unknown protein [Arabidopsis thaliana]
NCBI Description
                   266074
Seq. No.
                   10302 2.R1011
Contig ID
5'-most EST
                   LIB3137-015-Q1-K1-G3
                   {\tt BLASTX}
Method
                   g1871184
NCBI GI
                   248
BLAST score
                   1.0e-20
E value
                   153
Match length
                   32
% identity
                  (U90439) unknown protein [Arabidopsis thaliana]
```



266075 Seq. No. Contig ID

10306 1.R1011 LIB83-014-Q1-E1-H7

Seq. No.

266076

Contig ID

5'-most EST

10306 2.R1011

5'-most EST

 $uC-zm\overline{f}lmo17068e02b2$

Seq. No.

266077

Contig ID

10308 1.R1011

5'-most EST

LIB3078-055-Q1-K1-G9

Seq. No.

266078

Contig ID 5'-most EST 10309 1.R1011 uC-zmflb73055c07b1

Method NCBI GI BLAST score BLASTX g4324597 1610

E value Match length

1.0e-180 474

% identity NCBI Description

67 (AF106324) sodium proton exchanger Nhx1 [Arabidopsis

thaliana]

Seq. No.

266079

Contig ID 5'-most EST 10311 1.R1011 LIB83-014-Q1-E1-D7

Seq. No.

266080

Contig ID 5'-most EST 10322 1.R1011 $uwh70\overline{0}207268.h1$

Seq. No.

266081

Contig ID 5'-most EST

10322 2.R1011 xsy700210289.hl

Seq. No.

266082

Contig ID

10327 1.R1011

5'-most EST

LIB3079-016-Q1-K1-D8

Method NCBI GI BLAST score BLASTX g100728 1904

E value Match length 0.0e+00372 95

% identity NCBI Description

aspartate transaminase (EC 2.6.1.1) AAT3 precursor - proso

millet >gi_1084464_pir__S53304 aspartate aminotransferase - proso millet >gi_20601_emb_CAA45024_ (X63430) aspartate

aminotransferase [Panicum miliaceum]

>gi_435459_dbj_BAA04993_ (D25323) aspartate

aminotransferase [Panicum miliaceum]

Seq. No. Contig ID 266083

10327_2.R1011 uC-zmflMo17064g12b1

5'-most EST Method

BLASTX



NCBI GI g100728 BLAST score 877 E value 2.0e-94 Match length 188 % identity 90

NCBI Description aspartate transaminase (EC 2.6.1.1) AAT3 precursor - proso millet >gi_1084464_pir__S53304 aspartate aminotransferase - proso millet >gi 20601 emb CAA45024 (X63430) aspartate

aminotransferase [Panicum miliaceum]

>gi 435459 dbj BAA04993 (D25323) aspartate

aminotransferase [Panicum miliaceum]

Seq. No. 266084

Contig ID 10330_1.R1011 5'-most EST xjt700095505.h1

Method BLASTX
NCBI GI g584777
BLAST score 2070
E value 0.0e+00
Match length 467
% identity 84

NCBI Description PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 1 PRECURSOR

(PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 1) (DAHP

SYNTHETASE 1) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE

SYNTHASE 1)

Seq. No. 266085

Contig ID 10330 2.R1011

5'-most EST LIB3088-042-Q1-K1-F12

Method BLASTX
NCBI GI g584778
BLAST score 363
E value 2.0e-34
Match length 72
% identity 93

NCBI Description PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 2 PRECURSOR

(PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 2) (DAHP

SYNTHETASE 2) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE

SYNTHASE 2) >gi 542033 pir_S40412

2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 2

precursor - tomato >gi_410488_emb_CAA79856_ (Z21793) phospho-2-dehydro-3-deoxyheptonate aldolase [Lycopersicon

esculentum]

Seq. No. 266086

Contig ID 10330_3.R1011

5'-most EST LIB3069-002-Q1-K1-D6

Method BLASTX
NCBI GI g584779
BLAST score 585
E value 1.0e-60
Match length 118
% identity 91

NCBI Description PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 2 PRECURSOR

(PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 2) (DAHP

SYNTHETASE 2) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE

SYNTHASE 2) >gi 294285 (M95201)



3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Solanum tuberosum] >gi 445609 prf 1909356A deoxyarabinoheptulosonate phosphate synthase [Solanum tuberosum]

Seq. No. 266087

Contig ID 10330 5.R1011 5'-most EST fdz701159828.hl

Seq. No. 266088

Contig ID 10332 1.R1011

5'-most EST LIB3079-021-Q1-K1-D7

Method BLASTX NCBI GI g1707640 BLAST score 252 E value 4.0e-45

Match length 127 75 % identity

(X98355) transcription factor GAMyb [Oryza sativa] NCBI Description

266089 Seq. No.

Contig ID 10339 1.R1011 5'-most EST uC-zmflB73112c06b2

Method BLASTX NCBI GI g576886 BLAST score 379 1.0e-56 E value Match length 194 % identity 57

(L37750) kaurene synthase A [Zea mays] NCBI Description

266090 Seq. No.

Contig ID 10343 1.R1011

5'-most EST LIB3062-037-Q1-K1-B8

Method BLASTX g2947060 NCBI GI BLAST score 624 E value 1.0e-64 242 Match length

% identity 54

(AC002521) putative membrane protein [Arabidopsis thaliana] NCBI Description

Seq. No. 266091

10343 2.R1011 Contig ID

5'-most EST LIB3079-036-Q1-K1-B10

BLASTX Method NCBI GI g2947060 BLAST score 474 E value 1.0e-47 Match length 113 76 % identity

NCBI Description (AC002521) putative membrane protein [Arabidopsis thaliana]

266092 Seq. No.

10343 3.R1011 Contig ID 5'-most EST xsy700214727.hl

5'-most EST

Method



```
Seq. No.
                   266093
                   10343 4.R1011
Contig ID
                   uC-zmflmo17329h05a1
5'-most EST
Method
                   BLASTX
                   g2947060
NCBI GI
BLAST score
                   505
                   7.0e-51
E value
Match length
                   139
                   69
% identity
                   (AC002521) putative membrane protein [Arabidopsis thaliana]
NCBI Description
                   266094
Seq. No.
Contig ID
                   10343 5.R1011
                   rvt700550632.hl
5'-most EST
                   266095
Seq. No.
                   10348 1.R1011
Contig ID
5'-most EST
                   LIB3066-034-Q1-K1-E1
                   266096
Seq. No.
Contig ID
                   10351 1.R1011
                   LIB14\overline{3}-041-Q1-E1-G2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g733555
BLAST score
                   147
                   7.0e-09
E value
Match length
                   132
                   32
% identity
                   (U23450) No definition line found [Caenorhabditis elegans]
NCBI Description
                   266097
Seq. No.
                   10352 1.R1011
Contig ID
                   ypc700804349.h1
5'-most EST
Method
                   BLASTX
                   g100905
NCBI GI
                   213
BLAST score
                   5.0e-17
E value
Match length
                   81
                   62
% identity
NCBI Description Opaque-2 protein - maize
                   266098
Seq. No.
                   10352 2.R1011
Contig ID
                   LIB3079-035-Q1-K1-D9
5'-most EST
                   BLASTX
Method
                   g129171
NCBI GI
                   240
BLAST score
                   3.0e-20
E value
                   109
Match length
                   56
% identity
                   OPAQUE-2 REGULATORY PROTEIN >gi 22388 emb CAA33550
NCBI Description
                   (X15544) opaque-2 protein [Zea mays]
                   266099
Seq. No.
                   10353 1.R1011
Contig ID
```

36987

LIB83-012-Q1-E1-F12

BLASTX



97

53

NCBI Description (AC005223) 40409 [Arabidopsis thaliana]

Match length

% identity

```
g1170601
NCBI GI
                  569
BLAST score
                  2.0e-58
E value
Match length
                  239
                  51
% identity
                  FRUIT PROTEIN PKIWI502 >gi 1085869 pir S48036 hypothetical
NCBI Description
                  protein - kiwi fruit >gi 450237 (L27809) pKIWI502
                  [Actinidia deliciosa]
                  266100
Seq. No.
                  10358 1.R1011
Contig ID
                  uC-zmflb73029d11b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3342802
                  823
BLAST score
                  1.0e-161
E value
Match length
                  331
                  90
% identity
                  (AF061838) putative cytosolic 6-phosphogluconate
NCBI Description
                  dehydrogenase [Zea mays]
                  266101
Seq. No.
                  10359 1.R1011
Contig ID
                  uC-zmflb73226h12b1
5'-most EST
                  BLASTX
Method
                  g3128176
NCBI GI
BLAST score
                  336
                  6.0e-31
E value
                  103
Match length
                  58
% identity
                  (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
                  266102
Seq. No.
                  10361_1.R1011
Contig ID
5'-most EST
                  nbm700466673.h1
                  BLASTX
Method
NCBI GI
                  q4204263
BLAST score
                   445
                   2.0e-43
E value
                  180
Match length
                   48
% identity
NCBI Description (AC005223) 40409 [Arabidopsis thaliana]
                   266103
Seq. No.
                   10361 2.R1011
Contig ID
5'-most EST
                  uC-zmflmo17323g06a1
Seq. No.
                   266104
Contig ID
                   10361 3.R1011
5'-most EST
                   nbm700475602.h1
Method
                   BLASTX
NCBI GI
                   g4204263
BLAST score
                   227
E value
                   8.0e-19
```



```
266105
Seq. No.
                  10361 4.R1011
Contig ID
5'-most EST
                  nbm700467921.hl
Seq. No.
                  266106
                  10366 1.R1011
Contig ID
5'-most EST
                  LIB3136-019-Q1-K1-E6
                  BLASTX
Method
                  g4544443
NCBI GI
                  355
BLAST score
                  3.0e - 33
E value
                  176
Match length
% identity
                  (AC006592) putative mitochondrial uncoupling protein
NCBI Description
                  [Arabidopsis thaliana]
                  266107
Seq. No.
Contig ID
                  10368 1.R1011
                  LIB3079-035-Q1-K1-A3
5'-most EST
                  266108
Seq. No.
                  10369 1.R1011
Contig ID
5'-most EST
                  LIB3067-028-Q1-K1-E11
                  BLASTX
Method
                  q4510348
NCBI GI
                  386
BLAST score
                  7.0e-37
E value
Match length
                  146
% identity
                  (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                   266109
Seq. No.
                   10373 1.R1011
Contig ID
                  wty700162827.h1
5'-most EST
                   BLASTX
Method
                   g3293547
NCBI GI
                   295
BLAST score
E value
                   6.0e-26
Match length
                   324
% identity
                   31
                  (AF072709) putative oxidoreductase [Streptomyces lividans]
NCBI Description
                   266110
Seq. No.
                   10376 1.R1011
Contig ID
                   pmx700091496.hl
5'-most EST
                   266111
Seq. No.
                   10379 1.R1011
Contig ID
5'-most EST
                   LIB3136-003-Q1-K1-G2
                   BLASTX
Method
                   g3461813
NCBI GI
                   177
BLAST score
                   6.0e-13
E value
                   54
Match length
```

(AC004138) putative sucrose/H+ symporter [Arabidopsis

61

% identity

NCBI Description



thaliana]

266112 Seq. No. Contig ID 10380 1.R1011 5'-most EST uC-zmroteosintel16d12b2 BLASTX Method q2498512 NCBI GI BLAST score 301 2.0e-54 E value 588 Match length 28 % identity LDLC PROTEIN >gi_1082264_pir__A53542 brefeldin A-sensitive NCBI Description Golgi protein LDLC - human >gi 575654 emb CAA84427_ (Z34975) ldlCp [Homo sapiens] 266113 Seq. No. Contig ID 10380 3.R1011 5'-most EST uC-zmroteosinte038h06b1 266114 Seq. No. 10381 1.R1011 Contig ID uC-zmflmo17187h12b1 5'-most EST BLASTX Method g3540182 NCBI GI 578 BLAST score E value 4.0e-59 386 Match length 37 % identity (AC004122) Unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 266115 10381 2.R1011 Contig ID uC-zmflmo17128g02b1 5'-most EST Method BLASTX g3540182 NCBI GI 172 BLAST score 5.0e-12 E value 86 Match length % identity 37 (AC004122) Unknown protein [Arabidopsis thaliana] NCBI Description 266116 Seq. No. 10381 3.R1011 Contig ID $uC-zm\overline{f}lmo17101d08b1$ 5'-most EST BLASTX Method g3540182 NCBI GI 196 BLAST score 3.0e-14E value 241 Match length 46 % identity (AC004122) Unknown protein [Arabidopsis thaliana] NCBI Description 266117 Seq. No.

Contig ID 10381_4.R1011 5'-most EST uC-zmflm017211f06b1

Seq. No. 266118



Contig ID 10381_7.R1011 5'-most EST uC-zmflb73041d06b1

Seq. No. 266119

Contig ID 10381_9.R1011

5'-most EST uC-zmflmo17184h09b1

Seq. No. 266120

Contig ID 10382 1.R1011

5'-most EST LIB3079-042-Q1-K2-A11

Method BLASTX
NCBI GI g4455244
BLAST score 277
E value 1.0e-24
Match length 89
% identity 57

NCBI Description (AL035523) MtN3-like protein [Arabidopsis thaliana]

Seq. No. 266121

Contig ID 10383 1.R1011

5'-most EST LIB14 $\overline{3}$ -018-Q1-E1-E12

Method BLASTX
NCBI GI g3250695
BLAST score 486
E value 2.0e-48
Match length 309
% identity 59

NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 266122

Contig ID 10385 1.R1011

5'-most EST LIB3059-027-Q1-K1-H4

Seq. No. 266123

Contig ID 10385 2.R1011

5'-most EST LIB3079-034-Q1-K1-H12

Seq. No. 266124

Contig ID 10385 3.R1011

5'-most EST uC-zmflmo17012d01b1

Seq. No. 266125

Contig ID 10391_1.R1011

5'-most EST LIB3079-034-Q1-K1-E6

Seq. No. 266126

Contig ID 10391 2.R1011

5'-most EST LIB3180-052-P2-M1-H8

Seq. No. 266127

Contig ID 10393_1.R1011

5'-most EST LIB3079-034-Q1-K1-E8

Seq. No. 266128

Contig ID 10396 1.R1011

5'-most EST LIB3079-034-Q1-K1-F11

Method BLASTX



```
g1871593
NCBI GI
BLAST score
                  179
E value
                  1.0e-12
                  115
Match length
                  39
% identity
                  (Z92669) lipC [Mycobacterium tuberculosis]
NCBI Description
                  266129
Seq. No.
                  10400 1.R1011
Contig ID
                  uC-zmflb73020a11b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4566614
BLAST score
                  561
E value
                  2.0e-57
Match length
                  137
                  78
% identity
                  (AF112887) actin depolymerizing factor [Populus alba x
NCBI Description
                  Populus tremula]
Seq. No.
                  266130
                  10400 2.R1011
Contig ID
                  LIB3115-001-Q1-K1-A5
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4566614
BLAST score
                  396
                  3.0e-38
E value
Match length
                  99
                  76
% identity
NCBI Description
                  (AF112887) actin depolymerizing factor [Populus alba x
                  Populus tremula]
                  266131
Seq. No.
                  10400 3.R1011
Contig ID
5'-most EST
                  LIB3156-010-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                  g4566614
BLAST score
                  174
                   3.0e-12
E value
Match length
                   46
% identity
                  72
NCBI Description
                  (AF112887) actin depolymerizing factor [Populus alba x
                   Populus tremula]
                   266132
Seq. No.
                   10400 4.R1011
Contig ID
                  wty700166478.h1
5'-most EST
Method
                   BLASTX
                  g4185515
NCBI GI
                   352
BLAST score
                   2.0e-33
E value
```

90 Match length 76 % identity

NCBI Description (AF102824) actin depolymerizing factor 6 [Arabidopsis

thaliana]

266133 Seq. No.

10403 1.R1011 Contig ID



```
LIB3079-034-Q1-K1-F9
5'-most EST
                  BLASTX
Method
                  g4455224
NCBI GI
BLAST score
                  389
E value
                  5.0e-37
                  418
Match length
                  31
% identity
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                  266134
Seq. No.
                  10405 1.R1011
Contig ID
                  LIB3062-044-Q1-K1-C4
5'-most EST
                  266135
Seq. No.
                  10406 1.R1011
Contig ID
5'-most EST
                  xmt700263386.h1
                  BLASTX
Method
                  g1841502
NCBI GI
BLAST score
                  1937
                  0.0e+00
E value
                   381
Match length
% identity
                   96
                   (Y11029) glutothione-dependent formaldehyde dehydrogenase
NCBI Description
                   [Zea mays]
                   266136
Seq. No.
Contig ID
                  10406 2.R1011
5'-most EST
                  LIB3079-031-Q1-K1-C9
Method
                  BLASTX
                  g1841502
NCBI GI
BLAST score
                   570
E value
                   1.0e-58
Match length
                   115
                   94
% identity
NCBI Description
                   (Y11029) glutothione-dependent formaldehyde dehydrogenase
                   [Zea mays]
                   266137
Seq. No.
                   10409 1.R1011
Contig ID
                   pmx700083758.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2804455
BLAST score
                   205
                   3.0e-21
E value
Match length
                   183
% identity
NCBI Description
                   (AF043699) similar to a human orf (GB:D13642) and human
                   UV-damaged DNA binding factor (GB:U32986) in separate
                   non-overlapping regions [Caenorhabditis elegans]
                   266138
Seq. No.
Contig ID
                   10413 1.R1011
5'-most EST
                   uC-zmroteosinte047a07b1
```

Method BLASTX
NCBI GI g3128311
BLAST score 541
E value 8.0e-55



Match length 359 % identity 34

NCBI Description (AF010496) hypothetical protein [Rhodobacter capsulatus]

Seq. No. 266139

Contig ID 10416_1.R1011

5'-most EST LIB3079-033-Q1-K1-A3

Method BLASTX
NCBI GI g1174853
BLAST score 773
E value 3.0e-82
Match length 161
% identity 84

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-18 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42)

>gi_481811_pir__S39483 ubiquitin-conjugating enzyme UBC2-1
- Arabidopsis thaliana >gi_22658_emb_CAA48378_ (X68306)
ubiquitin-conjugating enzyme [Arabidopsis thaliana]

Seq. No. 266140

Contig ID 10416 2.R1011

5'-most EST LIB143-038-Q1-E1-B8

67

Method BLASTX
NCBI GI g1174853
BLAST score 542
E value 3.0e-55
Match length 150

% identity

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-18 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42)

>gi_481811_pir__S39483 ubiquitin-conjugating enzyme UBC2-1
- Arabidopsis thaliana >gi_22658_emb_CAA48378_ (X68306)
ubiquitin-conjugating enzyme [Arabidopsis thaliana]

Seq. No. 266141

Contig ID 10418 1.R1011

5'-most EST LIB3079-026-Q1-K1-G3

Method BLASTN
NCBI GI g1167556
BLAST score 35
E value 9.0e-10

Match length 107 % identity 83

NCBI Description Oryza sativa glycine-rich cell wall protein (Angrp-1) gene,

complete cds

Seq. No. 266142

Contig ID 10423_1.R1011 5'-most EST pmx700082710.h1

Method BLASTX
NCBI GI g3738297
BLAST score 492
E value 2.0e-49
Match length 204
% identity 22

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                  266143
Contig ID
                  10424 1.R1011
                  LIB3079-034-Q1-K1-B9
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3928090
BLAST score
                  205
                  6.0e-16
E value
Match length
                  86
                  47
% identity
                  (AC005770) putative MTN3 protein [Arabidopsis thaliana]
NCBI Description
                  266144
Seq. No.
Contig ID
                  10426 1.R1011
5'-most EST
                  LIB3079-054-Q1-K1-F4
                  266145
Seq. No.
Contig ID
                  10430 1.R1011
5'-most EST
                  uC-zmflmo17168b06b1
                  266146
Seq. No.
                  10435 1.R1011
Contig ID
                  LIB3079-034-Q1-K1-A5
5'-most EST
                  266147
Seq. No.
                  10437 1.R1011
Contig ID
                  uC-zmflmo17152e05b1
5'-most EST
                  BLASTX
Method
                  q3914467
NCBI GI
BLAST score
                  1621
                  0.0e+00
E value
Match length
                   465
                  70
% identity
                  26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
NCBI Description
                   >qi 1864003 dbj BAA19252 (AB001422) 21D7 [Nicotiana
                   tabacum]
                   266148
Seq. No.
                  10437_2.R1011
Contig ID
5'-most EST
                  LIB3152-041-P1-K1-B8
Method
                   BLASTX
                   g3914468
NCBI GI
BLAST score
                   156
                   3.0e-10
E value
Match length
                   122
                   34
% identity
                  26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
NCBI Description
                   >gi_478411_pir__JQ2257 nuclear antigen 21D7 - carrot
                   >gi 217911 dbj BAA02696 (D13434) 21D7 antigen [Daucus
                   carota]
                   266149
Seq. No.
```

Contig ID 10437_3.R1011 5'-most EST wty700172136.h1

Method BLASTX
NCBI GI g3914467
BLAST score 244
E value 2.0e-20



Match length 56 86 % identity 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) NCBI Description >gi 1864003 dbj_BAA19252_ (AB001422) 21D7 [Nicotiana tabacum] 266150 Seq. No. 10437 4.R1011 Contia ID uC-zmflmo17329b09a1 5'-most EST BLASTX Method g3914467 NCBI GI BLAST score 364 1.0e-34 E value 96 Match length 71 % identity 26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) NCBI Description >gi_1864003_dbj_BAA19252_ (AB001422) 21D7 [Nicotiana tabacum] 266151 Seq. No. 10437 5.R1011 Contig ID LIB3061-046-Q1-K1-C6 5'-most EST 266152 Seq. No. 10438 1.R1011 Contig ID LIB3150-050-Q1-N1-E3 5'-most EST Seq. No. 266153 10441 1.R1011 Contig ID LIB3069-052-Q1-K1-G10 5'-most EST 266154 Seq. No. 10441 3.R1011 Contig ID xjt700096410.h1 5'-most EST 266155 Seq. No. Contig ID 10443 1.R1011 5'-most EST ntr700072089.h1 Method BLASTX NCBI GI q4263695 BLAST score 200 6.0e-19 E value Match length 283 25 % identity (AC006223) putative myosin II heavy chain [Arabidopsis NCBI Description thaliana] Seq. No. 266156 Contig ID 10455 1.R1011 LIB3079-033-Q1-K1-G7 5'-most EST

Seq. No. 266157

Contig ID 10456_1.R1011

5!-most EST uC-zmflmo17233g08a1

Seq. No. 266158

Contig ID 10459_1.R1011



```
5'-most EST
                   uC-zmflmo17201f01b1
                   BLASTX
Method
                   g4585976
NCBI GI
BLAST score
                   791
                   3.0e-84
E value
                   205
Match length
                   72
% identity
                   (AC005287) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   266159
Seq. No.
                   10459 2.R1011
Contig ID
                   uC-zmflb73121a02b2
5'-most EST
Method
                   BLASTX
                   g4585976
NCBI GI
BLAST score
                   505
                   4.0e-51
E value
                   169
Match length
                   59
% identity
                   (AC005287) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   266160
Seq. No.
                   10459 3.R1011
Contig ID
                   tzu700205743.h1
5'-most EST
                   BLASTX
Method
                   q4585976
NCBI GI
                   246
BLAST score
                   9.0e-21
E value
Match length
                   61
                   72
% identity
                   (AC005287) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   266161
Seq. No.
                   10460_1.R1011
Contig ID
                   LIB3115-015-P1-K1-D9
5'-most EST
                   BLASTN
Method
                   q206371
NCBI GI
BLAST score
                   103
E value
                   2.0e-50
                   508
Match length
                   100
% identity
NCBI Description Rat(Sprague-Dawley) prolactin gene:exons IV, V and flanks
                   266162
Seq. No.
                   10461_1.R1011
Contig ID
                   LIB3069-006-Q1-K1-G5
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2655291
BLAST score
                   870
E value
                   1.0e-93
                   191
Match length
% identity
                   (AF032974) germin-like protein 4 [Oryza sativa]
NCBI Description
                   266163
Seq. No.
                   10461 2.R1011
Contig ID
                   uC-zmflb73039e04b1
5'-most EST
```

36997

BLASTX

Method

BLAST score

Match length

E value

782

268

5.0e-83



```
NCBI GI
                   g2655291
BLAST score
                   513
                   5.0e-52
E value
                   110
Match length
                   88
% identity
                  (AF032974) germin-like protein 4 [Oryza sativa]
NCBI Description
Seq. No.
                   266164
                   10465 1.R1011
Contig ID
5'-most EST
                   uC-zm\overline{f}lmo17099e09b1
                   266165
Seq. No.
                   10468 1.R1011
Contig ID
                   LIB3079-041-Q1-K1-B8
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4105719
BLAST score
                   1068
                   1.0e-117
E value
Match length
                   215
                   98
% identity
                  (AF050128) cell wall invertase Incw2; beta-fructosidase
NCBI Description
                   [Zea mays]
                   266166
Seq. No.
Contig ID
                   10468 2.R1011
                   uC-zmroteosinte012g05b1
5'-most EST
Method
                   BLASTX
                   g3372518
NCBI GI
BLAST score
                   341
                   4.0e-32
E value
Match length
                   75
% identity
                   88
NCBI Description
                  (AF050631) invertase [Zea mays]
Seq. No.
                   266167
Contig ID
                   10471_1.R1011
5'-most EST
                   ntr70\overline{0}076516.h1
Method
                   BLASTX
NCBI GI
                   q2224915
BLAST score
                   607
                   5.0e-63
E value
Match length
                   149
                   73
% identity
NCBI Description
                  (U95968) beta-expansin [Oryza sativa]
                   266168
Seq. No.
Contig ID
                   10472 1.R1011
5'-most EST
                   LIB3136-051-Q1-K1-C12
                   266169
Seq. No.
Contig ID
                   10473 1.R1011
5'-most EST
                   uC-zmflb73198b05b1
Method
                   BLASTX
NCBI GI
                   g3281861
```



% identity 55
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

 Seq. No.
 266170

 Contig ID
 10473_3.R1011

 5'-most EST
 xsy700209753.h1

Seq. No. 266171

Contig ID 10473 5.R1011 5'-most EST gct701172662.h1

Seq. No. 266172

Contig ID 10476_1.R1011 5'-most EST rvt700549956.h1

Seq. No. 266173

Contig ID 10477_1.R1011 5'-most EST vux700156629.h1

Seq. No. 266174

Contig ID 10477 2.R1011

5'-most EST LIB3136-040-P1-K1-A11

Seq. No. 266175

Contig ID 10477_3.R1011 5'-most EST dyk700106516.h1

Seq. No. 266176

Contig ID 10483 1.R1011 5'-most EST gct701167924.h1

Method BLASTX
NCBI GI g1076287
BLAST score 374
E value 6.0e-44
Match length 167

% identity 50

NCBI Description amine acid permease - Arabidopsis thaliana

>gi_510236_emb_CAA50672_ (X71787) amine acid permease

[Arabidopsis thaliana]

Seq. No. 266177

Contig ID 10494 1.R1011

5'-most EST uC-zmroteosinte099c12b2

Method BLASTX
NCBI GI g1572801
BLAST score 649
E value 2.0e-67
Match length 283
% identity 45

NCBI Description (U70854) F38A5.1 gene product [Caenorhabditis elegans]

Seq. No. 266178

Contig ID 10495_1.R1011

5'-most EST uC-zmroteosinte034d09b1

Method BLASTX
NCBI GI g3928085
BLAST score 682



E value 1.0e-71
Match length 204
% identity 60

NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 266179

Contig ID 10498 2.R1011

5'-most EST LIB3079-032-Q1-K1-F12

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 9.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 266180

Contig ID 10499_1.R1011 5'-most EST uC-zmflb73380h07a1

Method BLASTX
NCBI GI g4587549
BLAST score 1219
E value 1.0e-134
Match length 391
% identity 62

NCBI Description (AC006577) Similar to gb_U55861 RNA binding protein

nucleolysin (TIAR) from Mus musculus and contains several PF 00076 RNA recognition motif domains. ESTs gb_T21032 and

gb T44127 come from this gene. [Arabidopsis t

Seq. No. 266181

Contig ID 10499_2.R1011

5'-most EST LIB3088-021-Q1-K1-D7

Method BLASTN
NCBI GI g3821780
BLAST score 34
E value 2.0e-09
Match length 34
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 266182

Contig ID 10499_3.R1011

5'-most EST uC-zmroteosinte025c10b1

Method BLASTX
NCBI GI g4587549
BLAST score 491
E value 2.0e-49
Match length 125
% identity 70

NCBI Description (AC006577) Similar to gb_U55861 RNA binding protein

nucleolysin (TIAR) from Mus musculus and contains several PF_00076 RNA recognition motif domains. ESTs gb_T21032 and

gb_T44127 come from this gene. [Arabidopsis t

Seq. No. 266183

Contig ID 10500 1.R1011



5'-most EST uC-zmflb73278d01b1

Method BLASTX
NCBI GI g4325041
BLAST score 1997
E value 0.0e+00
Match length 654
% identity 81

NCBI Description (AF117339) FtsH-like protein Pftf precursor [Nicotiana

tabacum]

Seq. No. 266184

Contig ID 10500_2.R1011 5'-most EST ymt700221338.h1

Seq. No. 266185

Contig ID 10500_3.R1011

5'-most EST LIB3136-038-P1-K1-G6

Seq. No. 266186

Contig ID 10505_1.R1011 5'-most EST ymt700222847.h1

Method BLASTX
NCBI GI g2342685
BLAST score 357
E value 2.0e-33
Match length 136

% identity 50

NCBI Description (AC000106) Contains similarity to Rhodococcus amidase

(gb_D16207). ESTs gb_T20504, gb_H36650, gb_N97423, gb_H36595

come from this gene. [Arabidopsis thaliana]

Seq. No. 266187

Contig ID 10506_1.R1011 5'-most EST wty700168565.h1

Seq. No. 266188

Contig ID 10507_1.R1011 5'-most EST cyk700049385.f1

Method BLASTX
NCBI GI g461899
BLAST score 620
E value 2.0e-64
Match length 198
% identity 62

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR

(PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_1076368_pir__B53422_peptidylprolyl isomerase

(EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi_405131 (L14845) cyclophilin [Arabidopsis thaliana] >gi_1322278

(U42724) cyclophilin [Arabidopsis thaliana]

Seq. No. 266189

Contig ID 10507_2.R1011

5'-most EST LIB3079-016-Q1-K1-H7

Method BLASTX NCBI GI g461899 BLAST score 223



E value 3.0e-18 Match length 94 % identity 56

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR

(PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_1076368_pir__B53422 peptidylprolyl isomerase (EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi_405131

(L14845) cyclophilin [Arabidopsis thaliana] >gi_1322278

(U42724) cyclophilin [Arabidopsis thaliana]

Seq. No. 266190

Contig ID 10508 1.R1011

5'-most EST uC-zmflmo17215f05b1

Method BLASTX
NCBI GI g3980413
BLAST score 1020
E value 1.0e-173
Match length 547
% identity 43

NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No. 266191

Contig ID 10508_2.R1011 5'-most EST uC-zmflb73296c01a1

Seq. No. 266192

Contig ID 10509_1.R1011 5'-most EST ymt700223494.h1

Method BLASTX
NCBI GI 94582435
BLAST score 166
E value 2.0e-11
Match length 69
% identity 45

NCBI Description (AC007196) putative selenium-binding protein [Arabidopsis

thaliana]

Seq. No. 266193

Contig ID 10518_1.R1011 5'-most EST nbm700473322.h1

Method BLASTN
NCBI GI g1657765
BLAST score 151
E value 2.0e-79
Match length 187
% identity 95

NCBI Description Zea mays retrotransposon Milt 5' LTR and primer binding

site DNA sequence

Seq. No. 266194

Contig ID 10524 1.R1011

5'-most EST LIB3079-031-Q1-K1-G12

Method BLASTX
NCBI GI g3264767
BLAST score 241
E value 3.0e-20
Match length 60



% identity

NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.

266195

Contig ID

10524 3.R1011

5'-most EST

LIB3060-003-Q1-K1-A9

Seq. No.

266196

Contig ID

10538 1.R1011

5'-most EST

LIB3059-044-Q1-K1-E6

Seq. No.

266197

Contig ID

10538 2.R1011

5'-most EST

LIB3079-032-Q1-K1-A7

Seq. No.

266198

Contig ID

10539 1.R1011

5'-most EST

LIB3079-032-Q1-K1-A6

Seq. No.

266199

Contig ID 5'-most EST 10546_1.R1011 ntr700074288.h1

Method

BLASTX

NCBI GI

q4538911

BLAST score

723

E value

4.0e-76

Match length

295

50

% identity NCBI Description

(AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No.

266200

Contig ID 5'-most EST 10546_2.R1011 pmx700083791.h1

Method

BLASTX

NCBI GI

g4263722

623

BLAST score E value

9.0e-65

Match length

180

% identity

64

NCBI Description

(AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No.

Method

266201

Contig ID

10546 3.R1011

5'-most EST

uC-zmflmo17118d12a1

NCBI GI

BLASTX g4263722

BLAST score

304

E value

1.0e-27

Match length

66

% identity NCBI Description

(AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No.

266202

Contig ID

10546 4.R1011

5'-most EST

tzu700206545.h1

Method

BLASTX

NCBI GI

g4538911



BLAST score 148 E value 3.0e-09 Match length 49 % identity 59

NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]

Seq. No. 266203

Contig ID 10546 10.R1011

5'-most EST LIB3152-036-P1-K1-C5

Seq. No. 266204

Contig ID 10547 1.R1011

5'-most EST LIB3079-006-Q1-K1-G4

Seq. No. 266205

Contig ID 10556_1.R1011 5'-most EST xsy700209165.h1

Method BLASTN
NCBI GI g1808687
BLAST score 101
E value 3.0e-49
Match length 286
% identity 82

NCBI Description S.stapfianus pSD.13 mRNA

Seq. No. 266206

Contig ID 10556_2.R1011

5'-most EST LIB189-009-Q1-E1-H2

Method BLASTN
NCBI GI g1808687
BLAST score 88
E value 2.0e-41
Match length 282

% identity 80

NCBI Description S.stapfianus pSD.13 mRNA

Seq. No. 266207

Contig ID 10556_3.R1011

5'-most EST LIB3067-022-Q1-K1-A7

Method BLASTN
NCBI GI g1808687
BLAST score 144
E value 4.0e-75
Match length 271
% identity 89

NCBI Description S.stapfianus pSD.13 mRNA

Seq. No. 266208

Contig ID 10556 4.R1011

5'-most EST LIB3088-001-Q1-K1-G12

Method BLASTN
NCBI GI g1808687
BLAST score 35
E value 4.0e-10

Match length 39 % identity 97

NCBI Description S.stapfianus pSD.13 mRNA

E value

Match length

% identity

3.0e-15

80



```
266209
Seq. No.
                  10556 5.R1011
Contig ID
                  uC-zm\overline{f}lmo17267d04b1
5'-most EST
Method
                  BLASTN
NCBI GI
                  q1808687
BLAST score
                  88
E value
                  1.0e-41
Match length
                  234
% identity
                   78
NCBI Description S.stapfianus pSD.13 mRNA
Seq. No.
                   266210
Contig ID
                  10556 6.R1011
5'-most EST
                  LIB3150-013-Q1-N1-D2
Method
                  BLASTN
                  g1808687
NCBI GI
                  83
BLAST score
                   9.0e-39
E value
Match length
                   235
% identity
                   74
NCBI Description S.stapfianus pSD.13 mRNA
                   266211
Seq. No.
                  10557_1.R1011
Contig ID
5'-most EST
                   cat700016364.rl
                   BLASTX
Method
NCBI GI
                   q2982309
BLAST score
                   210
E value
                   2.0e-16
Match length
                   47
                   77
% identity
NCBI Description
                  (AF051239) probable ubiquitin activating enzyme 2 [Picea
                   mariana]
Seq. No.
                   266212
                   10560 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73260h04b2
Method
                   BLASTX
NCBI GI
                   g2497528
BLAST score
                   545
E value
                   3.0e-64
Match length
                   259
% identity
                   54
                  KINESIN-LIKE PROTEIN KIF2 (KINESIN-RELATED PROTEIN XKIF2)
NCBI Description
                   >gi 1171151 (U36486) kinesin-related protein XKIF2 [Xenopus
                   laevis]
                   266213
Seq. No.
                   10560 2.R1011
Contig ID
5'-most EST
                   fdz701165833.h1
                   BLASTN
Method
NCBI GI
                   g1185555
BLAST score
                   44
```



NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc4) gene, partial cds

Seq. No. 266214

Contig ID 10561 1.R1011

5'-most EST LIB3079-031-Q1-K1-F11

Seq. No. 266215

Contig ID 10564_1.R1011 5'-most EST gwl700616639.h1

Seq. No. 266216

Contig ID 10564_2.R1011 5'-most EST fdz701165233.h1

Seq. No. 266217

Contig ID 10565_1.R1011 5'-most EST pmx700088211.h1

Method BLASTX
NCBI GI g3328101
BLAST score 933
E value 1.0e-100

Match length 564 % identity 40

NCBI Description (AF073995) beta-galactosidase [synthetic construct]

Seq. No. 266218

Contig ID 10566_1.R1011 5'-most EST ntr700077059.h1

Seq. No. 266219

Contig ID 10566 2.R1011

5'-most EST LIB3067-045-Q1-K1-F11

Seq. No. 266220

Contig ID 10567_1.R1011 5'-most EST uC-zmflB73044c12b1

Method BLASTX
NCBI GI g3096922
BLAST score 240
E value 7.0e-20
Match length 82
% identity 60

NCBI Description (AL023094) putative protein [Arabidopsis thaliana]

Seq. No. 266221

Contig ID 10569_1.R1011

5'-most EST LIB3079-031-Q1-K1-F12

Method BLASTX
NCBI GI g1170409
BLAST score 163
E value 1.0e-10
Match length 49
% identity 65

NCBI Description HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22)

>gi_549887 (U09336) homeobox protein [Arabidopsis thaliana]
>gi_549888 (U09337) homeobox protein [Arabidopsis thaliana]

```
>gi 4490724_emb_CAB38927.1_ (AL035709) homeobox protein
HAT22 [Arabidopsis thaliana]
266222
10570 1.R1011
wty700172138.h1
BLASTX
```

q2736286 NCBI GI BLAST score 1062 1.0e-116 E value Match length 221 88 % identity

Seq. No.

Contig ID

5'-most EST Method

(AF031079) isopentenyl diphosphate isomerase I [Camptotheca NCBI Description

acuminata]

266223 Seq. No. Contig ID 10571 1.R1011

uC-zmflmo17342a02a1 5'-most EST

Method BLASTX NCBI GI q3860249 BLAST score 170 E value 7.0e-12 87

Match length % identity 44

(AC005824) unknown protein [Arabidopsis thaliana] NCBI Description

266224 Seq. No.

Contig ID 10572 1.R1011

5'-most EST LIB189-032-Q1-E1-C11

266225 Seq. No.

10575 1.R1011 Contig ID 5'-most EST uC-zmrob73033a02b1

Method BLASTX g1169128 NCBI GI 559 BLAST score 3.0e-57 E value Match length 132 80 % identity

SERINE/THREONINE-PROTEIN KINASE CTR1 >gi 166680 (L08789) NCBI Description protein kinase [Arabidopsis thaliana] >gi 166682 (L08790)

protein kinase [Arabidopsis thaliana]

266226 Seq. No.

10576_1.R1011 Contig ID

 $uC-zm\overline{f}lmo17150g09b1$ 5'-most EST

Method BLASTX NCBI GI q4337176 BLAST score 183 8.0e-13 E value 193 Match length % identity

NCBI Description (AC006416) T31J12.4 [Arabidopsis thaliana]

266227 Seq. No.

10576 2.R1011 Contig ID 5'-most EST hbs701185312.h1



266228 Seq. No.

10583 1.R1011 Contig ID $uC-zm\overline{f}1b73016c05b1$ 5'-most EST

BLASTX Method g4204793 NCBI GI 633 BLAST score 4.0e-66 E value 154 Match length 79 % identity

(U52079) P-glycoprotein [Solanum tuberosum] NCBI Description

266229 Seq. No.

10585 1.R1011 Contig ID

LIB3150-041-Q1-N1-D10 5'-most EST

266230 Seq. No.

10586 1.R1011 Contig ID

LIB3079-024-Q1-K1-B7 5'-most EST

BLASTN Method g3821780 NCBI GI 36 BLAST score

1.0e-10 E value 48 Match length 67 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 266231

10590 1.R1011 Contig ID

LIB3115-022-P1-K1-C7 5'-most EST

BLASTX Method NCBI GI g3023751 BLAST score 328 7.0e-30 E value 236 Match length 37 % identity

NCBI Description 70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS

ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383
peptidylprolyl isomerase (EC 5.2.1.8) - wheat

>gi 854626 emb CAA60505_ (X86903) peptidylprolyl isomerase

[Triticum aestivum]

266232 Seq. No.

10596 1.R1011 Contig ID

uC-zmflmo17035e12b1 5'-most EST

BLASTX Method NCBI GI q2864614 BLAST score 454 E value 5.0e-45 Match length 202 49 % identity

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

266233 Seq. No.

10604 1.R1011 Contig ID $cyk70\overline{0}052259.f1$ 5'-most EST

Method BLASTX

```
a3033392
NCBI GI
BLAST score
                  916
                  8.0e-99
E value
Match length
                  362
% identity
                  51
                   (AC004238) putative translation initiation factor
NCBI Description
                  EIF-2B-epsilon subunit [Arabidopsis thaliana]
                  266234
Seq. No.
                  10608 1.R1011
Contig ID
5'-most EST
                  LIB3180-033-P2-M2-C3
Method
                  BLASTX
                  q2398829
NCBI GI
                  680
BLAST score
E value
                  2.0e-71
                  198
Match length
                  68
% identity
                  (Y11220) mitochondrial uncoupling protein [Solanum
NCBI Description
                  tuberosum]
                  266235
Seq. No.
                  10608 2.R1011
Contig ID
5'-most EST
                  LIB3152-014-P1-K1-D8
Method
                  BLASTX
                  q3335378
NCBI GI
BLAST score
                   328
                   3.0e - 30
E value
Match length
                  161
% identity
                   44
                  (AC003028) Myb-related transcription activator [Arabidopsis
NCBI Description
                  thaliana]
                   266236
Seq. No.
Contig ID
                   10609 1.R1011
5'-most EST
                  LIB3069-028-Q1-K1-B7
Method
                  BLASTX
                  q1706551
NCBI GI
                   224
BLAST score
                   1.0e-17
E value
Match length
                  85
                   47
% identity
                  GLUCAN ENDO-1, 3-BETA-GLUCOSIDASE PRECURSOR
NCBI Description
                   ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                   (BETA-1,3-ENDOGLUCANASE) >gi 924953 (U30323) beta
                   1,3-glucanase [Triticum aestivum]
                   266237
Seq. No.
```

 Seq. No.
 266237

 Contig ID
 10609_2.R1011

 5'-most EST
 LIB3079-031-Q1-K1-A2

 Method
 BLASTX

 NCBI GI
 g4335750

 BLAST score
 184

 E value
 1.0e-13

Match length 64 % identity 47

NCBI Description (AC006284) putative beta-1,3-endoglucanase [Arabidopsis

thaliana]



Seq. No. 266238 Contig ID 10614_1.R1011

5'-most EST uwc700150413.h1

Seq. No. 266239 Contig ID 10616 1.R1011

5'-most EST uC-zmflmo17321g06b1

Method BLASTX
NCBI GI g3183321
BLAST score 205
E value 2.0e-15
Match length 156
% identity 33

NCBI Description HYPOTHETICAL 28.1 KD PROTEIN C4F8.03 IN CHROMOSOME I

 $>gi_2330820_emb_CAB11050_$ (Z98530) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 266240 Contig ID 10618_1.R1011

5'-most EST xyt700342764.h1 Method BLASTX

Method BLASTX
NCBI GI 94504161
BLAST score 276
E value 8.0e-24
Match length 218
% identity 21

NCBI Description G-rich RNA sequence binding factor 1

>gi_2500579_sp_Q12849_GRF1_HUMAN G-RICH_SEQUENCE_FACTOR-1 (GRSF-1) >gi_517196 (U07231) G-rich_sequence_factor-1 [Homo

sapiens]

Seq. No. 266241

Contig ID 10618_2.R1011 5'-most EST LIB83-005-Q1-E1-B8

Seq. No. 266242

Contig ID 10618_3.R1011 5'-most EST uC-zmflb73179c01b1

Seq. No. 266243

Contig ID 10618_5.R1011 5'-most EST uwc700153490.h1

Seq. No. 266244

Contig ID 10619_1.R1011

5'-most EST LIB3079-030-Q1-K1-F7

Seq. No. 266245

Contig ID 10621_1.R1011

5'-most EST uC-zmflmo17297e09b1

Method BLASTX
NCBI GI g2262105
BLAST score 745
E value 3.0e-79
Match length 197
% identity 68



NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 266246

Contig ID 10622 1.R1011

5'-most EST uC-zmroteosinte003c05b1

Method BLASTX
NCBI GI g4106818
BLAST score 456
E value 8.0e-45
Match length 399
% identity 34

NCBI Description (AF083395) phospholipase A2-activating protein [Homo

sapiens]

Seq. No. 266247

Contig ID 10627 1.R1011

5'-most EST LIB3079-030-Q1-K1-G7

Seq. No. 266248

Contig ID 10628 1.R1011

5'-most EST LIB3079-030-Q1-K1-G8

Seq. No. 266249

Contig ID 10633_1.R1011 5'-most EST uC-zmflb73160b01a1

Seq. No. 266250

Contig ID 10634_1.R1011 5'-most EST cyk700050072.f1

Method BLASTX
NCBI GI 94467134
BLAST score 499
E value 1.0e-50
Match length 132
% identity 70

NCBI Description (AL035540) protein kinase like protein [Arabidopsis

thaliana]

Seq. No. 266251

Contig ID 10635_1.R1011

5'-most EST LIB3180-062-P2-M1-H5

Method BLASTX
NCBI GI g2129636
BLAST score 224
E value 2.0e-18
Match length 117
% identity 43

NCBI Description lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase

[Arabidopsis thaliana]

Seq. No. 266252

Contig ID 10635 2.R1011

5'-most EST LIB3153-009-Q1-K1-A3

Method BLASTX
NCBI GI g4314378
BLAST score 257
E value 2.0e-33



Match length 179 % identity 44

NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 266253

Contig ID 10636 1.R1011

5'-most EST uC-zmflMo17064b06b1

Method BLASTX
NCBI GI g2979553
BLAST score 286
E value 3.0e-25
Match length 143
% identity 40

NCBI Description (AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No. 266254

Contig ID 10638_1.R1011 5'-most EST uC-zmrob73079h09b1

Method BLASTX
NCBI GI g4522012
BLAST score 842
E value 4.0e-90
Match length 282
% identity 58

NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 266255

Contig ID 10638_2.R1011

5'-most EST LIB3079-022-Q1-K1-A10

Seq. No. 266256

Contig ID 10638_3.R1011 5'-most EST uC-zmflb73054h12b1

Method BLASTX
NCBI GI g4522012
BLAST score 570
E value 8.0e-64
Match length 217
% identity 56

NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 266257

Contig ID 10638 4.R1011

5'-most EST LIB3180-037-P2-M2-A7

Seq. No. 266258

Contig ID 10638_9.R1011 5'-most EST cyk700049105.f1

Method BLASTX
NCBI GI 94522012
BLAST score 196
E value 3.0e-15
Match length 68
% identity 51

NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 266259

```
641 1.R1011
Contig ID
                  LIB3079-030-Q1-K1-E7
5'-most EST
                   266260
Seq. No.
                   10649 1.R1011
Contig ID
                  wyr700242541.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3822036
                   941
BLAST score
                   1.0e-132
E value
                   283
Match length
                   83
% identity
                  (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
NCBI Description
                   266261
Seq. No.
                   10649 2.R1011
Contig ID
                   dyk700106144.hl
5'-most EST
                   BLASTN
Method
NCBI GI
                   q3822035
                   101
BLAST score
                   3.0e-49
E value
                   374
Match length
                   99
% identity
                   Zea mays endo-1,3-1,4-beta-D-glucanase mRNA, complete cds
NCBI Description
                   266262
Seq. No.
                   10656 1.R1011
Contig ID
                   qmh700027596.f1
5'-most EST
Seq. No.
                   266263
                   10658 1.R1011
Contig ID
                   LIB3067-009-Q1-K1-A10
5'-most EST
                   BLASTX
Method
                   g1707032
NCBI GI
                   440
BLAST score
                   3.0e-44
E value
                   204
Match length
                   45
% identity
                   (U80445) coded for by C. elegans cDNA yk13g5.3; coded for
NCBI Description
                   by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA
                   CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for
                   by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA
                   yk65h8
                   266264
Seq. No.
                   10661_1.R1011
Contig ID
                   wty700170064.h1
5'-most EST
                   BLASTX
Method
                   q3252807
NCBI GI
BLAST score
                   698
                    2.0e-73
E value
                   274
Match length
                    51
 % identity
                   (AC004705) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    266265
 Seq. No.
                    10665 1.R1011
 Contig ID
```



```
dyk700103309.h1
5'-most EST
                  BLASTX
Method
                  q2213583
NCBI GI
                  568
BLAST score
                  6.0e-58
E value
                  226
Match length
                  49
% identity
                  (AC000348) T7N9.3 [Arabidopsis thaliana]
NCBI Description
                  266266
Seq. No.
                  10665 3.R1011
Contig ID
5'-most EST
                  uC-zmromo17016b10a1
                  266267
Seq. No.
                  10666 1.R1011
Contig ID
5'-most EST
                  LIB3079-030-Q1-K1-A8
                  266268
Seq. No.
                  10666 3.R1011
Contig ID
5'-most EST
                  xdb70\overline{0}340329.h1
                  266269
Seq. No.
                  10670 1.R1011
Contig ID
5'-most EST
                  LIB3079-041-Q1-K1-F10
Method
                   BLASTX
                   g2621082
NCBI GI
BLAST score
                   148
                   5.0e-09
E value
                   126
Match length
% identity
                   37
                  (AE000796) conserved protein [Methanobacterium
NCBI Description
                   thermoautotrophicum]
                   266270
Seq. No.
                   10671_1.R1011
Contig ID
5'-most EST
                   LIB3079-029-Q1-K1-F6
Method
                   BLASTX
NCBI GI
                   q3150415
BLAST score
                   369
                   3.0e-35
E value
Match length
                   93
% identity
                   (AC004165) sec13-related protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3420046 (AC004680) sec13-related protein [Arabidopsis
                   thaliana]
Seq. No.
                   266271
                   10671 2.R1011
Contig ID
5'-most EST
                   xsy700214856.hl
Method
                   BLASTX
NCBI GI
                   g3150415
BLAST score
                   236
```

E value 1.0e-19 Match length 62 60 % identity

NCBI Description (AC004165) sec13-related protein [Arabidopsis thaliana] >gi 3420046 (AC004680) sec13-related protein [Arabidopsis



thaliana]

Seq. No. 266272 Contig ID 10676 2.R

Contig ID 10676_2.R1011 5'-most EST rv1700455062.h1

Method BLASTX
NCBI GI 94587585
BLAST score 950
E value 1.0e-103
Match length 315
% identity 63

NCBI Description (AC007232) hypothetical protein [Arabidopsis thaliana]

Seq. No. 266273

Contig ID 10689_1.R1011 5'-most EST wen700334456.h1

Method BLASTX
NCBI GI g2576411
BLAST score 484
E value 2.0e-48
Match length 155
% identity 64

NCBI Description (AF012833) similar to dynamin-like protein encoded by

GenBank Accession Number X99669 [Arabidopsis thaliana]

Seq. No. 266274

5'-most EST uC-zmflmo17293a11b1

Method BLASTX
NCBI GI g3549667
BLAST score 1024
E value 1.0e-112
Match length 267
% identity 73

NCBI Description (AL031394) Arabidopsis dynamin-like protein ADL2

[Arabidopsis thaliana]

Seq. No. 266275

Contig ID 10690_1.R1011 5'-most EST fdz701165761.h1

Method BLASTX
NCBI GI g4432834
BLAST score 170
E value 1.0e-11
Match length 83
% identity 47

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 266276

Contig ID 10690_2.R1011 5'-most EST hvj700620711.h1

Method BLASTX
NCBI GI 94432834
BLAST score 160
E value 2.0e-10
Match length 83
% identity 45

```
(AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                   266277
Seq. No.
                   10694 1.R1011
Contig ID
                   wyr70\overline{0}242351.h1
5'-most EST
                   BLASTX
Method
                   q2723473
NCBI GI
                   558
BLAST score
                   3.0e-57
E value
                   114
Match length
                   97
% identity
                   (D89726) defender against apoptotic death 1 protein [Oryza
NCBI Description
                   sativa] >gi_2723883_dbj_BAA24104_ (D89727) defender against
                   apoptotic death 1 protein [Oryza sativa]
                   266278
Seq. No.
                   10696 1.R1011
Contig ID
                   uC-zmflb73084c10b2
5'-most EST
                   BLASTX
Method
NCBI GI
                   q22122
                   1853
BLAST score
                   0.0e + 00
E value
                   379
Match length
                   93
% identity
                   (X04050) alcohol dehydrogenase 1 [Zea mays] >gi_3420021
NCBI Description
                   (AF050457) alcohol dehydrogenase 1 [Zea mays]
                   266279
Seq. No.
                   10696 2.R1011
Contig ID
5'-most EST
                   uC-zmflmo17073a02b1
                   BLASTX
Method
                   q3420019
NCBI GI
BLAST score
                   421
                   3.0e-41
E value
Match length
                   83
                   98
% identity
                   (AF050456) putative alcohol dehydrogenase 1 [Sorghum
NCBI Description
                   bicolor]
Seq. No.
                   266280
                   10696 3.R1011
Contig ID
                   rvt700552424.h1
5'-most EST
                   BLASTN
Method
                   g22121
NCBI GI
BLAST score
                   150
                   6.0e-79
E value
                   214
Match length
                   97
% identity
NCBI Description Maize alcohol dehydrogenase 1 gene (Adh1-1F)
                   266281
Seq. No.
                   10696 6.R1011
Contig ID
5'-most EST
                   LIB3117-013-Q1-K1-F10
                   BLASTX
Method
                   g1351874
NCBI GI
```

438

3.0e-43

BLAST score

E value



92 Match length 91 % identity

ALCOHOL DEHYDROGENASE 1 >gi_553077 (L08590) alcohol NCBI Description dehydrogenase 1 [Zea mays] >gi_951357 (L08588) alcohol

dehydrogenase 1 [Zea luxurians]

266282 Seq. No.

10697 1.R1011 Contig ID cyk700048791.f1 5'-most EST

266283 Seq. No.

10703 1.R1011 Contig ID cyk700051726.f1 5'-most EST

266284 Seq. No.

10707 1.R1011 Contig ID

LIB3279-049-P1-K1-D7 5'-most EST

266285 Seq. No.

10708 1.R1011 Contig ID

5'-most EST LIB3079-029-Q1-K1-D2

266286 Seq. No.

10712 1.R1011 Contig ID $xsy70\overline{0}213832.h1$ 5'-most EST

266287 Seq. No.

10720 1.R1011 Contig ID

LIB3079-030-Q1-K1-B9 5'-most EST

266288 Seq. No.

10721 1.R1011 Contig ID

uC-zmflb73077f04b2 5'-most EST

BLASTX Method q3738285 NCBI GI BLAST score 533 E value 5.0e-54

151 Match length 69 % identity

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

266289 Seq. No.

10721 3.R1011 Contig ID 5'-most EST uC-zmflmo17418b04a1

266290 Seq. No. Contig ID 10728_1.R1011

LIB3079-028-Q1-K1-G6 5'-most EST

Method BLASTX NCBI GI q4220541 BLAST score 366 1.0e-34 E value Match length 185 48 % identity

(AL035356) Rab geranylgeranyl transferase like protein NCBI Description

[Arabidopsis thaliana]



Contig ID 10729_1.R1011

5'-most EST LIB3079-028-Q1-K1-G8

Seq. No. 266292

Contig ID 10730_1.R1011 5'-most EST ceu700430205.h1

Seq. No. 266293

Contig ID 10735_1.R1011 5'-most EST uwc700154042.h1

Seq. No. 266294

Contig ID 10742_1.R1011

5'-most EST uC-zmflmo17261h02b1

Seq. No. 266295

Contig ID 10742_2.R1011 5'-most EST uC-zmrob73077a09b1

Seq. No. 266296

Contig ID 10745_1.R1011 5'-most EST tfd700570016.h1

Method BLASTX
NCBI GI g2388577
BLAST score 252
E value 2.0e-21

Match length 132 % identity 45

NCBI Description (AC000098) Similar to Arabidopsis putative ion-channel

PID:g2262157 (gb AC002329). [Arabidopsis thaliana]

Seq. No. 266297

Contig ID 10747_1.R1011

5'-most EST LIB3079-028-Q1-K1-F2

Seq. No. 266298

Contig ID 10748_1.R1011 5'-most EST uC-zmflb73272h09b1

5'-most EST uC-zmflb73272h09b Method BLASTX

NCBI GI g3360289
BLAST score 2078
E value 0.0e+00
Match length 483
% identity 85

NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase

1 [Zea mays]

Seq. No. 266299

Contig ID 10748_2.R1011 5'-most EST wty700169673.h1

Method BLASTX
NCBI GI g3360289
BLAST score 539
E value 4.0e-55
Match length 173
% identity 68



```
(AF023164) leucine-rich repeat transmembrane protein kinase
NCBI Description
                   1 [Zea mays]
                   266300
Seq. No.
                   10749 1.R1011
Contig ID
                  LIB3118-007-Q1-K1-E3
5'-most EST
                   BLASTX
Method
                   g2191165
NCBI GI
                   327
BLAST score
                   1.0e-29
E value
                   106
Match length
                   56
% identity
                   (AF007270) A IG002P16.14 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   266301
Seq. No.
                   10749 2.R1011
Contig ID
                   LIB3088-020-Q1-K1-G9
5'-most EST
Seq. No.
                   266302
                   10750 1.R1011
Contig ID
                   xjt700095441.h1
5'-most EST
                   266303
Seq. No.
                   10754 1.R1011
Contig ID
                   uC-zmflb73061e04b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3182915
BLAST score
                   321
                   4.0e-56
E value
                   179
Match length
                   56
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1842150_dbj_BAA19225
                   (AB001051) ADP-ribosylation factor [Dugesia japonica]
                   266304
Seq. No.
                   10767 1.R1011
Contig ID
5'-most EST
                   uC-zmroteosinte035e05b2
                   BLASTX
Method
NCBI GI
                   q1839188
BLAST score
                   359
                   3.0e-35
E value
                   177
Match length
% identity
                  (U86081) root hair defective 3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   266305
Contig ID
                   10771 1.R1011
5'-most EST
                   LIB3079-027-Q1-K1-E5
Method
                   BLASTX
                   q3426039
NCBI GI
                   511
BLAST score
E value
                   1.0e-51
                   195
Match length
 % identity
                   55
```

NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

```
266306
Seq. No.
                   10773_1.R1011
Contig ID
                   uC-zm\overline{f}lmo17268c09b1
5'-most EST
                   BLASTX
Method
                   g1652704
NCBI GI
                   332
BLAST score
                   2.0e-30
E value
                   231
Match length
                   34
% identity
                   (D90907) hypothetical protein [Synechocystis sp.]
NCBI Description
                   266307
Seq. No.
                   10774 1.R1011
Contig ID
                   uC-zmroB73014e12b1
5'-most EST
                   BLASTX
Method
                   g3395938
NCBI GI
                   877
BLAST score
                   3.0e-94
E value
                   232
Match length
                   51
% identity
                   (AF076924) polypyrimidine tract-binding protein homolog
NCBI Description
                   [Arabidopsis thaliana]
                   266308
Seq. No.
                   10774 2.R1011
Contig ID
                   uC-zm\overline{f}1b73185d11b1
5'-most EST
                   BLASTN
Method
                   g3511235
NCBI GI
                   40
BLAST score
                   6.0e-13
E value
                   64
Match length
                   91
% identity
                   Zea mays starch branching enzyme IIb (ae) gene, complete
NCBI Description
                   cds
                   266309
Seq. No.
Contig ID
                   10777 1.R1011
5'-most EST
                   uC-zmflmo17133e02b1
                   BLASTX
Method
                   a3241943
NCBI GI
                   386
BLAST score
                    3.0e-37
E value
                   148
Match length
% identity
NCBI Description (AC004625) hypothetical protein [Arabidopsis thaliana]
```

10778 _1.R1011 Contig ID

uC-zmflmo17307c10b1 5'-most EST

BLASTX Method q4457221 NCBI GI 239 BLAST score E value 1.0e-19 Match length 89

54 % identity

(AF127797) putative bZIP DNA-binding protein [Capsicum NCBI Description

chinense]



```
266311
Seq. No.
                  10782 1.R1011
Contig ID
                  LIB3079-045-Q1-K1-A6
5'-most EST
Seq. No.
                  266312
                  10783 1.R1011
Contig ID
                  LIB3137-016-Q1-K1-A8
5'-most EST
                   BLASTX
Method
                   g2190550
NCBI GI
                   711
BLAST score
                   1.0e-104
E value
                   322
Match length
                   62
% identity
                   (AC001229) ESTs gb T45673,gb_N37512 come from this gene.
NCBI Description
                   [Arabidopsis thaliana]
                   266313
Seq. No.
                   10784 1.R1011
Contig ID
                   LIB3159-011-Q1-K1-C7
5'-most EST
                   BLASTX
Method
                   g4455363
NCBI GI
BLAST score
                   334
                   1.0e-32
E value
                   158
Match length
                   51
% identity
                   (AL035524) Medicago nodulin N21-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   266314
Seq. No.
                   10787 1.R1011
Contig ID
                   kyv70\overline{0}142505.h1
5'-most EST
                   BLASTX
Method
                   g3924611
NCBI GI
                   744
BLAST score
                   7.0e-79
E value
                   305
Match length
                   54
% identity
                  (AF069442) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   266315
Seq. No.
                   10788 1.R1011
Contig ID
                   xmt700264959.h1
 5'-most EST
                   BLASTX
Method
                   g2980641
NCBI GI
                    535
BLAST score
                    9.0e-55
E value
Match length
                    129
 % identity
NCBI Description (Y11250) multi resistance protein [Arabidopsis thaliana]
                    266316
 Seq. No.
                    10789 1.R1011
 Contig ID
                    LIB83-014-Q1-E1-F7
 5'-most EST
```

Contig ID 10790_1.R1011



```
uC-zmflb73265g11b4
5'-most EST
                  BLASTX
Method
                  g3169028
NCBI GI
                  160
BLAST score
                  2.0e-10
E value
                  68
Match length
                  41
% identity
                  (AL023702) putative cationic amino acid transporter
NCBI Description
                   [Streptomyces coelicolor]
                  266318
Seq. No.
                  10790 2.R1011
Contig ID
                  LIB3079-026-Q1-K1-D2
5'-most EST
                  266319
Seq. No.
                  10791 1.R1011
Contig ID
                  LIB3079-016-Q1-K1-A10
5'-most EST
                  BLASTN
Method
                   g799029
NCBI GI
                   322
BLAST score
                   0.0e+00
E value
                   380
Match length
                   97
% identity
NCBI Description Z.mays BET1 mRNA
                   266320
Seq. No.
                   10791 3.R1011
Contig ID
                   LIB3115-004-Q1-K1-D10
5'-most EST
Method
                   BLASTN
                   g799029
NCBI GI
                   207
BLAST score
                   1.0e-113
E value
                   327
Match length
                   98
% identity
NCBI Description Z.mays BET1 mRNA
                   266321
Seq. No.
                   10795_1.R1011
Contig ID
                   xjt700096767.hl
5'-most EST
                   BLASTX
Method
                   g4587611
NCBI GI
                   526
BLAST score
                   2.0e-53
E value
                   139
Match length
                   75
 % identity
                   (AC006951) putative 40S ribosomal protein S17 [Arabidopsis
 NCBI Description
                   thaliana]
                   266322
 Seq. No.
                   10795 2.R1011
 Contig ID
                   LIB3150-089-P1-N1-H5
 5'-most EST
                   BLASTX
 Method
```

NCBI GI q4587611 529 BLAST score 1.0e-53 E value 139 Match length 76 % identity

NCBI Description (AC006951) putative 40S ribosomal protein S17 [Arabidopsis thaliana]

Seq. No. 266323

Contig ID 10795_5.R1011 5'-most EST pmx700090847.h1

Method BLASTX
NCBI GI g4587611
BLAST score 286
E value 8.0e-26
Match length 60
% identity 90

NCBI Description (AC006951) putative 40S ribosomal protein S17 [Arabidopsis

thaliana]

Seq. No. 266324

Contig ID 10799_1.R1011

5'-most EST LIB3079-055-Q1-K1-C6

Method BLASTX
NCBI GI g1172874
BLAST score 210
E value 5.0e-16
Match length 200
% identity 32

NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR

>gi_479589_pir__S34823 dehydration-induced protein RD22 Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
[Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene

[Arabidopsis thaliana]

Seq. No. 266325

Contig ID 10799_2.R1011

5'-most EST LIB3150-075-P1-N1-F5

Seq. No. 266326

Contig ID 10802_1.R1011 5'-most EST rvt700551068.h1

Seq. No. 266327

Contig ID 10809_1.R1011

5'-most EST LIB3079-025-Q1-K1-F8

Seq. No. 266328

Contig ID 10811_1.R1011 5'-most EST uwc700154653.h1

Method BLASTX
NCBI GI g2980641
BLAST score 1386
E value 1.0e-154
Match length 530
% identity 29

NCBI Description (Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No. 266329

Contig ID 10811_2.R1011

5'-most EST LIB3137-014-Q1-K1-A5

Method BLASTX

```
q2980641
NCBI GI
                   142
BLAST score
                   1.0e-08
E value
                   79
Match length
                   37
% identity
                  (Y11250) multi resistance protein [Arabidopsis thaliana]
NCBI Description
                   266330
Seq. No.
                   10811 4.R1011
Contig ID
                   vux700161710.hl
5'-most EST
                   BLASTX
Method
                   g3142303
NCBI GI
                   160
BLAST score
                   5.0e-11
E value
                   56
Match length
                   61
% identity
                   (AC002411) Strong similarity to MRP-like ABC transporter
NCBI Description
                   gb_U92650 from A. thaliana and canalicular multi-drug
                   resistance protein gb_L49379 from Rattus norvegicus.
                   [Arabidopsis thaliana]
                   266331
Seq. No.
                   10815 1.R1011
Contig ID
                   ceu70\overline{0}423935.h1
5'-most EST
                   266332
Seq. No.
                   10818 1.R1011
Contig ID
                   wty700167309.hl
5'-most EST
                   BLASTX
Method
                   q4467125
NCBI GI
                   1617
BLAST score
                   0.0e + 00
E value
                   399
Match length
                   76
% identity
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   266333
                   10824 1.R1011
Contig ID
                   uC-zmflmo17051f08b1
5'-most EST
                   BLASTX
Method
                   q2984225
NCBI GI
BLAST score
                    445
E value
                    2.0e-43
                   242
Match length
                    42
 % identity
NCBI Description (AE000766) enolase-phosphatase E-1 [Aquifex aeolicus]
 Seq. No.
                    266334
                    10825 1.R1011
 Contig ID
                    tzu700207027.h1
 5'-most EST
                    BLASTX
```

Method BLASTX
NCBI GI 9461498
BLAST score 2271
E value 0.0e+00
Match length 482
% identity 91

NCBI Description ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC



TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_320619_pir__S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421) alanine aminotransferase [Panicum miliaceum]

```
266335
Seq. No.
                  10825 2.R1011
Contig ID
                  LIB3150-094-P2-K1-C8
5'-most EST
                  BLASTX
Method
                  g3694807
NCBI GI
                  336
BLAST score
                   2.0e-31
E value
                  85
Match length
                   78
% identity
                  (AF055898) alanine aminotransferase [Zea mays]
NCBI Description
                   266336
Seq. No.
                   10825 4.R1011
Contig ID
                   ypc700801716.h1
5'-most EST
                   BLASTN
Method
                   g296203
NCBI GI
                   65
BLAST score
                   3.0e-28
E value
                   101
Match length
                   91
% identity
NCBI Description P. miliaceum mRNA for alanine aminotransferase
Seq. No.
                   266337
                   10825 5.R1011
Contig ID
                   LIB3150-068-P2-K1-G4
5'-most EST
                   BLASTX
Method
                   g3694807
NCBI GI
                   643
BLAST score
                   9.0e-80
E value
                   178
Match length
                   92
% identity
                  (AF055898) alanine aminotransferase [Zea mays]
NCBI Description
                   266338
Seq. No.
                   10828 1.R1011
Contig ID
                   uC-zmflb73206h01b1
5'-most EST
                   BLASTX
Method
                   q3005931
NCBI GI
                   517
BLAST score
                   1.0e-52
E value
                   154
Match length
                   62
% identity
NCBI Description (AJ005016) ABC transporter [Homo sapiens]
                   266339
Seq. No.
                   10830 1.R1011
Contig ID
                   LIB3079-025-Q1-K1-F12
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4006886
BLAST score
                   183
```

2.0e-13

49

E value Match length



% identity (Z99708) putative protein [Arabidopsis thaliana] NCBI Description 266340 Seq. No. 10831 1.R1011 Contig ID LIB3079-025-Q1-K1-D5 5'-most EST BLASTN Method g347854 NCBI GI 78 BLAST score 1.0e-35 E value 214 Match length 84 % identity Saccharum hybrid cultivar H65-7052 glucose transporter NCBI Description mRNA, complete cds 266341 Seq. No. 10832 1.R1011 Contig ID $uC-zm\overline{f}lb73019h03a1$ 5'-most EST BLASTX Method g3377843 NCBI GI 656 BLAST score 2.0e-68 E value 290 Match length 53 % identity (AF076274) contains similarity to rat p47 protein NCBI Description (GB:AB002086) [Arabidopsis thaliana] 266342 Seq. No. 10833 1.R1011 Contig ID LIB3079-025-Q1-K1-B8 5'-most EST BLASTX Method q2827534 NCBI GI 186 BLAST score 2.0e-25 E value 300 Match length 29 % identity (AL021633) predicted protein [Arabidopsis thaliana] NCBI Description 266343 Seq. No. 10836 1.R1011 Contig ID LIB3062-022-Q1-K1-E5 5'-most EST 266344 Seq. No. 10836 2.R1011 Contig ID LIB3079-025-Q1-K1-C2 5'-most EST Seq. No. 266345 10836 3.R1011 Contig ID 5'-most EST wyr700238014.hl 266346 Seq. No. 10841 1.R1011 Contig ID

Contig ID 10841_1.RIU11 5'-most EST LIB189-012-Q1-E1-E4

Method BLASTX
NCBI GI g3790100
BLAST score 2337
E value 0.0e+00



Match length 562 % identity

(AF095520) pyrophosphate-dependent phosphofructokinase beta NCBI Description

subunit [Citrus X paradisi]

266347 Seq. No.

10841 2.R1011 Contig ID

uC-zmflmo17021a07b1 5'-most EST

BLASTX Method g3377841 NCBI GI 549 BLAST score 4.0e-56 E value 116 Match length 89 % identity

(AF075598) contains similarity to phosphofructokinases NCBI Description

(Pfam; PFK.hmm, score; 36.60) [Arabidopsis thaliana]

266348 Seq. No.

10844 1.R1011 Contig ID

 $LIB30\overline{5}9-013-Q1-K1-C6$ 5'-most EST

BLASTX Method g2655029 NCBI GI BLAST score 602 2.0e-62 E value 116 Match length 97

% identity

(AF019296) starch synthase isoform zSTSII-1 [Zea mays] NCBI Description

266349 Seq. No.

10846 1.R1011 Contig ID

 $LIB31\overline{5}0-059-Q1-N1-G6$ 5'-most EST

BLASTX Method g2829912 NCBI GI 418 BLAST score 5.0e-41E value 135 Match length

56 % identity

(ACO02291) Similar ATP-dependent RNA Helicase [Arabidopsis NCBI Description

thaliana]

266350 Seq. No.

10847_1.R1011 Contig ID

uC-zmflmo17125f03b1 5'-most EST

BLASTX Method q2104681 NCBI GI 423 BLAST score 4.0e-41E value Match length 186 53 % identity

NCBI Description (X97907) transcription factor [Vicia faba]

266351 Seq. No.

10847 2.R1011 Contig ID

 $LIB31\overline{5}0-056-Q1-N1-H7$ 5'-most EST

266352 Seq. No.

10849 1.R1011 Contig ID



```
5'-most EST
                  xjt700094481.hl
                  266353
Seq. No.
                  10852 1.R1011
Contig ID
                  uwc700153727.hl
5'-most EST
Method
                  BLASTX
                   g2244797
NCBI GI
BLAST score
                   352
                   1.0e-32
E value
                   194
Match length
                   43
% identity
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   266354
Seq. No.
                   10854 1.R1011
Contig ID
                   LIB3079-025-Q1-K1-B12
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4432835
BLAST score
                   461
                   1.0e-45
E value
                   134
Match length
                   60
% identity
                   (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                   266355
Seq. No.
                   10854 2.R1011
Contig ID
                   uC-zm\overline{f}lmo17327a07b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4432835
                   195
BLAST score
                   6.0e-15
E value
                   50
Match length
                   68
% identity
                   (AC006283) unknown protein [Arabidopsis thaliana]
NCBI Description
                   266356
Seq. No.
                   10856 1.R1011
Contig ID
                   uC-zmflmo17335h05b1
5'-most EST
Method
                   BLASTX
                   g4586117
NCBI GI
                   1222
BLAST score
                   1.0e-134
E value
Match length
                   497
                   62
% identity
                   (AL049638) putative protein [Arabidopsis thaliana]
NCBI Description
                   266357
Seq. No.
                   10860 1.R1011
Contig ID
                   uC-zmflmo17a05b1
 5'-most EST
                   BLASTX
Method
                   g3757521
NCBI GI
                    687
 BLAST score
 E value
                    7.0e-72
                    273
Match length
                    51
 % identity
 NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]
```

```
266358
Seq. No.
                   10860_3.R1011
Contig ID
                   uC-zm\overline{f}lmo17158a02b1
5'-most EST
                   BLASTX
Method
                   g3757521
NCBI GI
                   271
BLAST score
                   2.0e-23
E value
                   144
Match length
                   42
% identity
                   (AC005167) unknown protein [Arabidopsis thaliana]
NCBI Description
                   266359
Seq. No.
                   10860 4.R1011
Contig ID
                   uC-zmflmo17293h12b1
5'-most EST
```

Method BLASTX
NCBI GI g3757521
BLAST score 351
E value 5.0e-48
Match length 148
% identity 64

NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No. 266360 Contig ID 10860_5.R1011

5'-most EST LIB3060-007-Q1-K1-F3

5'-most EST uC-zmflmo17155e09b1

Seq. No. 266362

Contig ID 10861_1.R1011

5'-most EST LIB3279-007-P1-K1-B12

Method BLASTX
NCBI GI g2505874
BLAST score 585
E value 3.0e-98
Match length 223
% identity 77

NCBI Description (Y12776) putative kinase [Arabidopsis thaliana]

Seq. No. 266363

Contig ID 10861_2.R1011 5'-most EST kyv700142463.h1

Method BLASTN
NCBI GI g168543
BLAST score 61
E value 1.0e-25
Match length 65
% identity 98

NCBI Description Zea mays putative ribosomal protein S8 mRNA, partial cds

Seq. No. 266364

Contig ID 10864_1.R1011

5'-most EST LIB3079-024-Q1-K1-H1

Seq. No. 266365

266372



```
10867 1.R1011
Contig ID
                  LIB3079-024-Q1-K1-H4
5'-most EST
                  BLASTN
Method
NCBI GI
                  q22513
                  82
BLAST score
                  6.0e-38
E value
                  160
Match length
                  90
% identity
NCBI Description Maize 316 bp insertion sequence 5' of waxy gene
                  266366
Seq. No.
                  10868 1.R1011
Contig ID
                  LIB3152-035-P1-K1-F7
5'-most EST
                  BLASTX
Method
                   g2911058
NCBI GI
                   500
BLAST score
                   3.0e-50
E value
                   206
Match length
                   53
% identity
                  (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                   266367
Seq. No.
                   10871 1.R1011
Contig ID
                   fwa700101915.hl
5'-most EST
                   2663.68
Seq. No.
                   10871 2.R1011
Contig ID
                   LIB3150-001-Q1-N1-D4
5'-most EST
                   266369
Seq. No.
                   10874 1.R1011
Contig ID
                   LIB3079-024-Q1-K1-E3
5'-most EST
                   BLASTX
Method
                   g2191187
NCBI GI
                   205
BLAST score
                   6.0e-16
E value
                   154
Match length
                   37
% identity
                   (AF007271) contains similarity to a DNAJ-like domain
NCBI Description
                   [Arabidopsis thaliana]
                   266370
Seq. No.
                   10875 1.R1011
Contig ID
                   LIB3079-024-Q1-K1-E4
5'-most EST
                   266371
Seq. No.
                   10881 1.R1011
Contig ID
 5'-most EST
                   LIB3079-024-Q1-K1-F4
                   BLASTX
Method
                   q3059129
NCBI GI
                   373
BLAST score
E value
                   1.0e-35
Match length
                   132
                    53
 % identity
                   (AJ000477) cytochrome P450 [Helianthus tuberosus]
 NCBI Description
```



10886 1.R1011 Contig ID rvt700548561.hl 5'-most EST

266373 Seq. No.

10889 1.R1011 Contig ID $qw170\overline{0}614527.h1$ 5'-most EST

BLASTX Method g1173327 NCBI GI 358 BLAST score 1.0e-33 E value 149 Match length 52 % identity

U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') NCBI Description

>gi_322619_pir__S30580 U2 snRNP protein A' - Arabidopsis thaliana >gi_17669_emb_CAA48890_ (X69137) U2 small nuclear ribonucleoprotein A' [Arabidopsis thaliana]

266374 Seq. No.

10892 1.R1011 Contig ID

LIB189-021-Q1-E1-G8 5'-most EST

266375 Seq. No.

10892 2.R1011 Contig ID

LIB3150-116-P2-K1-F11 5'-most EST

266376 Seq. No.

10893 1.R1011 Contig ID

LIB3136-038-P1-K1-A8 5'-most EST

BLASTX Method q2244904 NCBI GI 189 BLAST score 4.0e-14E value 164 Match length 19 % identity

(Z97339) similar to hypothetical protein C02F5.7 - Caenorha NCBI Description

[Arabidopsis thaliana]

266377 Seq. No.

10896 1.R1011 Contig ID

uC-zmflmo17201e11a1 5'-most EST

266378 Seq. No.

10898 1.R1011 Contig ID pmx700091727.h1 5'-most EST

266379 Seq. No.

10902 1.R1011 Contig ID 5'-most EST uC-zmflb73163h11b2

266380 Seq. No.

10902 2.R1011 Contig ID

5'-most EST uC-zmflb73163g10b2

266381 Seq. No.

10904 1.R1011 Contig ID

uC-zmflmo17223b08b1 5'-most EST

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266382
Seq. No.
                  10909 1.R1011
Contig ID
5'-most EST
                  LIB3079-023-Q1-K1-G5
                  266383
Seq. No.
Contig ID
                  10923 1.R1011
                  wyr700235575.h1
5'-most EST
                  BLASTX
Method
                  q2239083
NCBI GI
BLAST score
                  242
                  3.0e-20
E value
                  134
Match length
% identity
                  43
NCBI Description
                  (Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase
                  [Dianthus caryophyllus] >gi 2239087 emb CAB06429 (Z84385)
                  anthranilate N-hydroxycinnamoyl/benzoyltransferase
                  [Dianthus caryophyllus]
                  266384
Seq. No.
                  10924 1.R1011
Contig ID
                  ymt700220065.h1
5'-most EST
```

Contig ID 10924_1.R1011
5'-most EST ymt700220065.h1
Method BLASTX
NCBI GI g3983665
BLAST score 1893
E value 0.0e+00
Match length 416
% identity 89

266385

NCBI Description (AB011271) importin-beta2 [Oryza sativa]

Contig ID 10924 2.R1011 LIB3180-001-P1-M1-D1 5'-most EST BLASTX Method g3983665 NCBI GI 627 BLAST score E value 1.0e-65 135 Match length 90 % identity

NCBI Description (AB011271) importin-beta2 [Oryza sativa]

 Seq. No.
 266386

 Contig ID
 10926_1.R1011

 5'-most EST
 uC-zmflb73326b04a1

Seq. No. 266387

Contig ID 10931_1.R1011

5'-most EST LIB3137-017-Q1-K1-C4

Method BLASTX
NCBI GI 94468813
BLAST score 817
E value 1.0e-116
Match length 267
% identity 76

NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

Seg. No. 266388

Contig ID 10934_1.R1011



5'-most EST uC-zmrob73012f03b1 Method BLASTX NCBI GI q3915847 BLAST score 908 5.0e-98 E value Match length 231 % identity 77 NCBI Description 40S RIBOSOMAL PROTEIN S2 >qi 2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana] 266389 Seq. No. Contig ID 10934 2.R1011 5'-most EST LIB3059-013-Q1-K1-D1 Method BLASTX q3915847 NCBI GI BLAST score 567 E value 2.0e-58 Match length 134 % identity 81 NCBI Description 40S RIBOSOMAL PROTEIN S2 >qi 2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana] Seq. No. 266390 Contig ID 10934 4.R1011 LIB3179-019-P1-K1-C7 5'-most EST Method BLASTX q3915847 NCBI GI BLAST score 223 E value 3.0e-18 Match length 65 % identity 66 NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana] Seq. No. 266391 10934 5.R1011 Contig ID xjt700096204.hl 5'-most EST BLASTX Method NCBI GI g133961 BLAST score 258 2.0e-22 E value Match length 61 % identity 82 NCBI Description 40S RIBOSOMAL PROTEIN S4 (OMNIPOTENT SUPRESSOR PROTEIN SUP44) (RP12) (S2E) >gi 70888 pir R3BYS2 ribosomal protein S2.e - yeast (Saccharomyces cerevisiae) >qi 172793 (M59375) ribosomal protein S4 [Saccharomyces cerevisiae] >gi 1322683 emb CAA96831 (Z72645) ORF YGL123w [Saccharomyces cerevisiae] >gi 1628451 emb CAA63835 (X94106) SUP44 [Saccharomyces cerevisiae] Seq. No. 266392

Contig ID 10934 7.R1011 5'-most EST ntr700077038.h1

Seq. No. 266393

Contig ID 10934_10.R1011



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5'-most EST
                  ymt700222615.h1
Seq. No.
                  266394
Contig ID
                  10937 1.R1011
5'-most EST
                  LIB3079-023-Q1-K1-D9
Seq. No.
                  266395
Contig ID
                  10938 1.R1011
5'-most EST
                  tfd700572457.h1
Method
                  BLASTX
NCBI GI
                  g2246380
BLAST score
                  320
                  1.0e-29
E value
Match length
                  82
% identity
                  71
                 (Z86095) peptidyl-prolyl cis-trans isomerase [Arabidopsis
NCBI Description
                  thaliana]
                  266396
Seq. No.
                  10940 1.R1011
Contig ID
5'-most EST
                  LIB3079-023-Q1-K1-E12
                  266397
Seq. No.
                  10940 2.R1011
Contig ID
                  fdz701165346.hl
5'-most EST
                  266398
Seq. No.
                  10941 1.R1011
Contig ID
                  uC-zmflb73361e08a2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4586038
BLAST score
                  554
                  7.0e-57
E value
Match length
                  139
% identity
                  72
NCBI Description (AC007109) putative heat shock protein [Arabidopsis
                  thaliana]
Seq. No.
                  266399
Contig ID
                  10941 2.R1011
                  wyr700239651.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4586038
BLAST score
                  775
E value
                  1.0e-103
Match length
                  313
% identity
NCBI Description (AC007109) putative heat shock protein [Arabidopsis
                  thaliana]
```

Seq. No. 266400 Contig ID 10942 1.R1011

5'-most EST uC-zmflmo17158e12b1

Seq. No. 266401

Contig ID 10942_3.R1011 5'-most EST rvt700550074.h1



```
266402
 Seq. No.
 Contig ID
                    10945 1.R1011
 5'-most EST
                    xjt700096966.h1
                    BLASTX
 Method
 NCBI GI
                    g3165391
 BLAST score
                    245
 E value
                    3.0e-20
                    210
 Match length
                    36
 % identity
 NCBI Description (AB014471) compaired with Cricetulus griseus SL15 mRNA;
                    GenBank Accession Number U55387 [Mus musculus]
                    266403
 Seq. No.
 Contig ID
                    10945 2.R1011
 5'-most EST
                    uC-zmflMo17085a07b1
 Seq. No.
                    266404
 Contig ID
                    10950 1.R1011
 5'-most EST
                    LIB3079-023-Q1-K1-C6
 Method
                    BLASTX
 NCBI GI
                    g1041712
                    508
BLAST score
                    2.0e-51
 E value
                    127
 Match length
 % identity
                    72
 NCBI Description (U30479) expansin Os-EXP3 [Oryza sativa]
                    266405
 Seq. No.
                    10951 1.R1011
 Contig ID
 5'-most EST
                    LIB3079-023-Q1-K1-C7
 Method
                    BLASTX
 NCBI GI
                    g1699024
 BLAST score
                    398
 E value
                    1.0e-38
 Match length
                    125
                    58
  % identity
 NCBI Description (U78866) gene1000 [Arabidopsis thaliana] >gi 1699057
                    (U78870) unknown [Arabidopsis thaliana]
  Seq. No.
                    266406
  Contig ID
                    10952 1.R1011
  5'-most EST
                    LIB3079-023-Q1-K1-C9
                    266407
  Seq. No.
                    10953 1.R1011
  Contig ID
  5'-most EST
                    LIB3061-001-Q1-K2-E1
 Method
                    BLASTX
 NCBI GI
                    g4582488
 BLAST score
                    515
  E value
                    1.0e-51
 Match length
                    375
  % identity
                    39
```

37035

NCBI Description (AL021768) putative protein [Arabidopsis thaliana]

266408

10954 1.R1011

Seq. No. Contig ID



```
LIB3088-001-Q1-K1-G6
5'-most EST
Method
                  BLASTX
                  g3183991
NCBI GI
BLAST score
                  461
                  1.0e-45
E value
                  209
Match length
% identity
                  46
NCBI Description (AJ005173) P69F protein [Lycopersicon esculentum]
                  266409
Seq. No.
                  10954 2.R1011
Contig ID
5'-most EST
                  uC-zmflmo17199a11b1
                  266410
Seq. No.
                  10954 4.R1011
Contig ID
                  nbm700476896.h1
5'-most EST
                  266411
Seq. No.
                  10963 1.R1011
Contig ID
                  LIB3079-023-Q1-K1-A9
5'-most EST
Seq. No.
                  266412
                  10966 1.R1011
Contig ID
5'-most EST
                  LIB3079-027-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  q82705
                  487
BLAST score
                  1.0e-48
E value
Match length
                  108
                  91
% identity
NCBI Description lipid body-associated major protein L3 - maize (fragment)
                  >gi 168513 (M17225) major protein L3 [Zea mays]
Seq. No.
                  266413
Contig ID
                  10968 1.R1011
                  LIB3079-022-Q1-K1-G11
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2262105
                  636
BLAST score
                  2.0e-66
E value
                  209
Match length
% identity
                  57
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
Seq. No.
                  266414
                  10977 1.R1011
Contig ID
5'-most EST
                  LIB3069-037-Q1-K1-B1
Method
                  BLASTX
                  g1421730
NCBI GI
```

Method BLASTX
NCBI GI g1421730
BLAST score 1099
E value 1.0e-120
Match length 251
% identity 83

NCBI Description (U43082) RF2 [Zea mays]

Seq. No. 266415

Contig ID 10978_1.R1011



pmx700086153.h1 5'-most EST BLASTX Method q3201619 NCBI GI BLAST score 650 8.0e-68 E value Match length 166 73 % identity (AC004669) dihydroxypolyprenylbenzoate methyltransferase NCBI Description [Arabidopsis thaliana] 266416 Seq. No. 10986 1.R1011 Contig ID xsy700212365.hl 5'-most EST BLASTX Method q3522938 NCBI GI 656 BLAST score 5.0e-68 E value 369 Match length 43 % identity NCBI Description (AC004411) unknown protein [Arabidopsis thaliana] 266417 Seq. No. 10986 2.R1011 Contig ID LIB3150-108-P2-K1-H4 5'-most EST 266418 Seq. No. 10987 1.R1011 Contig ID $uC-zm\overline{f}1b73283e12b2$ 5'-most EST 266419 Seq. No. 10987 2.R1011 Contig ID $dyk70\overline{0}104215.h1$ 5'-most EST 266420 Seq. No. 10988 1.R1011 Contig ID $uC-zm\overline{f}lmo17248c10b1$ 5'-most EST BLASTX Method g267146 NCBI GI 1523 BLAST score 1.0e-170 E value 396 Match length 73 % identity DNA TOPOISOMERASE I >gi_99762_pir__S22864 DNA topoisomerase NCBI Description (EC 5.99.1.2) I - Arabidopsis thaliana >gi_16558_emb_CAA40763_ (X57544) topoisomerase I
[Arabidopsis thaliana] >gi_445137_prf__1908437A topoisomerase I [Arabidopsis thaliana] 266421 Seq. No. 10989 1.R1011 Contig ID uC-zmflmo17242c03b1 5'-most EST BLASTX Method a2911057 NCBI GI

Method BLASIX
NCBI GI g2911057
BLAST score 715
E value 2.0e-75
Match length 249
% identity 53



NCBI Description (AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana]

Seq. No. 266422

Contig ID 10989_2.R1011 5'-most EST xsy700211003.h1

Method BLASTX
NCBI GI g2911057
BLAST score 193
E value 6.0e-15
Match length 83
% identity 48

NCBI Description (AL021961) caffeoyl-CoA O-methyltransferase - like protein

[Arabidopsis thaliana]

Seq. No. 266423

Contig ID 10989 3.R1011 5'-most EST tfd700571450.h1

Method BLASTX
NCBI GI g684942
BLAST score 186
E value 8.0e-14
Match length 63
% identity 52

NCBI Description (U20736) S-adenosyl-L-methionine:trans-caffeoyl-CoA

3-O-methyltransferase [Medicago sativa subsp. sativa]

Seq. No. 266424

Contig ID 10989_4.R1011 5'-most EST wyr700242093.h1

Method BLASTX
NCBI GI g2960356
BLAST score 166
E value 1.0e-18
Match length 74
% identity 66

NCBI Description (AJ224894) caffeoyl-CoA 3-O-methyltransferase [Populus balsamifera subsp. trichocarpa] >gi 3334838 emb CAA11496

balsamifera subsp. trichocarpa; >gi_3334838_emb_CAA11496_ (AJ223621) caffeoyl CoA 3-O-methyltransferase [Populus

balsamifera subsp. trichocarpa]

Seq. No. 266425

Contig ID 10989_5.R1011 5'-most EST dyk700105414.h1

Method BLASTX
NCBI GI g2911057
BLAST score 363
E value 1.0e-34
Match length 120
% identity 56

NCBI Description (AL021961) caffeoyl-CoA O-methyltransferase - like protein

[Arabidopsis thaliana]

Seq. No. 266426

Contig ID 10992 1.R1011

5'-most EST $uC-zm\overline{f}lmo17158g05b1$



Contig ID 10999 1.R1011

5'-most EST LIB3079-022-Q1-K1-B2

Seq. No. 266428

Contig ID 11005_1.R1011 5'-most EST xjt700094984.h1

Method BLASTX
NCBI GI g3135273
BLAST score 231
E value 5.0e-19
Match length 135
% identity 33

NCBI Description (AC003058) hypothetical protein [Arabidopsis thaliana]

>qi 4191773 (AC005917) putative WD-40 repeat protein

[Arabidopsis thaliana]

Seq. No. 266429

Contig ID 11006 1.R1011

5'-most EST LIB3279-006-P1-K1-F2

Seq. No. 266430

Contig ID 11007_1.R1011 5'-most EST uC-zmflm017233c12b1

Seq. No. 266431

Contig ID 11007_2.R1011 5'-most EST pmx700085791.h1

Seq. No. 266432

Contig ID 11010_1.R1011

5'-most EST LIB3079-021-Q1-K1-H10

Method BLASTX
NCBI GI 94006859
BLAST score 282
E value 7.0e-25
Match length 167
% identity 42

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 266433

Contig ID 11011 1.R1011

5'-most EST LIB3079-021-Q1-K1-A9

Method BLASTX
NCBI GI g2245004
BLAST score 232
E value 3.0e-19
Match length 121
% identity 40

NCBI Description (Z97341) similarity to membrane transport protein

[Arabidopsis thaliana]

Seq. No. 266434

Contig ID 11012_1.R1011 5'-most EST uC-zmflmo17287b10a1

Seq. No. 266435



Contig ID 11014 1.R1011

5'-most EST LIB3079-021-Q1-K1-H4

Seq. No. 266436

Contig ID 11014 2.R1011

5'-most EST LIB83-012-Q1-E1-G11

266437 Seq. No.

11015 1.R1011 Contig ID 5'-most EST clt700043388.f1

Method BLASTX NCBI GI g401114 BLAST score 1196 1.0e-132 E value Match length 233 % identity 98

NCBI Description SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE

GLUCOSYLTRANSFERASE) >gi_82726_pir__JQ1329 sucrose-phosphate synthase (EC 2.4.1.14) - maize >gi_168626

(M97550) sucrose phosphate synthase [Zea mays]

Seq. No. 266438

Contig ID 11026 1.R1011 5'-most EST fC-zmle700088007á1

266439 Seq. No.

11026 3.R1011 Contig ID

5'-most EST uC-zmflmo17129d02b1

266440 Seq. No.

Contig ID 11026 4.R1011

5'-most EST uC-zmflmo17194c03a1

Seq. No. 266441

11027 1.R1011 Contig ID 5'-most EST $xmt70\overline{0}265564.h1$

Method BLASTX NCBI GI q3319776 BLAST score 586 1.0e-60 E value Match length 127 % identity 96

NCBI Description (AJ007665) seryl-tRNA synthetase [Zea mays]

266442 Seq. No.

Contig ID 11027 2.R1011 5'-most EST rv1700454272.h1

Method BLASTX NCBI GI g3319776 BLAST score 1254 E value 1.0e-139 Match length 247 % identity 97

NCBI Description (AJ007665) seryl-tRNA synthetase [Zea mays]

Seq. No. 266443

Contig ID 11027_4.R1011



```
uC-zmflb73300a08b1
5'-most EST
                  BLASTX
Method
                  q3319776
NCBI GI
BLAST score
                  274
                  4.0e-24
E value
                  158
Match length
                  87
% identity
                  (AJ007665) seryl-tRNA synthetase [Zea mays]
NCBI Description
                  266444
Seq. No.
                  11029 1.R1011
Contig ID
                  LIB3136-019-Q1-K1-F9
5'-most EST
                  266445
Seq. No.
                  11030 1.R1011
Contig ID
                  yyf700348355.hl
5'-most EST
Method
                  BLASTX
                  g2982297
NCBI GI
                  1096
BLAST score
                   1.0e-120
E value
Match length
                   232
                   90
% identity
                  (AF051233) KIAA0107-like protein [Picea mariana]
NCBI Description
                  266446
Seq. No.
                   11030 2.R1011
Contig ID
                   uC-zmflb73073d08b3
5'-most EST
                   BLASTX
Method
                   q2982297
NCBI GI
                   650
BLAST score
E value
                   8.0e-68
                   184
Match length
                   73
% identity
                  (AF051233) KIAA0107-like protein [Picea mariana]
NCBI Description
                   266447
Seq. No.
                   11030 3.R1011
Contig ID
                   xjt700095552.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2494625
BLAST score
                   173
E value
                   3.0e-12
                   110
Match length
                   38
% identity
NCBI Description HYPOTHETICAL PROTEIN KIAA0107 >gi 285951_dbj_BAA03497_
                   (D14663) KIAA0107 [Homo sapiens]
                   266448
Seq. No.
                   11031 1.R1011
Contig ID
                   LIB3079-021-Q1-K1-H9
5'-most EST
                   BLASTN
Method
                   g4416300
NCBI GI
                   104
BLAST score
                   3.0e-51
E value
                   123
Match length
```

% identity 97
NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster



```
region, complete sequence
                  266449
Seq. No.
Contig ID
                  11039 1.R1011
                  LIB3079-021-Q1-K1-D9
5'-most EST
                  266450
Seq. No.
                  11041 1.R1011
Contig ID
5'-most EST
                  LIB3059-011-Q1-K1-B7
Method
                  BLASTX
NCBI GI
                  g1711507
                  607
BLAST score
                  7.0e-63
E value
Match length
                  117
                   95
% identity
```

NCBI Description SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19) >gi 624221 (U19030) signal recognition particle 19 kDa

protein subunit SRP19 [Oryza sativa]

266451 Seq. No. Contig ID 11041_2.R1011 5'-most EST uC-zmflb73275g11b1 Method BLASTX NCBI GI g1711507 BLAST score 484 E value 3.0e-57 Match length 116

93

% identity SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19) NCBI Description

>qi 624221 (U19030) signal recognition particle 19 kDa

protein subunit SRP19 [Oryza sativa]

266452 Seq. No. 11046 1.R1011 Contig ID $ypc70\overline{0}807442.h1$ 5'-most EST

Method BLASTX NCBI GI q141617 BLAST score 362 E value 3.0e - 34Match length 145 % identity 54

ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1) NCBI Description

>gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize
>gi_22515_emb_CAA37595_ (X53515) zein Zc1 [Zea mays]

>gi 168666 (M16460) 16-kDa zein protein [Zea mays]

Seq. No. 266453

11053 1.R1011 Contig ID

5'-most EST LIB3088-025-Q1-K1-G8

Method BLASTN NCBI GI g2062705 BLAST score 34 2.0e-09 E value Match length 34 100 % identity

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds



Contig ID 11053 3.R1011 rvt700551468.hl 5'-most EST

266455 Seq. No.

11058 1.R1011 Contig ID

LIB3079-052-Q1-K1-D2 5'-most EST

266456 Seq. No.

11059 1.R1011 Contig ID

LIB3079-021-Q1-K1-D5 5'-most EST

Method BLASTX g4204295 NCBI GI BLAST score 171 5.0e-12E value Match length 106 % identity 40

(AC003027) lcl prt seq No definition line found NCBI Description

[Arabidopsis thaliana]

266457 Seq. No.

11060 1.R1011 Contig ID

LIB143-001-Q1-E1-A1 5'-most EST

Seq. No. 266458

11066 1.R1011 Contig ID

LIB3061-036-Q1-K1-G5 5'-most EST

Method BLASTX NCBI GI g3763845 BLAST score 450 1.0e-44E value 113 Match length 76

% identity

(AB018375) early nodulin [Oryza sativa] NCBI Description

>gi_3763847_dbj_BAA33814_ (AB018376) early nodulin [Oryza

sativa]

266459 Seq. No.

11066 2.R1011 Contig ID

LIB3061-001-Q1-K1-H10 5'-most EST

BLASTX Method g3763845 NCBI GI 453 BLAST score 6.0e-45E value 115 Match length 75 % identity

(AB018375) early nodulin [Oryza sativa] NCBI Description

>gi 3763847_dbj_BAA33814_ (AB018376) early nodulin [Oryza

sativa]

266460 Seq. No.

11066 4.R1011 Contig ID

LIB3150-082-P2-N2-H10 5'-most EST

BLASTN Method q3763846 NCBI GI

BLAST score 67



3.0e-29 E value Match length 163 85 % identity Oryza sativa OsENOD93a mRNA for early nodulin, complete cds NCBI Description 266461 Seq. No. 11068 1.R1011 Contig ID LIB3079-031-Q1-K1-H9 5'-most EST BLASTX Method g82654 NCBI GI 376 BLAST score 7.0e - 36E value 128 Match length 60 % identity 10K zein precursor - maize >gi_22541_emb_CAA30409_ (X07535) NCBI Description 10kDa zein (AA 1 - 150) [Zea mays] 266462 Seq. No. 11068 2.R1011 Contig ID LIB3118-008-Q1-K1-A8 5'-most EST BLASTN Method g984524 NCBI GI 325 BLAST score 0.0e+00E value 498 Match length 73 % identity Zea mays high-methionine zein DZS18 (dzs18) gene, complete NCBI Description cds 266463 Seq. No. 11068 3.R1011 Contig ID LIB3117-009-Q1-K1-C5 5'-most EST BLASTX Method NCBI GI q82654 150 BLAST score 7.0e-10 E value Match length 30 97 % identity 10K zein precursor - maize >gi_22541 emb CAA30409 (X07535) NCBI Description 10kDa zein (AA 1 - 150) [Zea mays] Seq. No. 266464 11068 6.R1011 Contig ID LIB3059-006-Q1-K1-D3 5'-most EST BLASTX Method NCBI GI q463152 BLAST score 156 E value 2.0e-10 Match length 42 74 % identity

NCBI Description (L29505) zein [Zea mays] >gi_1094858_prf__2106415A Met-rich

seed storage protein [Zea mays]

Seq. No. 266465

Contig ID 11068_7.R1011

5'-most EST LIB3151-009-Q1-K1-B9

Method BLASTN



NCBI GI g22540
BLAST score 129
E value 3.0e-66
Match length 257
% identity 92

NCBI Description Maize mRNA for 10kDa zein

Seq. No. 266466

Contig ID 11068_10.R1011 5'-most EST LIB3117-009-Q1-K1-D4

Method BLASTN
NCBI GI g984524
BLAST score 83
E value 3.0e-39
Match length 99
% identity 96

NCBI Description Zea mays high-methionine zein DZS18 (dzs18) gene, complete

cds

Seq. No. 266467

Contig ID 11070 1.R1011

5'-most EST LIB3116-034-P1-K1-A2

Method BLASTX
NCBI GI g2129929
BLAST score 727
E value 8.0e-77
Match length 149
% identity 93

NCBI Description DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB2 -

tomato >gi_1049068 (U28403) RNA polymerase II subunit 2

[Solanum lycopersicum]

Seq. No. 266468

Contig ID 11070_2.R1011

5'-most EST LIB3115-005-Q1-K1-G3

Method BLASTX
NCBI GI g2129929
BLAST score 984
E value 1.0e-107
Match length 194
% identity 95

NCBI Description DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB2 -

tomato >gi 1049068 (U28403) RNA polymerase II subunit 2

[Solanum lycopersicum]

Seq. No. 266469

Contig ID 11070 3.R1011

5'-most EST uC-zmroteosintel18e07b1

Method BLASTX
NCBI GI g2736117
BLAST score 921
E value 1.0e-100
Match length 178
% identity 98

NCBI Description (AF020839) RPB140 [Hordeum vulgare]

Seq. No. 266470



Contig ID 11070_4.R1011 5'-most EST uC-zmflmo17269g06a1

Seq. No. 266471

Contig ID 11072_1.R1011 5'-most EST uC-zmflb73190a11b1

Method BLASTX
NCBI GI g1174470
BLAST score 682
E value 2.0e-71
Match length 221
% identity 61

NCBI Description OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)

(INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A

integral membrane protein [Mus musculus]

Seq. No. 266472

Contig ID 11073_1.R1011 5'-most EST bdu700382122.h1

Method BLASTX
NCBI GI g1172557
BLAST score 788
E value 3.0e-84
Match length 163
% identity 96

NCBI Description OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT

ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
>gi_422030 pir__ S34146 porin por1 - maize
>gi_626044 pir__ A55017 porin, plastid - maize
>gi_313136 emb_CAA51828 (X73429) porin [Zea mays]

Seq. No. 266473

Contig ID 11077_1.R1011

5'-most EST uC-zmflb73066d01b1

Method BLASTX
NCBI GI g3738284
BLAST score 298
E value 3.0e-26
Match length 234
% identity 41

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 266474

Contig ID 11077_4.R1011 5'-most EST ceu700428747.h1

Seq. No. 266475

Contig ID 11079_1.R1011 5'-most EST uC-zmflb73237d06b2

Method BLASTX
NCBI GI g2245378
BLAST score 803
E value 1.0e-85
Match length 231
% identity 68

NCBI Description (U83245) auxin response factor 1 [Arabidopsis thaliana]

E value

Match length

9.0e-60



```
266476
Seq. No.
Contig ID
                  11080 1.R1011
5'-most EST
                  LIB3066-027-Q1-K1-G7
                  BLASTX
Method
NCBI GI
                  g2983600
BLAST score
                  1015
E value
                   1.0e-110
Match length
                   399
% identity
                   51
NCBI Description (AE000725) argininosuccinate synthase [Aquifex aeolicus]
                   266477
Seq. No.
                   11083 1.R1011
Contig ID
5'-most EST
                  LIB3061-046-Q1-K1-G12
                  BLASTX
Method
NCBI GI
                   g542190
BLAST score
                   458
                   2.0e-45
E value
Match length
                   92
                   100
% identity
                  hypothetical protein 1087 - maize >gi 459269_emb_CAA54960_
NCBI Description
                   (X78029) transcribed sequence 1087 [Zea mays]
                   266478
Seq. No.
Contig ID
                   11087 1.R1011
5'-most EST
                   xjt700093517.h1
Method
                   BLASTX
NCBI GI
                   g4587557
BLAST score
                   497
                   7.0e-50
E value
Match length
                   188
% identity
                   59
                   (AC006577) Similar to gb_U21858 transcription initiation
NCBI Description
                   factor TFIID 31KD subunit (TAFII32) from Homo sapiens.
                   [Arabidopsis thaliana]
                   266479
Seq. No.
                   11090 1.R1011
Contig ID
                   uC-zmflb73008e04b1
5'-most EST
                   BLASTX
Method
                   g1885312
NCBI GI
                   410
BLAST score
                   6.0e-40
E value
Match length
                   153
% identity
                   61
                  (X91660) similar to Xyloglucan endotransglycosylase (XET)
NCBI Description
                   [Hordeum vulgare]
                   266480
Seq. No.
                   11093 1.R1011
Contig ID
                   uC-zmflmo17290e09b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2894599
BLAST score
                   582
```



% identity NCBI Description (AL021889) putative protein [Arabidopsis thaliana] Seq. No. 266481 11093 3.R1011 Contig ID 5'-most EST uC-zmrob73051b07a1 266482 Seq. No. Contig ID 11093 5.R1011 gct701167821.hl 5'-most EST Method BLASTX g4510423 NCBI GI 174 BLAST score 5.0e-13E value Match length 41 83 % identity NCBI Description (AC006929) unknown protein [Arabidopsis thaliana] 266483 Seq. No. Contig ID 11094 1.R1011 5'-most EST uC-zmflb73279g08b1 Seq. No. 266484 Contig ID. 11095 1.R1011 uC-zmflmo17150b06b1 5'-most EST Method BLASTX NCBI GI q633110 BLAST score 2495 E value 0.0e+00Match length 596 % identity 82 (D31843) plasma membrane H+-ATPase [Oryza sativa] NCBI Description 266485 Seq. No. Contig ID 11095 4.R1011 5'-most EST uC-zmflb73139b05b1 BLASTX Method q633110 NCBI GI BLAST score 446 3.0e-44E value 181 Match length 69 % identity NCBI Description (D31843) plasma membrane H+-ATPase [Oryza sativa] Seq. No. 266486 11097 1.R1011 Contig ID LIB3079-020-Q1-K1-G2 5'-most EST BLASTX Method q2245069 NCBI GI BLAST score 579 E value 2.0e-59 Match length 197 51 % identity

NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No. 266487

Contig ID 11098_1.R1011



```
LIB3079-020-Q1-K1-G3
5'-most EST
                  BLASTX
Method
                   g3367568
NCBI GI
                   343
BLAST score
                   5.0e-32
E value
                   206
Match length
                   41
% identity
                   (AL031135) protein kinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   266488
Seq. No.
                   11100 1.R1011
Contig ID
                   ntr700072230.hl
5'-most EST
                   266489
Seq. No.
                   11100 3.R1011
Contig ID
                   uC-zmromo17017a06a1
5'-most EST
                   266490
Seq. No.
                   11101 1.R1011
Contig ID
                   ymt700222073.hl
5'-most EST
                   BLASTX
Method
                   g3928150
NCBI GI
                   218
BLAST score
                   1.0e-17
E value
                   84
Match length
% identity
                   51
                  (AJ131049) hypothetical protein [Cicer arietinum]
NCBI Description
                   266491
Seq. No.
                   11103 1.R1011
Contig ID
                   uC-zmflmo17198d06b1
5'-most EST
                   BLASTX
Method
                   g2739368
NCBI GI
BLAST score
                   878
E value
                   3.0e - 94
Match length
                   260
                   66
% identity
                  (AC002505) cyclin-like protein [Arabidopsis thaliana]
NCBI Description
                   266492
Seq. No.
                   11104 1.R1011
Contig ID
                   uC-zmflb73053d02b2
5'-most EST
                   266493
Seq. No.
Contig ID
                   11105 1.R1011
                   LIB3062-027-Q1-K1-G3
5'-most EST
Method
                   BLASTX
                   q4503169
NCBI GI
                   260
BLAST score
                   4.0e-22
E value
                   155
Match length
                   37
% identity
                   cut (Drosophila)-like 1 (CCAAT displacement protein)
```

NCBI Description

>gi_457517 (L12579) alternatively spliced [Homo sapiens]



```
11106 1.R1011
Contig ID
                  LIB148-058-Q1-E1-C8
5'-most EST
                   266495
Seq. No.
                   11108 1.R1011
Contig ID
                   uC-zm\overline{f}1Mo17002g09b1
5'-most EST
                   BLASTX
Method
                   g3927831
NCBI GI
                   1283
BLAST score
                   1.0e-141
E value
                   427
Match length
                   60
% identity
                   (AC005727) similar to mouse ankyrin 3 [Arabidopsis
NCBI Description
                   thaliana]
                   266496
Seq. No.
                   11108 2.R1011
Contig ID
                   uC-zmflMo17063h11b1
5'-most EST
                   BLASTX
Method
                   g3927831
NCBI GI
                   398
BLAST score
                   2.0e-38
E value
                   158
Match length
                   49
% identity
                   (AC005727) similar to mouse ankyrin 3 [Arabidopsis
NCBI Description
                   thaliana]
                   266497
Seq. No.
                   11108 3.R1011
Contig ID
                   LIB189-021-Q1-E1-B8
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3927831
                   227
BLAST score
                   1.0e-18
E value
                   91
Match length
                   46
% identity
                   (AC005727) similar to mouse ankyrin 3 [Arabidopsis
NCBI Description
                   thaliana]
                   266498
Seq. No.
                   11110 1.R1011
Contig ID
5'-most EST
                   LIB143-040-Q1-E1-F3
                   266499
Seq. No.
                   11111 1.R1011
Contig ID
                   rvt700550414.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4539423
BLAST score
                   1424
                   1.0e-166
E value
Match length
                   390
                    75
 % identity
                    (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
NCBI Description
                    [Arabidopsis thaliana]
```

266500

11112 1.R1011

Seq. No.

Contig ID



```
LIB3079-020-Q1-K1-E8
5'-most EST
                   BLASTX
Method
                   g2827551
NCBI GI
BLAST score
                   356
                   2.0e-33
E value
                   150
Match length
                   43
% identity
                   (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
                   266501
Seq. No.
                   11113 1.R1011
Contig ID
5'-most EST
                   LIB3062-058-Q1-K1-E3
Method
                   BLASTX
                   g1946358
NCBI GI
BLAST score
                   432
                   4.0e-42
E value
                   110
Match length
                   68
% identity
                   (U93215) unknown protein [Arabidopsis thaliana]
NCBI Description
                   266502
Seq. No.
                   11113 2.R1011
Contig ID
5'-most EST
                   ceu70\overline{0}433538.h1
                   266503
Seq. No.
                   11114_1.R1011
Contig ID
5'-most EST
                   ntr700075601.hl
Method
                   BLASTX
                   q2702269
NCBI GI
                   272
BLAST score
                   8.0e-24
E value
                   118
Match length
                   50
% identity
                  (AC003033) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   266504
Contig ID
                   11116 1.R1011
                   uC-zmroB73014c02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4510349
BLAST score
                   225
                   4.0e-18
E value
                   78
Match length
% identity
                   63
                   (AC006921) putative bZIP transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   266505
Seq. No.
                   11116 2.R1011
Contig ID
5'-most EST
                   LIB3067-032-Q1-K1-G3
                   266506
Seq. No.
                   11119 1.R1011
Contig ID
                   pmx700090980.h1
```

5'-most EST pmx700090 Method BLASTX NCBI GI g2832680

BLAST score 743



```
E value
                  9.0e-79
                  208
Match length
% identity
                  37
                  (ALO21712) putative protein [Arabidopsis thaliana]
NCBI Description
                  266507
Seq. No.
                  11123 1.R1011
Contig ID
                  LIB3136-019-Q1-K1-B11
5'-most EST
                  266508
Seq. No.
                  11125 1.R1011
Contig ID
                  LIB3152-006-P1-K1-D3
5'-most EST
                  BLASTX
Method
                  g1707017
NCBI GI
BLAST score
                  765
                  2.0e-81
E value
                  230
Match length
                   63
% identity
                  (U78721) RNA helicase isolog [Arabidopsis thaliana]
NCBI Description
                   266509
Seq. No.
                   11129 1.R1011
Contig ID
                   uC-zmrob73004f03b1
5'-most EST
                   BLASTX
Method
                   g2160163
NCBI GI
BLAST score
                   268
                   1.0e-22
E value
Match length
                   121
% identity
                   54
                  (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                   266510
Seq. No.
                   11129 2.R1011
Contig ID
                   xmt700267733.h1
5'-most EST
                   BLASTX
Method
                   q2160163
NCBI GI
BLAST score
                   400
                   8.0e-39
E value
                   116
Match length
                   66
% identity
                  (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                   266511
Seq. No.
                   11130 1.R1011
Contig ID
                   nbm700474379.h1
5'-most EST
                   266512
Seq. No.
Contig ID
                   11131 1.R1011
5'-most EST
                   wty700167340.hl
                   BLASTX
Method
                   q4510379
NCBI GI
BLAST score
                   323
E value
                   2.0e-29
Match length
                   175
                   41
% identity
NCBI Description (AC007017) hypothetical protein [Arabidopsis thaliana]
```

NCBI GI

E value

BLAST score

Match length

g3150410

2.0e-70

673

289



```
266513
Seq. No.
Contia ID
                    11132 1.R1011
5'-most EST
                    wty700168108.h1
Method
                    BLASTX
NCBI GI
                    g2245132
BLAST score
                    176
E value
                    2.0e-12
Match length
                    115
% identity
                    37
NCBI Description
                    (Z97344) syntaxin [Arabidopsis thaliana]
                    266514
Seq. No.
                    11133 1.R1011
Contig ID
5'-most EST
                    tfd700576521.h1
Method
                    BLASTX
NCBI GI
                    q464806
BLAST score
                    262
                    3.0e-22
E value
Match length
                    225
% identity
                    30
                    SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72)
NCBI Description
                    >gi_423182_pir__A40692 signal recognition particle 72K
chain - dog >gi_297768_emb_CAA48014_ (X67813) signal
recognition particle,72 kDa subunit [Canis familiaris]
Seq. No.
                    266515
Contig ID
                    11139 1.R1011
5'-most EST
                    LIB3279-016-P1-K1-G10
Method
                    BLASTX
NCBI GI
                    g3548801
BLAST score
                    368
E value
                    9.0e-35
                    180
Match length
% identity
                    40
NCBI Description
                    (AC005313) putative transmembrane protein [Arabidopsis
                    thaliana] >gi 4335768 gb AAD17445 (AC006284) putative
                    integral membrane protein [Arabidopsis thaliana]
                    266516
Seq. No.
                    11140 1.R1011
Contig ID
                    dyk700104575.h1
5'-most EST
                    BLASTX
Method
                    g2388911
NCBI GI
BLAST score
                    547
E value
                    2.0e-55
Match length
                    226
                    48
% identity
                   (Z98974) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
Seq. No.
                    266517
                    11143 1.R1011
Contig ID
5'-most EST
                    pmx700091425.h1
                    BLASTX
Method
```



% identity 49 NCBI Description (AC004165) unknown protein [Arabidopsis thaliana]

Seq. No. 266518

Contig ID 11145_1.R1011

5'-most EST LIB3079-020-Q1-K1-B3

Seq. No. 266519

Contig ID 11146_1.R1011

5'-most EST LIB3079-020-Q1-K1-A12

Seq. No. 266520

Contig ID 11153_1.R1011

5'-most EST LIB3079-012-Q1-K1-G7

Seq. No. 266521

Contig ID 11162_1.R1011 5'-most EST xsy700213018.h1

Method BLASTX
NCBI GI g4128197
BLAST score 347
E value 5.0e-32
Match length 193
% identity 45

NCBI Description (U75273) acyl-CoA binding protein [Arabidopsis thaliana]

Seq. No. 266522

Contig ID 11163_1.R1011

5'-most EST uC-zmroteosinte042a09b1

Seq. No. 266523

Contig ID 11164_1.R1011

5'-most EST LIB3068-052-Q1-K1-A11

Method BLASTX
NCBI GI g4559358
BLAST score 347
E value 2.0e-32
Match length 99
% identity 64

NCBI Description (AC006585) putative steroid binding protein [Arabidopsis

thaliana]

Seq. No. 266524

Contig ID 11164_2.R1011 5'-most EST fC-zmf1700611858a1

Method BLASTX
NCBI GI g2982328
BLAST score 1220
E value 1.0e-134
Match length 263
% identity 89

NCBI Description (AF051249) pyruvate dehydrogenase El beta subunit [Picea

mariana]

Seq. No. 266525

Contig ID 11164_5.R1011 5'-most EST fC-zmse700613259r1



Method BLASTX g4530522 NCBI GI 283 BLAST score 3.0e-25E value 61 Match length 87 % identity

(AF124755) pyruvate dehydrogenase E1 beta subunit [Pinus NCBI Description

banksiana]

266526 Seq. No.

11164 9.R1011 Contig ID qmh700029780.f15'-most EST

266527 Seq. No.

11165 1.R1011 Contig ID

LIB3152-028-P1-K1-C1 5'-most EST

BLASTX Method g2801701 NCBI GI 585 BLAST score 7.0e-60 E value 305 Match length 40 % identity

(AF042379) spindle pole body protein spc97 homolog GCP2 NCBI Description

[Homo sapiens]

266528 Seq. No.

11167 1.R1011 Contig ID $xmt70\overline{0}266991.h1$ 5'-most EST

BLASTX Method g4519671 NCBI GI 340 BLAST score 3.0e-31 E value 131 Match length

53 % identity

(AB017693) transfactor [Nicotiana tabacum] NCBI Description

Seq. No. 266529

11168 1.R1011 Contig ID

LIB3079-019-Q1-K1-F3 5'-most EST

266530 Seq. No.

11172 1.R1011 Contig ID ymt700219749.h15'-most EST

BLASTN Method q3873174 NCBI GI 36 BLAST score E value 5.0e-10

Match length 56 % identity 91

Genomic sequence for Arabidopsis thaliana BAC F14N23, NCBI Description

complete sequence [Arabidopsis thaliana]

266531 Seq. No.

11172 2.R1011 Contig ID uC-zmflb73147c05b1 5'-most EST

Method BLASTX NCBI GI g3341679



BLAST score 338 E value 3.0e-31 Match length 284 % identity 30

NCBI Description (AC003672) dynamin-like protein phragmoplastin 12

[Arabidopsis thaliana]

Seq. No. 266532

Contig ID 11172_3.R1011

5'-most EST uC-zmflmo17368b01a1

Seq. No. 266533

Contig ID 11173_1.R1011 5'-most EST tfd700572647.h1

Seq. No. 266534

Contig ID 11174 1.R1011

5'-most EST LIB3180-019-P2-M1-C5

Method BLASTX
NCBI GI g3548810
BLAST score 354
E value 5.0e-33
Match length 217
% identity 35

% identity 35 NCBI Description (AC005313) putative chloroplast nucleoid DNA binding

protein [Arabidopsis thaliana]

Seq. No. 266535

Contig ID 11181_1.R1011

5'-most EST LIB3079-019-Q1-K1-D6

Seq. No. 266536

Contig ID 11184_1.R1011 5'-most EST vux700160635.h1

Method BLASTX
NCBI GI g4056507
BLAST score 190
E value 3.0e-14
Match length 63
% identity 59

NCBI Description (AC005896) putative RNA binding protein [Arabidopsis

thaliana]

Seq. No. 266537

Contig ID 11187_1.R1011 5'-most EST yyf700348104.h1

Method BLASTX
NCBI GI g3219355
BLAST score 374
E value 3.0e-35
Match length 221
% identity 42

NCBI Description (AF062371) ROOT HAIRLESS 1 [Arabidopsis thaliana]

Seq. No. 266538

Contig ID 11189_1.R1011

5'-most EST LIB3079-019-Q1-K1-B11



266539 Seq. No. 11190 1.R1011 Contig ID 5'-most EST $nbm70\overline{0464976.h1}$ Method BLASTX g3983665 NCBI GI BLAST score 896 E value 5.0e-97 179 Match length 98 % identity (AB011271) importin-beta2 [Oryza sativa] NCBI Description 266540 Seq. No. 11194 1.R1011 Contig ID 5'-most EST uC-zmflmo17151d05b1 Method BLASTX NCBI GI q2345148 894 BLAST score 3.0e-96 E value Match length 201 % identity 83 (AF014821) developmentally regulated GTP binding protein NCBI Description [Pisum sativum] 266541 Seq. No. 11194 2.R1011 Contig ID xyt700343545.h1 5'-most EST BLASTX Method q2058456 NCBI GI 1264 BLAST score E value 1.0e-147 284 Match length 93 % identity (U66408) GTP-binding protein [Arabidopsis thaliana] NCBI Description >gi_2345150_gb_AAB67830_ (AF014822) developmentally regulated GTP binding protein [Arabidopsis thaliana] 266542 Seq. No. 11195 1.R1011 Contig ID LIB3059-046-Q1-K1-H4 5'-most EST Method BLASTX g3549657 NCBI GI BLAST score 193 2.0e-14 E value 82 Match length % identity 41 (AL031394) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 266543
Contig ID 11198 1.R1011

5'-most EST uC-zmflmo17152b11b1

Seq. No. 266544

Contig ID 11203_1.R1011

5'-most EST LIB143-021-Q1-E1-B8

Method BLASTX NCBI GI g563235



BLAST score 1415 E value 1.0e-157 Match length 280 % identity 94

NCBI Description (U15964) xyloglucan endo-transglycosylase homolog; similar

to Triticum aestivum endo-xyloglucan transferase, PIR Accession Number E49539 [Zea mays] >gi_563927 (U15781) xyloglucan endo-transglycosylase homolog [Zea mays]

>gi_1097378_prf__2113418A xyloglucan endotransglycosylase

homolog [Zea mays]

Seq. No. 266545

Contig ID 11203_2.R1011

5'-most EST uC-zmflmo17220b06b1

Method BLASTX
NCBI GI g563235
BLAST score 346
E value 1.0e-32
Match length 91
% identity 73

NCBI Description (U15964) xyloglucan endo-transglycosylase homolog; similar

to Triticum aestivum endo-xyloglucan transferase, PIR Accession Number E49539 [Zea mays] >gi_563927 (U15781) xyloglucan endo-transglycosylase homolog [Zea mays]

>gi 1097378 prf 2113418A xyloglucan endotransglycosylase

homolog [Zea mays]

Seq. No. 266546

Contig ID 11204 1.R1011

5'-most EST LIB3079-018-Q1-K1-H12

Seq. No. 266547

Contig ID 11216_1.R1011

5'-most EST LIB3079-018-Q1-K1-F10

Method BLASTX
NCBI GI g3287696
BLAST score 147
E value 3.0e-09
Match length 42
% identity 67

NCBI Description (AC003979) Strong similarity to phosphoribosylanthranilate

transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region.

[Arabidopsis thaliana]

Seq. No. 266548

Contig ID 11217 1.R1011

5'-most EST LIB3079-018-Q1-K1-F11

Method BLASTX
NCBI GI g2739372
BLAST score 779
E value 5.0e-83
Match length 276
% identity 59

NCBI Description (AC002505) hypothetical protein [Arabidopsis thaliana]

Seq. No. 266549

Match length

% identity

59

56



```
11224 1.R1011
Contig ID
                  fwa700101387.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4503363
BLAST score
                  664
E value
                  1.0e-69
Match length
                  192
                  65
% identity
NCBI Description
                  UNKNOWN >gi 3062806 dbj BAA25646 (D86198)
                  dolichol-phosphate-mannose synthase [Homo sapiens]
                  266550
Seq. No.
                  11226 1.R1011
Contig ID
5'-most EST
                  LIB3079-018-Q1-K1-G10
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
                  1.0e-10
E value
                  36
Match length
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  266551
Contig ID
                  11228 1.R1011
5'-most EST
                  uC-zmflb73166e12b2
Method
                  BLASTX
NCBI GI
                  q4406804
BLAST score
                  1343
                   1.0e-149
E value
Match length
                   325
% identity
                  (AC006304) proline iminopeptidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   266552
Contig ID
                   11228 2.R1011
5'-most EST
                  LIB83-012-Q1-E1-C8
Method
                   BLASTX
NCBI GI
                   g2911044
BLAST score
                   374
                   1.0e-35
E value
Match length
                   115
% identity
                   65
                  (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   266553
                   11228 3.R1011
Contig ID
                  hbs701184248.h1
5'-most EST
                   266554
Seq. No.
                   11228 4.R1011
Contig ID
5'-most EST
                  ntr700073852.h1
                   BLASTX
Method
                   g1710151
NCBI GI
BLAST score
                   163
E value
                   3.0e-11
```



```
NCBI Description (U72711) proline iminopeptidase [Arabidopsis thaliana]
                   266555
Seq. No.
                   11228 5.R1011
Contig ID
                   LIB3159-007-Q1-K1-B10
5'-most EST
                   BLASTX
Method
                   g2911044
NCBI GI
                   472
BLAST score
                   5.0e-47
E value
                   133
Match length
                   68
% identity
                   (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                   266556
Seq. No.
                   11228 6.R1011
Contig ID
5'-most EST
                   qmh700027057.f1
                   BLASTX
Method
                   g4406804
NCBI GI
                   188
BLAST score
                   1.0e-18
E value
                   67
Match length
                   75
% identity
                   (AC006304) proline iminopeptidase [Arabidopsis thaliana]
NCBI Description
                   266557
Seq. No.
                   11228 7.R1011
Contig ID
5'-most EST
                   uC-zmflmo17131c07a1
                   266558
Seq. No.
                   11239 1.R1011
Contig ID
5'-most EST
                   xjt70\overline{0}096408.h1
                   BLASTX
Method
                   g2507426
NCBI GI
BLAST score
                   1593
                   0.0e + 00
E value
Match length
                   566
% identity
                   64
                   ALANYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                   (ALANINE--TRNA LIGASE) (ALARS) >gi_1673365 emb CAA80380
                   (Z22673) mitochondrial tRNA-Ala synthetase [Arabidopsis
                   thaliana]
                   266559
Seq. No.
                   11239 2.R1011
Contig ID
                   LIB3117-007-Q1-K1-E3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2065021
BLAST score
                   209
E value
                   4.0e-16
                   70
Match length
                   57
% identity
                   (Y12555) alanyl t-RNA synthetase [Arabidopsis thaliana]
NCBI Description
```

37060

266560

11241 1.R1011

LIB3066-032-Q1-E1-D6

Seq. No.

Contig ID 5'-most EST



Seq. No. 266561

Contig ID 11241 2.R1011

5'-most EST LIB3066-032-Q1-E1-G3

Seq. No. 266562

Contig ID 11241_3.R1011

5'-most EST LIB3069-027-Q1-K1-D8

Seq. No. 266563

Contig ID 11241 18.R1011

5'-most EST LIB3069-016-Q1-K1-E1

Seq. No. 266564

Contig ID 11241 20.R1011

5'-most EST LIB3069-016-Q1-K1-C7

Seq. No. 266565

Contig ID 11241 21.R1011

5'-most EST LIB3069-027-Q1-K1-E1

Seq. No. 266566

Contig ID 11241 25.R1011

5'-most EST LIB3069-027-Q1-K1-E5

Seq. No. 266567

Contig ID 11245_1.R1011 5'-most EST LIB83-007-Q1-E1-F9

Method BLASTX

NCBI GI g4115538

BLAST score 276 E value 3.0e-24

Match length 193 % identity 33

NCBI Description (AB012116) UDP-glycose:flavonoid glycosyltransferase [Vigna

mungo]

Seq. No. 266568

Contig ID 11254 1.R1011

5'-most EST LIB143-037-Q1-E1-C6

Method BLASTX
NCBI GI g4314378
BLAST score 641
E value 1.0e-66

Match length 335 % identity 39

NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 266569

Contig ID 11254_2.R1011

5'-most EST LIB3116-011-Q1-K1-H4

Method BLASTX
NCBI GI g3482914
BLAST score 152
E value 6.0e-10
Match length 72

Match length 72 % identity 36

NCBI Description (AC003970) Similar to nodulins and lipase [Arabidopsis



```
thaliana]
                  266570
Seq. No.
                  11254 3.R1011
Contig ID
                  ntr700074845.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2129636
BLAST score
                  328
E value
                  4.0e-32
Match length
                  224
% identity
                  39
                 lipase - Arabidopsis thaliana >gi 1145627 (U38916) lipase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  266571
                  11254 5.R1011
Contig ID
                  nbm700471645.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4314378
BLAST score
                  143
                  6.0e-09
E value
                  67
Match length
% identity
                  37
NCBI Description
                 (AC006232) putative lipase [Arabidopsis thaliana]
Seq. No.
                  266572
Contig ID
                  11254 6.R1011
5'-most EST
                  wty700166293.hl
                  266573
Seq. No.
Contig ID
                  11263 1.R1011
                  LIB3079-017-Q1-K1-H4
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4512682
BLAST score
                  299
                  5.0e-27
E value
                  88
Match length
% identity
NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]
Seq. No.
                   266574
```

Contig ID 11263_2.R1011 5'-most EST wty700167023.h1

Method BLASTX
NCBI GI g4512682
BLAST score 354
E value 2.0e-33
Match length 119
% identity 57

NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]

Seq. No. 266575

Contig ID 11276_1.R1011

5'-most EST LIB3137-005-Q1-K1-A9

Seq. No. 266576

Contig ID 11276 2.R1011



LIB3066-047-Q1-K1-H2 5'-most EST Method BLASTX NCBI GI g4519539 1244 BLAST score E value 1.0e-137 339 Match length 68 % identity (AB016256) NAD-dependent sorbitol dehydrogenase [Malus NCBI Description domestica] 266577 Seq. No. Contig ID 11276 3.R1011 5'-most EST LIB3151-022-Q1-K1-A4 266578 Seq. No. 11276 4.R1011 Contig ID uC-zmflb73208a11b1 5'-most EST 266579 Seq. No. Contig ID 11276 8.R1011 LIB3079-015-Q1-K1-B10 5'-most EST BLASTX Method NCBI GI g4519539 BLAST score -205 E value 7.0e-1688 Match length % identity 45 (AB016256) NAD-dependent sorbitol dehydrogenase [Malus NCBI Description domestica] Seq. No. 266580 Contig ID 11282 1.R1011 uC-zmflmo17217h05b1 5'-most EST BLASTX Method NCBI GI q1001935 BLAST score 1262 E value 1.0e-139 Match length 267 % identity 93 NCBI Description (X81199) ZMM1 [Zea mays] >gi 1167914 (U31522) MADS box protein [Zea mays] 266581 Seq. No. 11282 3.R1011 Contig ID 5'-most EST yyf700350565.h1 Method BLASTX NCBI GI g1001935 531 BLAST score 3.0e-54E value Match length 110 95 % identity NCBI Description (X81199) ZMM1 [Zea mays] >gi 1167914 (U31522) MADS box

protein [Zea mays]

Seq. No. 266582

Contig ID 11283 1.R1011

5'-most EST LIB3066-006-Q1-K1-D8



Method BLASTX g3138799 NCBI GI BLAST score 1125 1.0e-123 E value Match length 221 97 % identity (AB014058) beta 6 subunit of 20S proteasome [Oryza sativa] NCBI Description Seq. No. 266583 11283 2.R1011 Contig ID 5'-most EST uC-zmflmo17219g12b1 BLASTX Method NCBI GI q3138799 BLAST score 262 E value 1.0e-22 Match length 50 96 % identity (AB014058) beta 6 subunit of 20S proteasome [Oryza sativa] NCBI Description 266584 Seq. No. Contig ID 11283_4.R1011 5'-most EST uC-zmroteosinte012g06b1 Method BLASTX NCBI GI g3138799 BLAST score 165 3.0e-14E value Match length 64 75 % identity (AB014058) beta 6 subunit of 20S proteasome [Oryza sativa] NCBI Description Seq. No. 266585 11293 1.R1011 Contig ID uC-zmflmo17181c06b1 5'-most EST Method BLASTX NCBI GI q2245108 BLAST score 574 E value 9.0e-59Match length 159 % identity (Z97343) EREBP-4 homolog [Arabidopsis thaliana] NCBI Description Seq. No. 266586 Contig ID 11299 1.R1011 5'-most EST LIB3079-017-Q1-K1-E8 Method BLASTX NCBI GI g1871192 BLAST score 254

E value 1.0e-21 197 Match length % identity 42

(U90439) Cys3His zinc finger protein isolog [Arabidopsis NCBI Description

thaliana]

266587 Seq. No.

11301 1.R1011 Contig ID

5'-most EST LIB3079-017-Q1-K1-F1



Seq. No. 266588

Contig ID 11305_1.R1011 5'-most EST uC-zmflB73010b10b1

Method BLASTX
NCBI GI g4185513
BLAST score 532
E value 4.0e-54
Match length 133
% identity 72

NCBI Description (AF102823) actin depolymerizing factor 5 [Arabidopsis

thaliana] >gi_4185517 (AF102825) actin depolymerizing

factor 5 [Arabidopsis thaliana]

Seq. No. 266589

Contig ID 11305 2.R1011

5'-most EST uC-zmroteosinte001f05b1

Seq. No. 266590

Contig ID 11305 3.R1011

5'-most EST uC-zmflmo17050g08b2

Method BLASTX
NCBI GI g4185513
BLAST score 582
E value 6.0e-60
Match length 143
% identity 74

NCBI Description (AF102823) actin depolymerizing factor 5 [Arabidopsis

thaliana] $>gi_4185517$ (AF102825) actin depolymerizing

factor 5 [Arabidopsis thaliana]

Seq. No. 266591

Contig ID 11305_4.R1011 5'-most EST uwc700154547.h1

Method BLASTX
NCBI GI g4185513
BLAST score 428
E value 6.0e-42
Match length 115
% identity 73

NCBI Description (AF102823) actin depolymerizing factor 5 [Arabidopsis

thaliana] >gi 4185517 (AF102825) actin depolymerizing

factor 5 [Arabidopsis thaliana]

Seq. No. 266592

Contig ID 11305 6.R1011

5'-most EST LIB3069-012-Q1-K1-H6

Method BLASTX
NCBI GI g4185513
BLAST score 190
E value 2.0e-14
Match length 58
% identity 59

NCBI Description (AF102823) actin depolymerizing factor 5 [Arabidopsis

thaliana] >gi_4185517 (AF102825) actin depolymerizing

factor 5 [Arabidopsis thaliana]

Seq. No. 266593



11305 7.R1011 Contig ID 5'-most EST uwc700152962.h1 Method BLASTX NCBI GI q4185513 BLAST score 221 E value 3.0e-18Match length 60 % identity NCBI Description (AF102823) actin depolymerizing factor 5 [Arabidopsis thaliana] >gi_4185517 (AF102825) actin depolymerizing factor 5 [Arabidopsis thaliana] 266594 Seq. No. Contig ID 11305 8.R1011 $xsy70\overline{0}217894.h1$

5'-most EST Method BLASTX NCBI GI q4185513 BLAST score 171 E value 2.0e-12 Match length 50 58 % identity

NCBI Description (AF102823) actin depolymerizing factor 5 [Arabidopsis thaliana] >gi_4185517 (AF102825) actin depolymerizing

factor 5 [Arabidopsis thaliana]

Seq. No. 266595

Contig ID 11306_1.RT011

LIB3079-006-Q1-K1-H9 5'-most EST

266596 Seq. No.

Contig ID 11308 1.R1011 wty700172668.hl 5'-most EST

Method BLASTX NCBI GI q4406759 BLAST score 194 E value 1.0e-14 74 Match length

51 % identity

NCBI Description (AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No. 266597

11311 1.R1011 Contig ID 5'-most EST uC-zmflMo17004d03b1

Seq. No. 266598

Contig ID 11311 3.R1011

5'-most EST LIB3150-040-Q1-N1-B10

Seq. No. 266599

11312 1.R1011 Contig ID $uC-zm\overline{f}1b73130b12b2$ 5'-most EST

Method BLASTX NCBI GI g2832642 BLAST score 204 E value 3.0e-15 Match length 270 % identity 31



NCBI Description (AL021710) putative protein [Arabidopsis thaliana]

Seq. No. 266600

Contig ID 11312 2.R1011

5'-most EST uC-zmroteosinte011f12b1

Seq. No. 266601

Contig ID 11313 1.R1011

5'-most EST LIB3079-017-Q1-K1-C8

Method BLASTX
NCBI GI g3874039
BLAST score 338
E value 2.0e-31
Match length 181
% identity 40

NCBI Description (Z75526) Weak similarity to Staphyloccus autolysin gene

(TR:G765072); cDNA EST EMBL:M89336 comes from this gene; cDNA EST yk505d12.3 comes from this gene [Caenorhabditis

elegans]

Seq. No. 266602

Contig ID 11314_1.R1011 5'-most EST wyr700235744.h1

Method BLASTX
NCBI GI g2821957
BLAST score 802
E value 1.0e-85
Match length 205
% identity 68

NCBI Description (AB006691) spermidine synthase 2 [Hyoscyamus niger]

Seq. No. 266603

Contig ID 11317_1.R1011

5'-most EST LIB30 $\overline{6}$ 0-047-Q1-K1-B9

Method BLASTX
NCBI GI g2191145
BLAST score 334
E value 3.0e-30
Match length 606

% identity 29

NCBI Description (AF007269) A IG002N01.4 gene product [Arabidopsis thaliana]

Seq. No. 266604

Contig ID 11317 4.R1011 5'-most EST uC-zmflb73218a12b2

Method BLASTN
NCBI GI g886820
BLAST score 45
E value 2.0e-16
Match length 49
% identity 98

NCBI Description Zea mays calcium-dependent protein kinase (MZECDPK2) mRNA,

complete cds

Seq. No. 266605

Contig ID 11320_1.R1011

5'-most EST LIB3068-019-Q1-K1-A6



Seq. No. 266606

Contig ID 11323 1.R1011

5'-most EST LIB3079-017-Q1-K1-C12

Seq. No. 266607

Contig ID 11325_1.R1011 5'-most EST uC-zmrob73049e07a1

Seq. No. 266608

Contig ID 11327_1.R1011 5'-most EST uC-zmflB73043d03b1

Seq. No. 266609

Contig ID 11329_1.R1011

5'-most EST LIB3079-017-Q1-K1-B11

Method BLASTX
NCBI GI g1006768
BLAST score 628
E value 2.0e-65
Match length 127
% identity 97

NCBI Description (X81200) ZMM2 [Zea mays]

Seq. No. 266610

Contig ID 11329 2.R1011

5'-most EST LIB3067-006-Q1-K1-A10

Method BLASTX
NCBI GI g2529340
BLAST score 326

E value 2.0e-30 Match length 100 % identity 76

NCBI Description (L81162) homologue; putative [Zea mays]

Seq. No. 266611

Contig ID 11330 1.R1011

5'-most EST LIB3079-017-Q1-K1-B12

Method BLASTX
NCBI GI g731632
BLAST score 263
E value 2.0e-22
Match length 183
% identity 36

NCBI Description HYPOTHETICAL 57.0 KD PROTEIN IN SOD2-RPL27 INTERGENIC

REGION >gi_626596_pir__S46784 hypothetical protein YHR009c - yeast (Saccharomyces cerevisiae) >gi_500703 (U10400)

Yhr009cp [Saccharomyces cerevisiae]

Seq. No. 266612

Contig ID 11332_1.R1011 5'-most EST uwc700151162.h1

Method BLASTX
NCBI GI g2282473
BLAST score 669
E value 1.0e-70
Match length 272



% identity 54

NCBI Description (AB005911) xanthine dehydrogenase [Bombyx mori]

Seq. No. 266613

Contig ID 11334_1.R1011 5'-most EST xsy700208735.h1

Seq. No. 266614

Contig ID 11334 2.R1011

5'-most EST uC-zmflmo17235g01b1

Seq. No. 266615

Contig ID 11334_6.R1011

5'-most EST uC-zmflm017092a11b1

Seq. No. 266616

Contig ID 11337_1.R1011
5'-most FST UC-zmrob73006d0

5'-most EST uC-zmrob73006d05a1 Method BLASTX

Method BLASTX
NCBI GI g4587584
BLAST score 2589
E value 0.0e+00
Match length 659
% identity 77

NCBI Description (AC007232) unknown protein [Arabidopsis thaliana]

Seq. No. 266617

Contig ID 11338_1.R1011 5'-most EST dyk700105374.h1

Seq. No. 266618

Contig ID 11341 1.R1011

5'-most EST LIB3068-060-Q1-K1-A4

Method BLASTX
NCBI GI g2623309
BLAST score 213
E value 1.0e-16
Match length 207
% identity 38

NCBI Description (AC002409) similar to tgacg-specific DNA-binding protein

[Arabidopsis thaliana]

Seq. No. 266619

Contig ID 11342 1.R1011 5'-most EST fdz701158492.h1

Method BLASTX
NCBI GI g1076390
BLAST score 1931
E value 0.0e+00
Match length 428
% identity 46

NCBI Description protein phosphatase 2A pDF2 - Arabidopsis thaliana

>gi 683504 emb CAA57529 (X82003) protein phosphatase 2A 65

kDa regulatory subunit [Arabidopsis thaliana]

Seq. No. 266620

Contig ID 11344_1.R1011

Seq. No.

Contig ID

266625

11345_5.R1011



```
5'-most EST
                  uC-zmflmo17270g05b1
                  BLASTX
Method
NCBI GI
                  g2760834
BLAST score
                  331
                  1.0e-30
E value
                  163
Match length
% identity
                  45
                  (AC003105) putative nitrate transporter [Arabidopsis
NCBI Description
                  thaliana]
                  266621
Seq. No.
                  11345_1.R1011
Contig ID
5'-most EST
                  hbs701186151.hl
                  BLASTX
Method
                  g3860308
NCBI GI
BLAST score
                  147
                  7.0e-09
E value
                  73
Match length
                  47
% identity
NCBI Description (AJ012681) hypothetical protein [Cicer arietinum]
                  266622
Seq. No.
Contig ID
                  11345_2.R1011
5'-most EST
                  LIB3067-028-Q1-K1-B10
Method
                  BLASTN
NCBI GI
                  q786131
                  68
BLAST score
                  1.0e-29
E value
Match length
                  164
                  85
% identity
NCBI Description Oryza sativa root-specific RCc3 mRNA, complete cds
Seq. No.
                  266623
                  11345_3.R1011
Contig ID
5'-most EST
                  uC-zmflb73124a08a1
Method
                  BLASTX
NCBI GI
                  g4204309
BLAST score
                  248
E value
                  2.0e-36
Match length
                  128
% identity
                  64
                  (AC003027) 1cl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  266624
Seq. No.
Contig ID
                  11345 4.R1011
5'-most EST
                  LIB3067-033-Q1-K1-H5
Method
                  BLASTX
NCBI GI
                  q4103618
BLAST score
                  271
E value
                  1.0e-23
                  83
Match length
% identity
                  60
NCBI Description (AF026382) HyPRP [Fragaria x ananassa]
```



5'-most EST LIB3079-058-Q1-K1-B5 Method BLASTX g4103618 NCBI GI BLAST score 271 1.0e-23 E value 83 Match length 60 % identity (AF026382) HyPRP [Fragaria x ananassa] NCBI Description 266626 Seq. No. 11345 6.R1011 Contig ID LIB3117-009-Q1-K1-B12 5'-most EST Method BLASTX q4103618 NCBI GI BLAST score 256 4.0e-22 E value 83 Match length 58 % identity (AF026382) HyPRP [Fragaria x ananassa] NCBI Description Seq. No. 266627 11364_1.R1011 Contig ID ypc700803957.h1 5'-most EST BLASTX Method NCBI GI q4455199 BLAST score 1143 1.0e-125 E value 333 Match length % identity NCBI Description (AL035440) putative protein [Arabidopsis thaliana] 266628 Seq. No. 11364 2.R1011 Contig ID 5'-most EST LIB3079-016-Q1-K1-G2 Seq. No. 266629 Contig ID 11365 1.R1011 uC-zmflmo17336b12b1 5'-most EST Method BLASTX NCBI GI q3334756 BLAST score 494 2.0e-49 E value Match length 113 % identity 84 NCBI Description (Y16672) putative arginine/serine-rich splicing factor [Medicago sativa] 266630 Seq. No. 11365 2.R1011 Contig ID 5'-most EST uC-zmroteosinte099a02b2

Seq. No. 266631

Contig ID 11365_3.R1011 5'-most EST xjt700094967.h1

Method BLASTX NCBI GI g3334756 BLAST score 491



2.0e-49 E value Match length 112 85 % identity NCBI Description (Y16672) putative arginine/serine-rich splicing factor [Medicago sativa] 266632 Seq. No. 11375_1.R1011 Contig ID 5'-most EST tzu700203268.h1 Method BLASTX g423112 NCBI GI BLAST score 154 9.0e-10 E value 101 Match length 34 % identity transcription factor TMF, TATA element modulatory factor -NCBI Description human 266633 Seq. No. Contig ID 11375 2.R1011

5'-most EST uC-zmflb73206f07b1 266634 Seq. No.

Contig ID 11377 1.R1011 uC-zmflmo17187d01b1 5'-most EST Method BLASTX q1708463 NCBI GI BLAST score 1031

1.0e-112 E value Match length 384 % identity 51

NCBI Description IAA-AMINO ACID HYDROLASE >gi_887785 (U23794) ILR1

[Arabidopsis thaliana]

Seq. No. 266635 Contig ID 11378 1.R1011 5'-most EST hbs701182230.hl Method BLASTX

NCBI GI g2980773 BLAST score 435 E value 2.0e-42 Match length 134 % identity 64

NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 266636

11381 1.R1011 Contig ID

LIB3067-033-Q1-K1-C5 5'-most EST

Seq. No. 266637

Contiq ID 11383 1.R1011

5'-most EST LIB3062-044-Q1-K1-D7

BLASTX Method NCBI GI g3176725 BLAST score 913 E value 8.0e-99 Match length 249



% identity 64 NCBI Description (AC002392) unknown protein [Arabidopsis thaliana]

Seq. No. 266638 Contig ID 11386_1.R1011

5'-most EST LIB3079-016-Q1-K1-D2

Method BLASTX
NCBI GI g3080426
BLAST score 207
E value 3.0e-16
Match length 126
% identity 38

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 266639

Contig ID 11388 1.R1011

5'-most EST LIB3079-016-Q1-K1-D4

Seq. No. 266640

Contig ID 11389 1.R1011

5'-most EST uC-zmflmo17204g05b1

Seq. No. 266641

Contig ID 11390 1.R1011

5'-most EST LIB3136-012-Q1-K1-D10

Seq. No. 266642

Contig ID 11390 2.R1011

5'-most EST LIB3079-040-Q1-K1-E3

Seq. No. 266643

Contig ID 11395_1.R1011 5'-most EST uC-zmflb73206e08b1

Seq. No. 266644

Contig ID 11395_2.R1011

5'-most EST LIB3079-012-Q1-K1-H9

Seq. No. 266645

Contig ID 11397_1.R1011 5'-most EST rvt700551628.h1

Method BLASTX
NCBI GI g2133266
BLAST score 384
E value 3.0e-60
Match length 287
% identity 46

NCBI Description chromosome scaffold protein sudA - Emericella nidulans

>gi_1103893 (U40146) chromosome scaffold protein

[Emericella nidulans]

Seq. No. 266646

Contig ID 11397_2.R1011

5'-most EST LIB3079-016-Q1-K1-B4

Method BLASTX
NCBI GI g4557060
BLAST score 441



2.0e-43 E value Match length 150 62 % identity

NCBI Description (AC007154) putative chromosome-associated polypeptide, 5'

partial [Arabidopsis thaliana]

266647 Seq. No.

11398 1.R1011 Contig ID uC-zmflb73188b03b1 5'-most EST

BLASTN Method g4416300 NCBI GI BLAST score 220 E value 1.0e-120 453 Match length 40 % identity

Zea mays chromosome 4 22 kDa zein-associated intercluster NCBI Description

region, complete sequence

266648 Seq. No.

11399 1.R1011 Contig ID

5'-most EST uC-zmroteosinte038a05b1

BLASTX Method NCBI GI q1928886 BLAST score 535 E value 4.0e-54 372 Match length % identity 36

(U92010) lin-10 protein homolog [Rattus norvegicus] NCBI Description

266649 Seq. No.

Contig ID 11401 1.R1011 xyt700342243.h1 5'-most EST

Method BLASTX NCBI GI q2244837 BLAST score 792 E value 2.0e-84 Match length 198 76 % identity

NCBI Description (Z97337) proteasome chain protein [Arabidopsis thaliana]

>gi_2511572_emb_CAA73618.1_ (Y13175) multicatalytic
endopeptidase [Arabidopsis thaliana] >gi_3421114 (AF043535)

20S proteasome beta subunit PBD2 [Arabidopsis thaliana]

266650 Seq. No.

11401 2.R1011 Contig ID 5'-most EST xyt700347105.hl

Method BLASTX q2244837 NCBI GI BLAST score 807 3.0e-86 E value 199 Match length 77 % identity

(Z97337) proteasome chain protein [Arabidopsis thaliana] NCBI Description

>gi_2511572_emb_CAA73618.1_ (Y13175) multicatalytic
endopeptidase [Arabidopsis thaliana] >gi_3421114 (AF043535) 20S proteasome beta subunit PBD2 [Arabidopsis thaliana]



Seq. No. 266651

Contig ID 11402_1.R1011

5'-most EST LIB3079-015-Q1-K1-H12

Method BLASTX
NCBI GI g4455232
BLAST score 831
E value 3.0e-89
Match length 192
% identity 74

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 266652

Contig ID 11402_2.R1011

5'-most EST uC-zmflMo17007h06b1

Method BLASTX
NCBI GI g4455232
BLAST score 215
E value 2.0e-17
Match length 51
% identity 71

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

Seq. No. 266653

Contig ID 11406_1.R1011

5'-most EST LIB3116-004-Q1-K2-B7

Seq. No. 266654

Contig ID 11408_1.R1011 5'-most EST cyk700047470.f1

Seq. No. 266655

Contig ID 11410_1.R1011

5'-most EST LIB3137-040-Q1-K1-F10

Method BLASTX
NCBI GI g542188
BLAST score 1388
E value 1.0e-154
Match length 400
% identity 70

NCBI Description OHP2 protein - maize >gi_168428 (L06478) opaque2

heterodimerizing protein 2 [Zea mays]

Seq. No. 266656

Contig ID 11410_3.R1011 5'-most EST uC-zmflb73296g10a1

Method BLASTX
NCBI GI g542188
BLAST score 492
E value 2.0e-49
Match length 97
% identity 99

NCBI Description OHP2 protein - maize >gi_168428 (L06478) opaque2

heterodimerizing protein 2 [Zea mays]

Seq. No. 266657

Contig ID 11410_5.R1011 5'-most EST wty700165459.h1



```
Method
                   BLASTX
NCBI GI
                   g542188
                   222
BLAST score
                   1.0e-18
E value
                   46
Match length
                   96
% identity
                  OHP2 protein - maize >gi_168428 (L06478) opaque2
NCBI Description
                  heterodimerizing protein 2 [Zea mays]
                   266658
Seq. No.
Contig ID
                   11411 1.R1011
                   LIB84-014-Q1-E1-C9
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4006876
                   169
BLAST score
                   2.0e-11
E value
Match length
                   117
                   40
% identity
                  (Z99707) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   266659
Seq. No.
                   11412 1.R1011
Contig ID
                   rvt700550388.hl
5'-most EST
                   BLASTX
Method
                   g4206765
NCBI GI
BLAST score
                   610
                   7.0e-63
E value
                   340
Match length
                   43
% identity
                  (AF104329) putative type 1 membrane protein [Arabidopsis
NCBI Description
                   thaliana]
                   266660
Seq. No.
                   11414_1.R1011
Contig ID
                   LIB3079-015-Q1-K1-H1
5'-most EST
Method
                   BLASTX
                   g2213884
NCBI GI
                   267
BLAST score
                   3.0e-23
E value
                   69
Match length
                   77
% identity
NCBI Description
                   (AF004166) 2-isopropylmalate synthase [Lycopersicon
                   pennellii]
                   266661
Seq. No.
                   11421 1.R1011
Contig ID
5'-most EST
                   LIB3079-015-Q1-K1-G10
Method
                   BLASTX
NCBI GI
                   q4249402
BLAST score
                   435
E value
                   7.0e-43
Match length
                   166
% identity
                   60
```

NCBI Description (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 266662 Contig ID 11423 1.R1011



```
5'-most EST
                  LIB3059-034-Q1-K1-C9
Seq. No.
                  266663
                  11427 1.R1011
Contig ID
5'-most EST
                  LIB3079-015-Q1-K1-G8
Seq. No.
                  266664
Contig ID
                  11437 1.R1011
5'-most EST
                  LIB3151-046-Q1-K1-A12
Method
                  BLASTX
NCBI GI
                  q4309969
BLAST score
                  409
E value
                  9.0e-40
Match length
                  154
% identity
                  50
NCBI Description (AC002983) putative phosphoglyceride transfer protein
                   [Arabidopsis thaliana]
Seq. No.
                  266665
Contig ID
                  11437 2.R1011
5'-most EST
                  tfd700575980.h1
Seq. No.
                  266666
Contig ID
                  11439 1.R1011
5'-most EST
                  LIB3136-028-Q1-K1-G5
Seq. No.
                  266667
                  11440 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73238b09b2
Method
                  BLASTX
NCBI GI
                  g4099148
BLAST score
                  930
E value
                  1.0e-100
Match length
                  224
                  82
% identity
NCBI Description (U84268) YLP [Hordeum vulgare]
Seq. No.
                  266668
                  11440 2.R1011
Contig ID
5'-most EST
                  uC-zmflmo17242e11b1
Method
                  BLASTX
NCBI GI
                  q4099148
BLAST score
                  835
E value
                  2.0e-89
Match length
                  224
% identity
                  75
NCBI Description (U84268) YLP [Hordeum vulgare]
                  266669
```

Seq. No.

11440 3.R1011 Contig ID

5'-most EST LIB3067-026-Q1-K1-D11

Seq. No. 266670

Contig ID 11440 5.R1011 5'-most EST uC-zmflb73238b09a1

Method BLASTN NCBI GI g4099147



```
BLAST score
                   37
                   3.0e-11
E value
Match length
                   45
                   96
% identity
NCBI Description
                  Hordeum vulgare vacuolar proton-translocating ATPase
                   subunit E (Ylp) mRNA, complete cds
                   266671
Seq. No.
                   11440 6.R1011
Contig ID
5'-most EST
                  hvj700619165.h1
                  BLASTX
Method
NCBI GI
                   q4099148
BLAST score
                   228
E value
                   1.0e-18
Match length
                   79
% identity
                   66
                  (U84268) YLP [Hordeum vulgare]
NCBI Description
Seq. No.
                   266672
Contig ID
                   11445 1.R1011
5'-most EST
                  LIB3079-015-Q1-K1-C2
Method
                   BLASTX
NCBI GI
                   g4567309
BLAST score
                   189
                   9.0e-14
E value
Match length
                   172
% identity
                   28
                  (AC005956) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   266673
Seq. No.
Contig ID
                   11447 1.R1011
5'-most EST
                   uC-zmflb73149e05b1
Method
                   BLASTX
NCBI GI
                   q4584525
BLAST score
                   1415
E value
                   1.0e-157
Match length
                   332
% identity
                   77
                   (AL049607) protein phosphatase 2C-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   266674
Seq. No.
                   11447 3.R1011
Contig ID
                   uC-zmflb73295a07a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4584525
BLAST score
                   158
E value
                   1.0e-10
Match length
                   33
```

% identity

NCBI Description (AL049607) protein phosphatase 2C-like protein [Arabidopsis

thaliana]

266675 Seq. No.

11447 7.R1011 Contig ID xsy700212409.h1 5'-most EST

Method BLASTX



NCBI GI q3482967 BLAST score 157 E value 1.0e-10 Match length 33 % identity 85

NCBI Description (AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi_4559345_gb_AAD23006.1_AC006585 1 (AC006585)

protein phosphatase 2C [Arabidopsis thaliana]

266676 Seq. No.

Contig ID 11450 1.R1011

5'-most EST uC-zmflMo17065h09b1

266677 Seq. No.

Contig ID 11451 1.R1011 5'-most EST nbm700477168.hl

Method BLASTX NCBI GI g2623297 BLAST score 412 E value 4.0e-40Match length 227 % identity 44

NCBI Description (AC002409) unknown protein [Arabidopsis thaliana]

>gi 3790583 (AF079180) RING-H2 finger protein RHC1a

[Arabidopsis thaliana]

266678 Seq. No.

Contig ID 11451 2.R1011 5'-most EST hbs701184583.h1

Method BLASTX NCBI GI q2623297 BLAST score 212 E value 1.0e-16 Match length 168 % identity 37

NCBI Description (AC002409) unknown protein [Arabidopsis thaliana]

>gi_3790583 (AF079180) RING-H2 finger protein RHC1a

[Arabidopsis thaliana]

Seq. No. 266679

Contig ID 11460 1.R1011

5'-most EST LIB3079-015-Q1-K1-A8

Method BLASTX NCBI GI g4325282 BLAST score 398 E value 1.0e-38 Match length 115 % identity

NCBI Description (AF123310) NAC domain protein NAM [Arabidopsis thaliana]

>gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM

[Arabidopsis thaliana]

266680 Seq. No.

11462 1.R1011 Contig ID

5'-most EST $uC-zm\overline{f}lmo17283a11b1$

Method BLASTX NCBI GI g3249105 BLAST score 468 8.0e-47E value Match length 127 % identity 68 (AC003114) Contains similarity to protein phosphatase 2C NCBI Description (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana] 266681 Seq. No. Contig ID 11466_1.R1011 yyf700351327.h1 5'-most EST Method BLASTX NCBI GI q4151068 BLAST score 2921 0.0e + 00E value Match length 645 % identity 84 (Y10862) ribonucleotide reductase [Nicotiana tabacum] NCBI Description 266682 Seq. No. 11466_2.R1011 Contig ID xyt700345178.h1 5'-most EST Method BLASTN NCBI GI q5091496 BLAST score 41 2.0e-13 E value Match length 150 % identity 89 Oryza sativa genomic DNA, chromosome 6, clone P0680A03, NCBI Description complete sequence Seq. No. 266683 Contig ID 11466 3.R1011 5'-most EST LIB3079-015-Q1-K1-B2 Method BLASTN NCBI GI q3452302 BLAST score 255

E value 1.0e-141

Match length 434 83 % identity

NCBI Description Zea mays retrotransposon Milt 3' LTR, partial sequence

266684 Seq. No.

11466 4.R1011 Contig ID

uC-zmflmo17152b05a1 5'-most EST

Method BLASTN NCBI GI q1657765 272 BLAST score E value 1.0e-151 364 Match length 95 % identity

Zea mays retrotransposon Milt 5' LTR and primer binding NCBI Description

site DNA sequence

266685 Seq. No.

11470 1.R1011 Contig ID

LIB3180-038-P2-M2-B2 5'-most EST

Method BLASTX



```
q2493494
NCBI GI
                   2156
BLAST score
                   0.0e + 00
E value
Match length
                   436
                   89
% identity
                  SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2)
NCBI Description
                   >gi 619351_bbs 153537 CP-MII.2=serine carboxypeptidase
                   [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436
                   aa]
                   266686
Seq. No.
                   11470 2.R1011
Contig ID
5'-most EST
                   kem700612258.h1
                   BLASTX
Method
                   q4455304
NCBI GI
                   289
BLAST score
                   3.0e-25
E value
Match length
                   110
                   51
% identity
                  (AL035528) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   266687
Seq. No.
                   11471 1.R1011
Contig ID
                   uC-zmflmo17073c04b1
5'-most EST
                   BLASTX
Method
                   g2088647
NCBI GI
                   975
BLAST score
                   1.0e-106
E value
                   358
Match length
                   54
% identity
                   (AF002109) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3158394 (AF036340) LRR-containing F-box protein
                   [Arabidopsis thaliana]
                   266688
Seq. No.
                   11471 2.R1011
Contig ID
5'-most EST
                   LIB3066-033-Q1-K1-C3
Method
                   BLASTX
                   a2088647
NCBI GI
BLAST score
                   379
                   2.0e-36
E value
Match length
                   134
                   55
% identity
                   (AF002109) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >qi 3158394 (AF036340) LRR-containing F-box protein
                   [Arabidopsis thaliana]
Seq. No.
                   266689
                   11471 3.R1011
Contig ID
                   vmt700222521.h1
5'-most EST
                   BLASTX
Method
                   g2088647
NCBI GI
                   397
BLAST score
```

2.0e-40 E value 162 Match length % identity

(AF002109) hypothetical protein [Arabidopsis thaliana] NCBI Description



>qi 3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana]

266690 Seq. No.

11484 1.R1011 Contig ID tfd700572233.h1 5'-most EST

BLASTX Method NCBI GI g3540195 BLAST score 414 E value 2.0e-40 Match length 195 % identity 21

(AC004260) Unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 266691

11484 2.R1011 Contig ID

LIB3079-015-Q1-K1-A1 5'-most EST

BLASTX Method NCBI GI g3540195 BLAST score 691 E value 8.0e-73 219 Match length 29 % identity

(AC004260) Unknown protein [Arabidopsis thaliana] NCBI Description

266692 Seq. No.

Contig ID 11487 1.R1011

LIB3079-014-Q1-K1-G5 5'-most EST

266693 Seq. No.

Contig ID 11491 1.R1011

LIB3118-012-Q1-K1-F5 5'-most EST

BLASTN Method NCBI GI q3282393 BLAST score 49 E value 3.0e-18 Match length 101

87 % identity

NCBI Description Oryza sativa aie2 mRNA, partial cds

Seq. No. 266694

11491 2.R1011 Contig ID 5'-most EST kyv700142574.h1

Method BLASTN NCBI GI g3282393 BLAST score 43 E value 2.0e-14 71 Match length 90 % identity

NCBI Description Oryza sativa aie2 mRNA, partial cds

266695 Seq. No.

11497 1.R1011 Contig ID

LIB3079-014-Q1-K1-F9 5'-most EST

Method BLASTX NCBI GI g3046693 BLAST score 652



```
3.0e-68
E value
                   138
Match length
                   83
% identity
NCBI Description
                   (AL022140) receptor like protein (fragment) [Arabidopsis
                   thaliana]
                   266696
Seq. No.
                   11497 2.R1011
Contig ID
5'-most EST
                   LIB3136-058-Q1-K1-D12
Method
                   BLASTX
NCBI GI
                   q4539329
                   338
BLAST score
E value
                   3.0e-45
                   176
Match length
                   55
% identity
                  (AL035679) ES43 like protein [Arabidopsis thaliana]
NCBI Description
                   266697
Seq. No.
                   11497 3.R1011
Contig ID
5'-most EST
                   vux700157287.hl
Method
                   BLASTX
                   g3046693
NCBI GI
BLAST score
                   235
                   8.0e-32
E.value
                   83
Match length
                   76
% identity
                  (AL022140) receptor like protein (fragment) [Arabidopsis
NCBI Description
                   thaliana]
                   266698
Seq. No.
Contig ID
                   11509 1.R1011
5'-most EST
                   LIB3067-033-Q1-K1-C2
Method
                   BLASTX
NCBI GI
                   g2648022
BLAST score
                   210
E value
                   2.0e-16
Match length
                   116
                   40
% identity
NCBI Description (Z97184) HKE2 [Homo sapiens]
Seq. No.
                   266699
                   11511 1.R1011
Contig ID
                   ymt700224033.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3292821
BLAST score
                   170
E value
                   8.0e-12
Match length
                   68
% identity
                   47
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
Seq. No.
                   266700
                   11512 1.R1011
Contig ID
                   LIB3079-014-Q1-K1-E1
5'-most EST
```

Seq. No. 266701

Contig ID 11517_1.R1011



```
5'-most EST
                  LIB3079-014-Q1-K1-C10
Method
                  BLASTX
NCBI GI
                  q3142300
BLAST score
                  948
E value
                  1.0e-116
Match length
                  321
                   62
% identity
NCBI Description
                  (AC002411) Contains similarity to pre-mRNA processing
                  protein PRP39 gb L29224 from S. cerevisiae. ESTs gb R64908
                  and gb_T88158, gb_N38703 and gb_AA651043 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  266702
Contig ID
                  11528 1.R1011
5'-most EST
                  wyr700239711.h1
                  BLASTX
Method
NCBI GI
                  q4336205
BLAST score
                  1401
E value
                  1.0e-156
Match length
                  279
% identity
                  95
NCBI Description
                 (AF077372) cytochrome b5 reductase [Zea mays]
Seq. No.
                  266703
Contig ID
                  11528 2.R1011
5'-most EST
                  LIB3068-011-Q1-K1-C6
Method
                  BLASTX
NCBI GI
                  q4336205
BLAST score
                  467
                  1.0e-46
E value
Match length
                  99
% identity
NCBI Description (AF077372) cytochrome b5 reductase [Zea mays]
Seq. No.
                  266704
                  11528 3.R1011
Contig ID
5'-most EST
                  LIB3068-007-Q1-K1-D6
Method
                  BLASTX
NCBI GI
                  q4336205
BLAST score
                  482
E value
                  1.0e-48
Match length
                  120
                  75
% identity
NCBI Description (AF077372) cytochrome b5 reductase [Zea mays]
Seq. No.
                  266705
                  11528 5.R1011
Contig ID
5'-most EST
                  uC-zmromo17009a11a1
Method
                  BLASTX
NCBI GI
                  g4336205
BLAST score
                  363
                  2.0e-34
E value
                  76
Match length
```

NCBI Description (AF077372) cytochrome b5 reductase [Zea mays] Seq. No. 266706

% identity



Contig ID 11528_6.R1011 5'-most EST nbm700469996.h1

Method BLASTX
NCBI GI g4336205
BLAST score 237
E value 1.0e-19
Match length 58
% identity 79

NCBI Description (AF077372) cytochrome b5 reductase [Zea mays]

Seq. No. 266707

Contig ID 11534_1.R1011 5'-most EST ntr700072585.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 2.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 266708

Contig ID 11534_2.R1011 5'-most EST LIB189-022-Q1-E1-F3

Seq. No. 266709

Contig ID 11537_1.R1011

5'-most EST LIB3079-013-Q1-K1-G5

Seq. No. 266710

Contig ID 11544_1.R1011 5'-most EST ymt700219964.h1

Seq. No. 266711

Contig ID 11544 2.R1011

5'-most EST LIB3079-013-Q1-K1-H2

Seq. No. 266712

Contig ID 11547_1.R1011

5'-most EST uC-zmflmo17294c10b1

Method BLASTX
NCBI GI g1084415
BLAST score 254
E value 1.0e-21
Match length 82
% identity 57

NCBI Description RNA-binding protein - Wood tobacco >gi 624925 dbj BAA05170

(D26182) RNA-binding glycine rich protein (RGP-2)

[Nicotiana sylvestris]

Seq. No. 266713

Contig ID 11547_2.R1011 5'-most EST xmt700265052.h1

Method BLASTX
NCBI GI g2366750
BLAST score 287
E value 3.0e-25



```
95
Match length
                   58
% identity
                  (D28862) RNA binding protein [Nicotiana sylvestris]
NCBI Description
                   266714
Seq. No.
                   11547 3.R1011
Contig ID
                   rvt700551368.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1084415
                   325
BLAST score
                   1.0e-29
E value
                   110
Match length
                   58
% identity
                  RNA-binding protein - Wood tobacco >gi_624925_dbj_BAA05170_
NCBI Description
                   (D26182) RNA-binding glycine rich protein (RGP-2)
                   [Nicotiana sylvestris]
                   266715
Seq. No.
                   11554_1.R1011
Contig ID
5'-most EST
                   wyr700239367.h1
Method
                   BLASTX
                   g2286153
NCBI GI
BLAST score
                   1625
                   0.0e + 00
E value
                   326
Match length
                   97
% identity
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
                   266716
Seq. No.
                   11554 2.R1011
Contig ID
5'-most EST
                   uC-zmflB73043c04b1
                   BLASTN
Method
NCBI GI
                   g3821780
BLAST score
                   36
E value
                   1.0e-10
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   266717
Seq. No.
Contig ID
                   11554 5.R1011
                   hvj700621716.h1
5'-most EST
Method
                   BLASTX
                   g2286153
NCBI GI
                   156
BLAST score
E value
                   2.0e-10
Match length
                   34
                   91
% identity
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
Seq. No.
                   266718
                   11554 9.R1011
Contig ID
```

xsy700214635.h1 5'-most EST

BLASTX Method g2286153 NCBI GI BLAST score 308 3.0e-28 E value



67 Match length % identity (AF007581) cytoplasmic malate dehydrogenase [Zea mays] NCBI Description Seq. No. 266719 11556 1.R1011 Contig ID $nbm70\overline{0}468438.h1$ 5'-most EST BLASTX Method NCBI GI q3668089 BLAST score 659 7.0e-69 E value Match length 289 52 % identity (AC004667) unknown protein [Arabidopsis thaliana] NCBI Description 266720 Seq. No. 11557 1.R1011 Contig ID uwc700155366.h1 5'-most EST Method BLASTX g3033384 NCBI GI BLAST score 1275 1.0e-141 E value 352 Match length 69 % identity (AC004238) putative CTP synthase [Arabidopsis thaliana] NCBI Description 266721 Seq. No. 11557 3.R1011 Contig ID cyk700052243.fl 5'-most EST Method BLASTX NCBI GI q3033384 181 BLAST score 5.0e-13E value 45 Match length 73 % identity (AC004238) putative CTP synthase [Arabidopsis thaliana] NCBI Description 266722 Seq. No. 11561 1.R1011 Contig ID 5'-most EST LIB3059-013-Q1-K1-F7 Method BLASTX NCBI GI g4538968 BLAST score 221 E value 7.0e-18 Match length 115 % identity NCBI Description (AL049488) putative protein kinase [Arabidopsis thaliana] 266723 Seq. No. 11568 1.R1011 Contig ID LIB3059-001-Q1-K2-B11 5'-most EST Method BLASTX

Method BLASTX
NCBI GI 94324409
BLAST score 239
E value 2.0e-19
Match length 201
% identity 32



NCBI Description (AF104119) intracellular chloride ion channel protein p64H1 [Rattus norvegicus]

Seq. No. 266724

Contig ID 11568 2.R1011 5'-most EST ymt700221662.h1

Method BLASTX
NCBI GI g2393724
BLAST score 159
E value 1.0e-10
Match length 114
% identity 34

NCBI Description (U80819) glutathione-S-transferase homolog [Mus musculus]

Seq. No. 266725

Contig ID 11568 3.R1011

5'-most EST LIB3117-004-Q1-K1-E2

Seq. No. 266726

Contig ID 11568_4.R1011 5'-most EST wty700168495.h1

Seq. No. 266727

Contig ID 11569 1.R1011

5'-most EST LIB3079-013-Q1-K1-E1

Seq. No. 266728

Contig ID 11570 1.R1011

5'-most EST uC-zmflmo17022g11b1

Method BLASTX
NCBI GI g1370172
BLAST score 573
E value 7.0e-59

Match length 146 % identity 75

NCBI Description (Z73935) RAB1X [Lotus japonicus]

Seq. No. 266729

Contig ID 11572 1.R1011

5'-most EST uC-zmflmo17078c05b1

Method BLASTX
NCBI GI g3150415
BLAST score 1182
E value 1.0e-130
Match length 275
% identity 78

NCBI Description (AC004165) sec13-related protein [Arabidopsis thaliana]

>gi_3420046 (AC004680) sec13-related protein [Arabidopsis

thaliana]

Seq. No. 266730

Contig ID 11572_2.R1011 5'-most EST ntr700077429.h1

Method BLASTX
NCBI GI g3150415
BLAST score 230
E value 3.0e-19



Match length 59 % identity 75

NCBI Description (AC004165) sec13-related protein [Arabidopsis thaliana] >gi 3420046 (AC004680) sec13-related protein [Arabidopsis

thaliana]

Seq. No. 266731

Contig ID 11575_1.R1011

5'-most EST LIB3079-013-Q1-K1-B9

Seq. No. 266732

Contig ID 11579_1.R1011 5'-most EST wen700333170.h1

Method BLASTX
NCBI GI g4432859
BLAST score 423
E value 3.0e-41
Match length 187
% identity 50

NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]

Seq. No. 266733

Contig ID 11590 1.R1011

5'-most EST LIB3079-013-Q1-K1-A5

Seq. No. 266734

Contig ID 11592 1.R1011

5'-most EST LIB3150-058-Q1-N1-G5

Method BLASTX
NCBI GI g2586129
BLAST score 1253
E value 1.0e-138
Match length 313

% identity 79

NCBI Description (U89509) b-keto acyl reductase [Zea mays]

Seq. No. 266735

Contig ID 11598_1.R1011 5'-most EST uC-zmflmo17175h07a1

Seq. No. 266736

Contig ID 11599 1.R1011

5'-most EST LIB3079-013-Q1-K1-B5

Method BLASTX
NCBI GI g2230757
BLAST score 544
E value 1.0e-55
Match length 184
% identity 61

NCBI Description (Y11969) dnaJ-like protein [Arabidopsis thaliana]

Seq. No. 266737

Contig ID 11600_1.R1011

5'-most EST LIB3079-013-Q1-K1-B6

Seq. No. 266738

Contig ID 11601 1.R1011



LIB3079-013-Q1-K1-A10 5'-most EST BLASTX Method g4325338 NCBI GI 233 BLAST score 2.0e-19 E value 69 Match length 59 % identity NCBI Description (AF128392) No definition line found [Arabidopsis thaliana] 266739 Seq. No. 11601 2.R1011 Contig ID $zuv70\overline{0}355169.h1$ 5'-most EST BLASTX Method q4325338 NCBI GI 349 BLAST score 3.0e-40E value 171 Match length 51 % identity NCBI Description (AF128392) No definition line found [Arabidopsis thaliana] 266740 Seq. No. 11603 1.R1011 Contig ID LIB3151-002-P1-K1-H4 5'-most EST BLASTX Method NCBI GI q3599968 840 BLAST score 4.0e-90 E value 230 Match length 69 % identity NCBI Description (AF032123) clp protease [Arabidopsis thaliana] 266741 Seq. No. 11608 1.R1011 Contig ID uC-zmroteosinte096e05b2 5'-most EST Method BLASTX g4454051 NCBI GI 868 BLAST score 4.0e-93 E value 357 Match length 49 % identity NCBI Description (AL035394) putative polygalacturonase [Arabidopsis thaliana] 266742 Seq. No. 11613 1.R1011 Contig ID LIB3079-012-Q1-K1-D8 5'-most EST 266743 Seq. No. 11619 1.R1011 Contig ID 5'-most EST LIB3079-001-Q1-K1-C9 266744 Seq. No. 11620 1.R1011 Contig ID tzu700204590.h1 5'-most EST BLASTX Method

37090

g4507855

1182

NCBI GI

BLAST score



```
1.0e-130
E value
                   542
Match length
                   45
% identity
                  Ubiquitin isopeptidase T >gi_1008542 (U35116) ubiquitin
NCBI Description
                   isopeptidase T [Homo sapiens]
                   266745
Seq. No.
                   11621 1.R1011
Contig ID
                   nbm70\overline{0}477144.h1
5'-most EST
                   BLASTX
Method
                   q3249070
NCBI GI
                   402
BLAST score
                   1.0e-38
E value
                   176
Match length
% identity
                   49
                   (AC004473) Contains similarity to siah binding protein 1
NCBI Description
                   (SiahBP1) gb_U51586 from Homo sapiens. ESTs gb_T43314,
                   gb T43315 and gb_R90521, gb_T75905 [Arabidopsis thaliana]
                   266746
Seq. No.
                   11622 1.R1011
Contig ID
                   uC-zm\overline{f}lmo17139b04b1
5'-most EST
Method
                   BLASTX
                   g4539348
NCBI GI
                   266
BLAST score
                   3.0e-23
E value
                   95
Match length
% identity
                   54
                  (AL035539) putative pollen allergen [Arabidopsis thaliana]
NCBI Description
                   266747
Seq. No.
                   11627 1.R1011
Contig ID
5'-most EST
                   rv1700454407.h1
                   BLASTX
Method
                   g2104530
NCBI GI
BLAST score
                   718
E value
                   3.0e-76
Match length
                   162
                   85
% identity
                   (AF001308) PROLIFERA [Arabidopsis thaliana] >gi 2104548
NCBI Description
                   (AF001535) AGAA.2, PROLIFERA [Arabidopsis thaliana]
                   266748
Seq. No.
                   11628 1.R1011
Contig ID
                   uC-zmflmo17159d12b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q585911
BLAST score
                   220
E value
                   5.0e-17
```

Match length 464 27 % identity

NCBI Description HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K (HNRNP K) (DC-STRETCH BINDING PROTEIN) (CSBP) (TRANSFORMATION

UPREGULATED NUCLEAR PROTEIN) (TUNP) >gi_284150_pir__A42058 heterogeneous nuclear ribonucleoprotein complex K, hnRNP K - human >qi 543380 pir S41495 dC stretch-binding protein CSBP - rat $\overline{>}$ gi_241 $\overline{4}$ 78 $\overline{b}\overline{b}s$ _74679 (S74678) heterogeneous



nuclear ribonucleoprotein complex K, hnRNP K [human, Peptide, 463 aa] [Homo sapiens] >gi_409389_dbj_BAA04566_ (D17711) dC-stretch binding protein (CSBP) [Rattus rattus]

 Seq. No.
 266749

 Contig ID
 11628_2.R1011

 5'-most EST
 uC-zmflB73022a12b1

Seq. No. 266750 Contig ID 11628_3.R1011

5'-most EST LIB3059-017-Q1-K1-F3

Seq. No. 266751

Contig ID 11628_6.R1011 5'-most EST rvt700550848.h1

Seq. No. 266752

Contig ID 11630_1.R1011 5'-most EST uC-zmflb73190d02b1

Seq. No. 266753

Contig ID 11630_3.R1011

5'-most EST LIB3069-047-Q1-K1-F7

Seq. No. 266754

Contig ID 11634_1.R1011 5'-most EST xsy700211629.h1

Method BLASTX
NCBI GI g3881978
BLAST score 1047
E value 1.0e-114
Match length 311

% identity 38

NCBI Description (Y11348) annexin-like protein [Medicago sativa]

Seq. No. 266755

Contig ID 11634_2.R1011 5'-most EST uC-zmflmo17323a03a1

Seq. No. 266756

Contig ID 11634_4.R1011 5'-most EST uC-zmflmo17368h10a1

Seq. No. 266757

Contig ID 11636_1.R1011

5'-most EST LIB3079-043-Q1-K1-F6

Seq. No. 266758

Contig ID 11636_3.R1011 5'-most EST uC-zmflb73094b09b2

Seq. No. 266759

Contig ID 11640_1.R1011

5'-most EST LIB189-015-Q1-E1-F1

Method BLASTX
NCBI GI g2618688
BLAST score 1111



1.0e-122 E value Match length 278

73 % identity

(AC002510) putative esterase D [Arabidopsis thaliana] NCBI Description

266760 Seq. No.

11641 1.R1011 Contig ID vux700158338.h1 5'-most EST

266761 Seq. No.

11642 1.R1011 Contig ID

5'-most EST LIB3150-058-Q1-N1-F11

266762 Seq. No.

11644 1.R1011 Contig ID

LIB3079-012-Q1-K1-B1 5'-most EST

266763 Seq. No.

11645 1.R1011 Contig ID

5'-most EST uC-zmroteosinte105e03b1

Method BLASTX g3790581 NCBI GI BLAST score 196 1.0e-14 E value Match length 52

% identity 58

(AF079179) RING-H2 finger protein RHB1a [Arabidopsis NCBI Description

thaliana]

266764 Seq. No.

Contig ID 11645 2.R1011 5'-most EST ypc700805869.hl

266765 Seq. No.

11650_3.R1011 Contig ID

5'-most EST LIB143-024-Q1-E1-D9

Method BLASTX NCBI GI q4507703 BLAST score 149 E value 2.0e-09 Match length 126 % identity 33

tumor suppressing subtransferable candidate 1 NCBI Description

>gi_2655037_gb_AAC51911_ (AF019952) tumor suppressing STF

cDNA 1 [Homo sapiens]

Seq. No. 266766

Contig ID 11650 4.R1011

5'-most EST LIB3079-012-Q1-K1-B5

Seq. No. 266767

11653 1.R1011 Contig ID

5'-most EST LIB3079-055-Q1-K1-A11

266768 Seq. No.

Contig ID 11654 1.R1011 5'-most EST $xmt70\overline{0}266010.h1$



Seq. No. 266769

Contig ID 11656_1.R1011 5'-most EST afb700381403.h1

Method BLASTX
NCBI GI 94504771
BLAST score 704
E value 1.0e-99
Match length 244
% identity 75

NCBI Description integrin beta 4 binding protein

>gi 3122258 sp P56537 IF6 HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 6 (EIF-6) (B4 INTEGRIN INTERACTOR) (CAB) >gi 2809383 (AF022229) translation initiation factor 6 [Homo sapiens] >gi 2910997 emb CAA72243 (Y11435) b4 integrin interactor [Homo sapiens] >gi 3335506 (AF047433)

b(2)gcn homolog [Homo sapiens]

Seq. No. 266770

Contig ID 11656_2.R1011 5'-most EST LIB143-002-Q1-E1-F2

Method BLASTX
NCBI GI g4504771
BLAST score 554
E value 1.0e-56

E value 1.0eMatch length 139
% identity 76

NCBI Description integrin beta 4 binding protein

>gi_3122258_sp_P56537_IF6_HUMAN EUKARYOTIC TRANSLATION
INITIATION FACTOR 6 (EIF-6) (B4 INTEGRIN INTERACTOR) (CAB)
>gi_2809383 (AF022229) translation initiation factor 6
[Homo sapiens] >gi_2910997_emb_CAA72243_ (Y11435) b4
integrin interactor [Homo sapiens] >gi_3335506 (AF047433)

b(2)gcn homolog [Homo sapiens]

Seq. No. 266771

Contig ID 11656_3.R1011

5'-most EST uC-zmflmo17055f11b1

Method BLASTX
NCBI GI g3355311
BLAST score 566
E value 2.0e-58
Match length 125
% identity 86

NCBI Description (AJ009737) eukaryotic translation initiation factor 6 [Beta

vulgaris]

Seq. No. 266772

Contig ID 11660_1.R1011 5'-most EST qmh700028478.f1

Seq. No. 266773

Contig ID 11665_1.R1011

5'-most EST LIB3079-059-Q1-K1-E7

Seq. No. 266774

Contig ID 11674 1.R1011



```
uC-zmflmo17074h04b1
5'-most EST
                  BLASTX
Method
                  q4455169
NCBI GI
BLAST score
                  591
                  5.0e-61
E value
                  204
Match length
                  57
% identity
                  (AL035521) putative aldehyde dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
                  266775
Seq. No.
                  11678 1.R1011
Contig ID
5'-most EST
                  LIB3079-011-Q1-K1-F5
                  BLASTX
Method
                  q4538929
NCBI GI
                  206
BLAST score
                  8.0e-16
E value
                  92
Match length
                  52
% identity
                  (AL049483) putative nucleic acid binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   266776
Seq. No.
                  11681_1.R1011
Contig ID
                  uC-zmflmo17238g06b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2988397
                   245
BLAST score
                   5.0e-20
E value
                  122
Match length
                   41
% identity
NCBI Description (AC004475) F23858_1 [Homo sapiens]
                   266777
Seq. No.
                   11681 2.R1011
Contig ID
5'-most EST
                   uC-zmflb73200g09b1
                   266778
Seq. No.
                   11681 4.R1011
Contig ID
                   uC-zmflb73256h03b1
5'-most EST
Seq. No.
                   266779
                   11681 5.R1011
Contig ID
5'-most EST
                   uC-zmflb73092c02a1
Method
                   BLASTX
NCBI GI
                   g2988397
BLAST score
                   152
                   2.0e-09
E value
Match length
                   38
% identity
NCBI Description (AC004475) F23858_1 [Homo sapiens]
                   266780
Seq. No.
```

11682 1.R1011 Contig ID

LIB3079-011-Q1-K1-G1 5'-most EST

BLASTX Method NCBI GI g4220537



```
BLAST score
                   361
                   7.0e-36
E value
                   182
Match length
                   49
% identity
                  (AL035356) PsRT17-1 like protein [Arabidopsis thaliana]
NCBI Description
                   266781
Seq. No.
                   11683_1.R1011
Contig ID
                   cat70\overline{0}016089.r1
5'-most EST
                   BLASTX
Method
                   g3935157
NCBI GI
                   434
BLAST score
                   8.0e-49
E value
Match length
                   164
                   57
% identity
                  (AC005106) T25N20.21 [Arabidopsis thaliana]
NCBI Description
                   266782
Seq. No.
                   11685 1.R1011
Contig ID
                   wyr700237832.hl
5'-most EST
                   266783
Seq. No.
                   11686 1.R1011
Contig ID
                   uC-zmroteosinte020g09b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2262172
BLAST score
                   265
                   8.0e-23
E value
                   150
Match length
                   46
% identity
                   (AC002329) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                   266784
Seq. No.
                   11688 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73208f12b1
Method
                   BLASTX
                   g3004550
NCBI GI
BLAST score
                   174
                   6.0e-12
E value
Match length
                   82
% identity
                   44
                  (AC003673) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   266785
Seq. No.
Contig ID
                   11689 1.R1011
5'-most EST
                   LIB3079-011-Q1-K1-D4
                   266786
Seq. No.
                   11689 2.R1011
Contig ID
5'-most EST
                   uC-zmflb73040e07b1
```

Seq. No. 266787

Contig ID 11689_3.R1011 5'-most EST tzu700205570.h1

Seq. No. 266788



11691_1.R1011 Contig ID ntr700071662.hl 5'-most EST

Method BLASTX NCBI GI q2239083 BLAST score 657 E value 1.0e-68 344 Match length 43 % identity

(Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase NCBI Description

[Dianthus caryophyllus] >gi_2239087_emb_CAB06429_ (Z84385)

anthranilate N-hydroxycinnamoyl/benzoyltransferase

[Dianthus caryophyllus]

266789 Seq. No.

11697 1.R1011 Contig ID

LIB3079-011-Q1-K1-E10 5'-most EST

BLASTX Method g4539301 NCBI GI BLAST score 283 3.0e-25E value Match length 128 45 % identity

(AL049480) putative mitochondrial protein [Arabidopsis NCBI Description

thaliana]

266790 Seq. No.

11698 1.R1011 Contig ID

LIB143-025-Q1-E1-H3 5'-most EST

BLASTX Method q4587546 NCBI GI BLAST score 345 4.0e-32 E value 117

Match length % identity

(AC006577) Belongs to the PF_00011 Hsp20/alpha crystallin NCBI Description

family. EST gb W4312 comes from this gene. [Arabidopsis

thaliana]

266791 Seq. No.

11704 1.R1011 Contig ID 5'-most EST xsy700209880.h1

Method BLASTX NCBI GI g4104058 BLAST score 318 E value 3.0e-29 Match length 122 % identity

(AF031195) blue copper-binding protein homolog [Triticum NCBI Description

aestivum]

Seq. No. 266792

11705 1.R1011 Contig ID $ceu70\overline{0}424428.h1$ 5'-most EST

BLASTX Method g4376915 NCBI GI BLAST score 155 E value 9.0e-12



Match length 83
% identity 49
NCBI Description (AE001646) Lipoate-Protein Ligase A [Chlamydia pneumoniae]
Seq. No. 266793
Contig ID 11710_1.R1011
5'-most EST uC-zmflb73066d05b1

Method BLASTX
NCBI GI g3297818
BLAST score 764
E value 4.0e-81
Match length 285
% identity 52

NCBI Description (AL031032) putative protein [Arabidopsis thaliana]

Seq. No. 266794

Contig ID 11714_1.R1011

5'-most EST LIB3069-028-Q1-K1-G1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 2.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 266795

Contig ID 11714_2.R1011 5'-most EST ypc700803019.h1

Seq. No. 266796

Contig ID 11714 3.R1011

5'-most EST LIB3150-006-Q1-N1-D9

Seq. No. 266797

Contig ID 11717_1.R1011

5'-most EST LIB3079-011-Q1-K1-C8

Method BLASTX
NCBI GI g2498731
BLAST score 581
E value 4.0e-60
Match length 162
% identity 68

NCBI Description PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1

>gi_1362013_pir__S57611 zeta-crystallin homolog Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768)

zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No. 266798

Contig ID 11719_1.R1011 5'-most EST uer700580707.h1

Method BLASTX
NCBI GI g231495
BLAST score 202
E value 1.0e-15
Match length 127
% identity 35



```
ACTIN 1 >gi_100021_pir__ S25488 actin - garden pea >gi_20637_emb_CAA47899_ (X67666) actin [Pisum sativum]
NCBI Description
                   266799
Seq. No.
                   11723 1.R1011
Contig ID
                   LIB3059-025-Q1-K1-D7
5'-most EST
                   BLASTX
Method
                   g3935184
NCBI GI
BLAST score
                   327
                   3.0e-30
E value
                   166
Match length
% identity
                   45
                   (AC004557) F17L21.27 [Arabidopsis thaliana]
NCBI Description
                   266800
Seq. No.
                   11724 1.R1011
Contig ID
                   LIB3079-011-Q1-K1-A4
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3047116
BLAST score
                   634
E value
                   8.0e-66
                   157
Match length
                   74
% identity
                   (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
                   266801
Seq. No.
                   11725 1.R1011
Contig ID
                   uC-zmflmo17173h12b1
5'-most EST
                   266802
Seq. No.
                   11726 1.R1011
Contig ID
                   vux700157313.h1
5'-most EST
                   BLASTX
Method
                   q4586031
NCBI GI
                   281
BLAST score
E value
                    7.0e-25
Match length
                   64
% identity
NCBI Description (AC007109) unknown protein [Arabidopsis thaliana]
                    266803
Seq. No.
                   11726 2.R1011
Contig ID
5'-most EST
                   LIB3068-038-Q1-K1-C10
                   BLASTX
Method
NCBI GI
                    q4586031
BLAST score
                    279
E value
                    2.0e-24
Match length
                    64
% identity
                    83
NCBI Description (AC007109) unknown protein [Arabidopsis thaliana]
Seq. No.
                    266804
                    11731 1.R1011
Contig ID
```

Contig ID 11/31_1.R1011 5'-most EST xjt700096383.h1

Method BLASTX NCBI GI g4454032 BLAST score 638



2.0e-66 E value 234 Match length 53 % identity

(AL035394) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

266805 11731 2.R1011 Contig ID

5'-most EST uC-zmflb73285d03b1

266806 Seq. No.

11734 1.R1011 Contig ID

5'-most EST LIB3079-010-Q1-K1-E8

266807 Seq. No.

11735 1.R1011 Contig ID

5'-most EST LIB189-008-Q1-E1-G2

266808 Seq. No.

11735 2.R1011 Contig ID

uC-zmroteosinte035g01b2 5'-most EST

Seq. No. 266809

11735 3.R1011 Contig ID qmh700028719.f1 5'-most EST

266810 Seq. No.

Contig ID 11735 4.R1011 5'-most EST wty700163432.hl

266811 Seq. No.

11735 5.R1011 Contig ID

LIB3079-010-Q1-K1-F5 5'-most EST

266812 Seq. No.

Contig ID 11739_1.R1011

5'-most EST LIB3136-023-Q1-K1-C1

Method BLASTX NCBI GI q3552013 BLAST score 205 1.0e-15 E value Match length 172

% identity

NCBI Description (AF086759) proline-rich protein precursor [Glycine max]

Seq. No. 266813

Contig ID 11746 1.R1011

5'-most EST LIB3068-039-Q1-K1-C12

266814 Seq. No.

11746 2.R1011 Contiq ID 5'-most EST pmx700087738.h1

Seq. No. 266815

11748 1.R1011 Contig ID

LIB3079-010-Q1-K1-D4 5'-most EST

Seq. No. 266816

% identity



```
11753 1.R1011
Contig ID
                  LIB3137-024-Q1-K1-G6
5'-most EST
Method
                  BLASTX
                  q2827661
NCBI GI
BLAST score
                  740
                  4.0e-78
E value
                  347
Match length
                   50
% identity
                  (AL021637) hyuC-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   266817
                   11753 2.R1011
Contig ID
                   uC-zmflm017093h06b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2827661
                   244
BLAST score
                   1.0e-20
E value
                   58
Match length
                   79
% identity
NCBI Description (AL021637) hyuC-like protein [Arabidopsis thaliana]
                   266818
Seq. No.
Contig ID
                   11753 3.R1011
5'-most EST
                   wty700164332.hl
                   BLASTX
Method
NCBI GI
                   q2827661
BLAST score
                   222
                   1.0e-18
E value
                   77
Match length
                   64
% identity
NCBI Description (AL021637) hyuC-like protein [Arabidopsis thaliana]
                   266819
Seq. No.
                   11756 1.R1011
Contig ID
5'-most EST
                   LIB3079-010-Q1-K1-E5
Method
                   BLASTX
                   g2443880
NCBI GI
BLAST score
                   200
                   3.0e-15
E value
                   117
Match length
                   39
% identity
NCBI Description (AC002294) Hypothetical protein [Arabidopsis thaliana]
                   266820
Seq. No.
                   11760 1.R1011
Contig ID
                   hbs701183772.h1
5'-most EST
                   266821
Seq. No.
                   11762 1.R1011
Contiq ID
5'-most EST
                   LIB3079-026-Q1-K1-A6
Method
                   BLASTX
                   g2980778
NCBI GI
BLAST score
                   209
E value
                   4.0e-16
Match length
                   83
```

37101

NCBI Description (AL022198) hypothetical protein [Arabidopsis thaliana]



Seq. No. 266822

Contig ID 11765 1.R1011

5'-most EST uC-zmflmo17321c02b1

Method BLASTX
NCBI GI g399015
BLAST score 1329
E value 1.0e-147
Match length 371
% identity 72

NCBI Description ADP, ATP CARRIER PROTEIN PRECURSOR (ADP/ATP TRANSLOCASE)

(ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT)

>gi 218145 dbj BAA02161 (D12637) ATP/ADP translocator

[Oryza sativa]

Seq. No. 266823

Contig ID 11765 2.R1011

5'-most EST LIB30 $\overline{67}$ -050-Q1-K1-B7

Method BLASTX
NCBI GI g2842480
BLAST score 386
E value 4.0e-37
Match length 102
% identity 76

NCBI Description (AL021749) ADP, ATP carrier-like protein [Arabidopsis

thaliana]

Seq. No. 266824

Contig ID 11767_1.R1011

5'-most EST LIB3079-009-Q1-K1-E7

Seq. No. 266825

Contig ID 11768 1.R1011

5'-most EST uC-zmflmo17268d10b1

Method BLASTX
NCBI GI g3834322
BLAST score 614
E value 3.0e-63
Match length 328
% identity 45

NCBI Description (AC005679) EST gb_R30300 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 266826

Contig ID 11772 1.R1011

5'-most EST LIB3079-009-Q1-K1-G7

Seq. No. 266827

Contig ID 11781_1.R1011 5'-most EST xmt700266273.h1

Method BLASTX
NCBI GI g3355483
BLAST score 256
E value 5.0e-22
Match length 73
% identity 60

NCBI Description (AC004218) gibberellin-regulated protein (GASA5)-like



[Arabidopsis thaliana]

266828 Seq. No. Contig ID 11782 1.R1011 LIB3079-010-Q1-K1-A4 5'-most EST

266829 Seq. No.

11786_1.R1011 Contig ID 5'-most EST yyf700350437.h1

Method BLASTX NCBI GI q1169544 BLAST score 1319 1.0e-146 E value 396 Match length 66 % identity

ERD1 PROTEIN PRECURSOR >gi_541859_pir__JN0901 ERD1 protein - Arabidopsis thaliana >gi_497629_dbj_BAA04506_ (D17582) NCBI Description

ERD1 protein [Arabidopsis thaliana]

266830 Seq. No.

11801 1.R1011 Contig ID

LIB3150-074-P1-N1-D10 5'-most EST

266831 Seq. No.

11801 2.R1011 Contig ID

5'-most EST LIB3067-001-Q1-K1-C8

266832 Seq. No.

11809 1.R1011 Contig ID 5'-most EST nbm700475473.h1

266833 Seq. No.

Contig ID 11815_1.R1011 5'-most EST xjt700095972.h1

Method BLASTX NCBI GI g2425064 BLAST score 1395 E value 1.0e-155 288 Match length

% identity 91

NCBI Description (AF019146) cysteine proteinase Mir2 [Zea mays]

Seq. No. 266834

11815_2.R1011 Contig ID

5'-most EST LIB143-046-Q1-E1-A11

Method BLASTX NCBI GI g2425064 BLAST score 808 E value 1.0e-86 Match length 177 88 % identity

NCBI Description (AF019146) cysteine proteinase Mir2 [Zea mays]

266835 Seq. No.

11816 1.R1011 Contig ID $nbm70\overline{0}476260.h1$ 5'-most EST

Method BLASTX



```
q2326372
NCBI GI
                   520
BLAST score
                   1.0e-52
E value
                   161
Match length
                   64
% identity
                  (Y14404) putative arabinose kinase [Arabidopsis thaliana]
NCBI Description
                   266836
Seq. No.
                   11817_1.R1011
Contig ID
                   LIB3150-074-P1-N1-B3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g799030
BLAST score
                   258
                   2.0e-22
E value
                   89
Match length
% identity
                   56
                  (Z49203) BET1 [Zea mays]
NCBI Description
                   266837
Seq. No.
                   11818 1.R1011
Contig ID
5'-most EST
                   wty700173010.h1
                   BLASTX
Method
                   g2288969
NCBI GI
BLAST score
                   592
E value
                   3.0e-61
                   148
Match length
                   79
% identity
                  (Y12862) glutathione transferase [Zea mays]
NCBI Description
                   266838
Seq. No.
                   11818 2.R1011
Contig ID
                   LIB3060-041-Q1-K1-C4
5'-most EST
                   BLASTX
Method
                   q2288969
NCBI GI
                   481
BLAST score
E value
                   2.0e-48
Match length
                   143
% identity
                  (Y12862) glutathione transferase [Zea mays]
NCBI Description
Seq. No.
                   266839
                   11820 1.R1011
Contig ID
5'-most EST
                   qmh700025801.f1
Method
                   BLASTX
NCBI GI
                   q3953463
BLAST score
                   296
E value
                   1.0e-26
                   87
Match length
% identity
                   61
NCBI Description (AC002328) F20N2.8 [Arabidopsis thaliana]
Seq. No.
                   266840
                   11826 1.R1011
Contig ID
```

5'-most EST uC-zmflb73100h09b1

Method BLASTX
NCBI GI g1881268
BLAST score 330



E value 9.0e-43 Match length 434 % identity 30

NCBI Description (AB001488) ATP-DEPENDENT RNA HELICASE DEAD HOMOLOG.

[Bacillus subtilis] >gi_2632758_emb_CAB12265_ (Z99106)

similar to ATP-dependent RNA helicase [Bacillus subtilis]

Seq. No. 266841

Contig ID 11828_1.R1011 5'-most EST uC-zmflb73066e01b1

Method BLASTX
NCBI GI g3858935
BLAST score 279
E value 8.0e-32
Match length 122
% identity 54

NCBI Description (AL021636) synaptobrevin-like protein [Arabidopsis

thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis

thaliana]

Seq. No. 266842

Contig ID 11828_2.R1011

5'-most EST LIB3150-040-Q1-N1-E1

57

Method BLASTX
NCBI GI g3858935
BLAST score 469
E value 9.0e-47
Match length 148

% identity

NCBI Description (AL021636) synaptobrevin-like protein [Arabidopsis

thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis

thaliana]

Seq. No. 266843

Contig ID 11830 1.R1011

5'-most EST LIB3069-010-Q1-K1-B9

Seq. No. 266844

Contig ID 11837_1.R1011 5'-most EST xsy700213241.h1

Method BLASTX
NCBI GI g2911060
BLAST score 420
E value 1.0e-40
Match length 368
% identity 34

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

>gi 3297826 emb CAA19884.1_ (AL031032) putative protein

[Arabidopsis thaliana]

Seq. No. 266845

Contig ID 11840_1.R1011

5'-most EST uC-zmflmo17151b09b1

Method BLASTX NCBI GI g2760325



```
BLAST score
                  513
                  1.0e-51
E value
                  183
Match length
                  58
% identity
                  (AC002130) F1N21.10 [Arabidopsis thaliana]
NCBI Description
                  266846
Seq. No.
                  11840 3.R1011
Contig ID
                  uC-zmroteosinte038e07b1
5'-most EST
                  BLASTX
Method
                  g2760325
NCBI GI
                  375
BLAST score
                  6.0e-36
E value
Match length
                  118
                  69
% identity
                  (AC002130) F1N21.10 [Arabidopsis thaliana]
NCBI Description
                  266847
Seq. No.
                  11841 1.R1011
Contig ID
                  xjt700092017.h1
5'-most EST
                  BLASTX
Method
                  g3643611
NCBI GI
                  546
BLAST score
                  1.0e-55
E value
                  131
Match length
                   75
% identity
NCBI Description (AC005395) putative casein kinase [Arabidopsis thaliana]
                   266848
Seq. No.
                   11844 1.R1011
Contig ID
5'-most EST
                  LIB3066-029-Q1-K1-C3
                   266849
Seq. No.
                   11845_1.R1011
Contig ID
                   LIB143-024-Q1-E1-C4
5'-most EST
                   BLASTX
Method
NCBI GI
                   a1843440
                   199
BLAST score
                   3.0e-15
E value
                   108
Match length
                   41
% identity
NCBI Description (Z70521) unknown [Cucumis melo]
Seq. No.
                   266850
                   11845 3.R1011
Contig ID
5'-most EST
                   uwc700154431.h1
Seq. No.
                   266851
Contig ID
                   11852 1.R1011
5'-most EST
                   uC-zmroteosinte030f04b1
Method
                   BLASTX
NCBI GI
                   q2511541
BLAST score
                   1685
E value
                   0.0e+00
```

37106

NCBI Description (AF020787) DNA-binding protein GBP16 [Oryza sativa]

393

Match length % identity



Seq. No. 266852

Contig ID 11852 2.R1011

5'-most EST LIB31 $\overline{5}$ 0-076-P1-N1-D8

Method BLASTX
NCBI GI g2511541
BLAST score 392
E value 5.0e-38
Match length 86
% identity 86

NCBI Description (AF020787) DNA-binding protein GBP16 [Oryza sativa]

Seq. No. 266853

Contig ID 11852 3.R1011

5'-most EST LIB3150-052-Q1-N1-G7

Method BLASTX
NCBI GI g2511541
BLAST score 633
E value 4.0e-66
Match length 142
% identity 85

NCBI Description (AF020787) DNA-binding protein GBP16 [Oryza sativa]

Seq. No. 266854

Contig ID 11852 7.R1011

5'-most EST LIB3180-001-P1-M1-E4

Seq. No. 266855

Contig ID 11853 1.R1011

5'-most EST LIB3079-008-Q1-K1-C12

Method BLASTX
NCBI GI g3421413
BLAST score 697
E value 9.0e-74
Match length 148
% identity 86

NCBI Description (AF081922) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa] >gi_3421415 (AF081923) protein

phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

Seq. No. 266856

Contig ID 11854_1.R1011 5'-most EST uC-zmflb73182f04b1

Method BLASTX
NCBI GI g1076534
BLAST score 298
E value 1.0e-36
Match length 180
% identity 52

NCBI Description monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - garden

pea >qi 497120 (U06461) monodehydroascorbate reductase

[Pisum sativum]

Seq. No. 266857

Contig ID 11864_1.R1011

5'-most EST LIB3061-052-Q1-K1-F9

Method BLASTX



a1706885 NCBI GI 750 BLAST score E value 3.0e-79 Match length 409 % identity 43 FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR NCBI Description (FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS) >gi 1345106 (U33557) folylpolyglutamate synthetase precursor [Mus musculus] Seq. No. 266858 11872 1.R1011 Contig ID dhd700198019.h15'-most EST Method BLASTX NCBI GI q3820531 BLAST score 473 E value 1.0e-75 Match length 244 % identity 53 NCBI Description (AF072736) beta-glucosidase [Pinus contorta] 266859 Seq. No. Contig ID 11875 1.R1011 5'-most EST zuv700353104.h1 266860 Seq. No. 11878 1.R1011 Contig ID LIB3079-051-Q1-K1-E9 5'-most EST Method BLASTX

NCBI GI q3168840

BLAST score 316

E value 9.0e - 29

Match length 79 81 % identity

NCBI Description (U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No. 266861

11882 1.R1011 Contig ID rv1700457479.h1 5'-most EST

Method BLASTX NCBI GI g4454482 BLAST score 458 E value 1.0e-45 Match length 165 58 % identity

NCBI Description (AC006234) hypothetical protein [Arabidopsis thaliana]

Seq. No. 266862

11885 1.R1011 Contig ID

5'-most EST uC-zmflmo17220d07b1

Method BLASTX NCBI GI g4539333 BLAST score 476 E value 2.0e-47 Match length 183 % identity 60

NCBI Description (AL035539) putative amino acid transport protein



[Arabidopsis thaliana]

266863 Seq. No. Contig ID

11887 1.R1011 5'-most EST LIB36-018-Q1-E1-A8

266864 Seq. No.

11887 2.R1011 Contig ID 5'-most EST mwy700442726.h1

266865 Seq. No.

Contig ID 11888 1.R1011

5'-most EST LIB3118-008-Q1-K1-G11

Method BLASTX NCBI GI g3868853 BLAST score 222 6.0e-36 E value 131 Match length 63 % identity

(AB013853) GPI-anchored protein [Vigna radiata] NCBI Description

Seq. No. 266866

11893 1.R1011 Contig ID

5'-most EST LIB143-018-Q1-E1-E5

266867 Seq. No.

Contig ID 11894 1.R1011

5'-most EST LIB3070-005-Q1-N1-A8

266868 Seq. No.

Contig ID 11896 1.R1011

LIB3079-007-Q1-K1-E5 5'-most EST

Method BLASTX g3738282 NCBI GI 272 BLAST score E value 9.0e-24Match length 139 % identity

NCBI Description (AC005309) putative RNA helicase [Arabidopsis thaliana]

Seq. No. 266869

11907 1.R1011 Contig ID pwr700451512.hl 5'-most EST

Method BLASTX NCBI GI g3335336 BLAST score 150 E value 5.0e-09 Match length 87 37 % identity

(AC004512) Contains similarity to DnaJ gene YM8520.10 NCBI Description

gb 825566 from from S. cerevisiae cosmid gb Z49705. ESTs gb Z47720 and gb Z29879 come from this gene. [Arabidopsis

thaliana]

Seq. No. 266870

Contig ID 11911 1.R1011

5'-most EST LIB3079-007-Q1-K1-C8



Seq. No. 266871

Contig ID 11912 1.R1011

5'-most EST LIB3079-007-Q1-K1-D10

Seq. No. 266872

Contig ID 11917_1.R1011 5'-most EST nwy700447219.h1

Method BLASTX
NCBI GI g3157951
BLAST score 875
E value 2.0e-94
Match length 200
% identity 89

NCBI Description (AC002131) Contains similarity to vesicle trafficking protein gb U91538 from Mus musculus. ESTs gb_F15494 and

gb F14097 come from this gene. [Arabidopsis thaliana]

Seq. No. 266873

Contig ID 11921 1.R1011

5'-most EST LIB3079-007-Q1-K1-E10

Seq. No. 266874

Contig ID 11922_1.R1011

5'-most EST LIB3067-022-Q1-K1-E10

Seq. No. 266875

Contig ID 11922 2.R1011 5'-most EST ceu700423980.h1

Seq. No. 266876

Contig ID 11926_1.R1011

5'-most EST LIB3079-007-Q1-K1-A9

Method BLASTX
NCBI GI g4206209
BLAST score 854
E value 4.0e-98
Match length 244
% identity 68

NCBI Description (AF071527) putative glucan synthase component [Arabidopsis

thaliana] >gi 4263042 gb AAD15311 (AC005142) putative

glucan synthase component [Arabidopsis thaliana]

Seq. No. 266877

Contig ID 11927_1.R1011 5'-most EST vux700160156.h1

Method BLASTN
NCBI GI g5579440
BLAST score 303
E value 1.0e-169
Match length 632
% identity 97

NCBI Description Zea mays histone acetyltransferase HAT B mRNA, complete cds

Seq. No. 266878

Contig ID 11927_2.R1011 5'-most EST xjt700094285.h1



BLASTN Method q5579440 NCBI GI BLAST score 355 0.0e+00E value 400 Match length 97 % identity

NCBI Description Zea mays histone acetyltransferase HAT B mRNA, complete cds

Seq. No. 266879

11927 3.R1011 Contig ID 5'-most EST uC-zmflb73247h09a2

Method BLASTN g5579440 NCBI GI BLAST score 483 0.0e+00E value Match length 587 96 % identity

NCBI Description Zea mays histone acetyltransferase HAT B mRNA, complete cds

266880 Seq. No.

11927 4.R1011 Contig ID pmx700086325.h1 5'-most EST

266881 Seq. No.

11927_6.R1011 Contig ID ymt700219876.h1 5'-most EST

Method BLASTX q2897875 NCBI GI BLAST score 892 1.0e-125 E value 237 Match length

97 % identity

NCBI Description (U90274) histone acetyltransferase HAT B [Zea mays]

Seq. No. 266882

11928 2.R1011 Contig ID uC-zmrob73002b09b1 5'-most EST

BLASTX Method q3912917 NCBI GI BLAST score 564 E value 1.0e-66 149 Match length 87 % identity

(AF001308) putative NAK-like ser/thr protein kinase NCBI Description

[Arabidopsis thaliana]

266883 Seq. No.

11931 1.R1011 Contig ID

5'-most EST LIB3079-038-Q1-K1-B7

266884 Seq. No.

11938 1.R1011 Contig ID pmx700089291.h1 5'-most EST

BLASTX Method NCBI GI g2467274 BLAST score 323 2.0e-29 E value



Match length 117 % identity 59

NCBI Description (Z99759) rna binding protein [Schizosaccharomyces pombe]

Seq. No. 266885

Contig ID 11938_3.R1011 5'-most EST pwr700450793.h1

Seq. No. 266886

Contig ID 11940 1.R1011

5'-most EST uC-zmflmo17150h04b1

Seq. No. 266887

Contig ID 11945 1.R1011

5'-most EST LIB3067-019-Q1-K1-B2

Method BLASTX
NCBI GI g543842
BLAST score 411
E value 3.0e-40
Match length 104
% identity 69

NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_477617_pir_A49520

ADP-ribosylation factor 1 - fruit fly (Drosophila

melanogaster) >gi_385340_bbs_133334 (S62079)

ADP-ribosylation factor 1, ARF 1 [Drosophila melanogaster,

Peptide, 182 aa] [Drosophila melanogaster]

Seq. No. 266888

Contig ID 11947_1.R1011

5'-most EST LIB3079-007-Q1-K1-G8

Method BLASTX
NCBI GI g4588012
BLAST score 1461
E value 1.0e-162
Match length 410
% identity 65

NCBI Description (AF085717) putative callose synthase catalytic subunit

[Gossypium hirsutum]

Seq. No. 266889

Contig ID 11948_1.R1011 5'-most EST wyr700243035.h1

Method BLASTX
NCBI GI 94544449
BLAST score 227
E value 1.0e-18
Match length 102
% identity 49

NCBI Description (AC006592) putative peroxidase [Arabidopsis thaliana]

Seq. No. 266890

Contig ID 11949_1.R1011

5'-most EST LIB3059-015-Q1-K1-F11

Seq. No. 266891

Contig ID 11950 1.R1011

5'-most EST LIB3079-007-Q1-K1-A4



```
BLASTX
Method
                  g1881412
NCBI GI
BLAST score
                  328
                  8.0e-30
E value
Match length
                  450
                  26
% identity
                  (Z83333) palA [Emericella nidulans]
NCBI Description
                  266892
Seq. No.
                  11956_1.R1011
Contig ID
5'-most EST
                  LIB3079-006-Q1-K1-G12
                  BLASTX
Method
NCBI GI
                   q2459411
BLAST score
                  195
                   2.0e-14
E value
Match length
                  123
                   41
% identity
                  (AC002332) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  266893
Seq. No.
Contig ID
                  11959_1.R1011
5'-most EST
                  LIB3079-006-Q1-K1-G9
                  BLASTX
Method
NCBI GI
                   g2582639
BLAST score
                   478
                   6.0e-48
E value
Match length
                   150
                   64
% identity
                  (AJ002414) hnRNP-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   266894
                   11961 1.R1011
Contig ID
5'-most EST
                   hvj700622789.hl
                   266895
Seq. No.
Contig ID
                   11961 2.R1011
5'-most EST
                   uC-zmflmo17151c11b1
Method
                   BLASTX
NCBI GI
                   g2244806
BLAST score
                   228
E value
                   3.0e-18
                   242
Match length
                   28
% identity
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   266896
Contig ID
                   11964 1.R1011
                   nbm700467735.h1
5'-most EST
Method
                   BLASTX
                   q3327204
NCBI GI
BLAST score
                   1567
                   0.0e+00
E value
```

Match length 600 % identity 61

NCBI Description (AB014595) KIAA0695 protein [Homo sapiens]

Seq. No. 266897



```
11966 1.R1011
Contig ID
                   uC-zm\overline{f}lmo17265g10b1
5'-most EST
                   BLASTX
Method
                   q3386609
NCBI GI
                   208
BLAST score
                   6.0e-16
E value
                   68
Match length
                   57
% identity
                   (AC004665) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   266898
Seq. No.
                   11968 1.R1011
Contig ID
                   fC-zmf1700464505a2
5'-most EST
                   266899
Seq. No.
                   11969 1.R1011
Contig ID
                   uC-zmflb73095e05b1
5'-most EST
                   BLASTX
Method
                   q4539324
NCBI GI
BLAST score
                   702
                   1.0e-73
E value
                   394
Match length
% identity
                   44
                   (AL035679) kinesin like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   266900
                   11969 4.R1011
Contig ID
5'-most EST
                   xdb70\overline{0}341951.h1
                   266901
Seq. No.
Contig ID
                   11969 5.R1011
                   uC-zm\overline{f}lb73285d10b1
5'-most EST
                   BLASTN
Method
                   q551289
NCBI GI
BLAST score
                    40
E value
                    8.0e-13
                   123
Match length
                    83
% identity
NCBI Description Z.mays (W22) phosphoglycerate mutase gene exons 2-8
Seq. No.
                    266902
Contig ID
                    11970 1.R1011
5'-most EST
                   LIB3118-014-Q1-K1-C6
                    266903
Seq. No.
Contig ID
                    11972 1.R1011
                    uC-zm\overline{f}1b73146c02b1
5'-most EST
                   BLASTX
Method
                    q4220480
NCBI GI
BLAST score
                    901
E value
                    8.0e-97
                    472
Match length
                    41
% identity
```

Seq. No. 266904

NCBI Description

(AC006069) unknown protein [Arabidopsis thaliana]



11974 1.R1011 Contig ID LIB3079-006-Q1-K1-C7 5'-most EST BLASTX Method g4455190 NCBI GI 445 BLAST score 9.0e-44E value 169 Match length 54 % identity (AL035440) putative protein [Arabidopsis thaliana] NCBI Description 266905 Seq. No.

11974 2.R1011 Contig ID

uC-zmroteosinte070f10b1 5'-most EST

BLASTX Method g4455190 NCBI GI 193 BLAST score 5.0e-18 E value 68 Match length 75 % identity

(AL035440) putative protein [Arabidopsis thaliana] NCBI Description

266906 Seq. No.

11979 1.R1011 Contig ID

LIB3152-045-P1-K1-G6 5'-most EST

BLASTX Method NCBI GI q169805 BLAST score 365 3.0e - 34E value 162 Match length 55 % identity

(L12252) [Oryza sativa DNA fragment with a miscellaneous NCBI Description

signal and an open reading frame.], gene product [Oryza

sativa]

266907 Seq. No.

11979 2.R1011 Contig ID 5'-most EST ypc700800868.hl

266908 Seq. No.

Contig ID 11980 1.R1011

LIB3069-055-Q1-K1-A9 5'-most EST

Method BLASTX NCBI GI q1709761 BLAST score 713 1.0e-104 E value Match length 247 % identity 81

PROTEASOME 27 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE NCBI Description

COMPLEX 27 KD SUBUNIT) >qi 1262146 emb CAA65660 (X96974)

proteasome subunit [Spinacia oleracea]

266909 Seq. No.

11983 1.R1011 Contig ID

LIB3067-048-Q1-K1-G6 5'-most EST

Method BLASTX g3878412 NCBI GI 159 BLAST score



3.0e-10 E value 175 Match length 27 % identity

(Z77666) cDNA EST EMBL:T01059 comes from this gene; cDNA NCBI Description EST EMBL: D71534 comes from this gene; cDNA EST EMBL: D74514 comes from this gene; cDNA EST EMBL: D66796 comes from this

gene; cDNA EST EMBL:C11630 comes from this gene; cDN

266910 Seq. No.

11985 1.R1011 Contig ID

LIB3136-016-Q1-K1-E2 5'-most EST

BLASTX Method g4504909 NCBI GI BLAST score 421 1.0e-67 E value Match length 424 36 % identity

karyopherin (importin) beta 3 >gi_2102696 (U72761) NCBI Description

karyopherin beta 3 [Homo sapiens]

266911 Seq. No.

11988 1.R1011 Contig ID uC-zmflb73207a02a1 5'-most EST

266912 Seq. No.

11989 1.R1011 Contig ID

uC-zmflmo17233h11a1 5'-most EST

Method BLASTX g2191136 NCBI GI 653 BLAST score

5.0e-68 E value 267 Match length 53 % identity

(AF007269) Similar to UTP-Glucose Glucosyltransferase; NCBI Description

coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290

[Arabidopsis thaliana]

266913 Seq. No.

11989 2.R1011 Contig ID qct701176050.hl 5'-most EST

BLASTX Method q1388078 NCBI GI 163 BLAST score 7.0e-11E value 128 Match length % identity

NCBI Description (U35826) thioredoxin h [Arabidopsis thaliana]

266914 Seq. No.

11989 3.R1011 Contig ID

uC-zmflmo17310a12a1 5'-most EST

Method BLASTX NCBI GI g2642648 BLAST score 342 9.0e-32 E value Match length 114



% identity (AF033852) cytosolic heat shock 70 protein; HSC70-3 NCBI Description [Spinacia oleracea] >gi_2660768 (AF034616) cytosolic heat shock 70 protein [Spinacia oleracea] >gi 2660770 (AF034617) cytosolic heat shock 70 protein [Spinacia oleracea] 266915 Seq. No. 11989 4.R1011 Contig ID 5'-most EST LIB3060-007-Q1-K1-A12 Method BLASTX NCBI GI q2459445 174 BLAST score 6.0e-12 E value 67 Match length 54 % identity (AC002332) putative ribonucleoprotein [Arabidopsis NCBI Description thaliana] 266916 Seq. No. Contig ID 11989 5.R1011 wev700405008.h1 5'-most EST Method BLASTN g22330 NCBI GI BLAST score 132 8.0e-68 E value Match length 140 99 % identity NCBI Description Z.mays Zmhoxla mRNA for homeobox protein 266917 Seq. No. Contig ID 11989 6.R1011 5'-most EST LIB3159-012-Q1-K1-D3 266918 Seq. No. Contig ID 11989 8.R1011 5'-most EST ceu700421934.h1 BLASTN Method NCBI GI g22330 BLAST score 132 7.0e-68 E value Match length 140 99 % identity NCBI Description Z.mays Zmhoxla mRNA for homeobox protein Seq. No. 266919 11989 9.R1011 Contig ID uC-zmflmo17223e11a1 5'-most EST BLASTN Method NCBI GI q22330 BLAST score 118 1.0e-59 E value

134 Match length 97 % identity

NCBI Description Z.mays Zmhoxla mRNA for homeobox protein

Seq. No. 266920

Contig ID 11989 10.R1011



```
5'-most EST
                  uC-zmroteosinte099f01b2
                  BLASTN
Method
                  g22330
NCBI GI
                  115
BLAST score
                  1.0e-57
E value
                  139
Match length
                  96
% identity
NCBI Description Z.mays Zmhoxla mRNA for homeobox protein
                  266921
Seq. No.
                  11989 15.R1011
Contig ID
5'-most EST
                  uer700583055.h1
                  266922
Seq. No.
                  11989 16.R1011
Contig ID
5'-most EST
                  LIB3157-001-Q1-K1-A12
                  BLASTN
Method
                  g22330
NCBI GI
                  98
BLAST score
                  1.0e-47
E value
                  131
Match length
                  93
% identity
NCBI Description Z.mays Zmhoxla mRNA for homeobox protein
                  266923
Seq. No.
                  11989 17.R1011
Contig ID
5'-most EST
                  LIB3060-036-Q1-K1-C4
                  266924
Seq. No.
                  11989 18.R1011
Contig ID
5'-most EST
                  xmt700264415.h1
                   266925
Seq. No.
Contig ID
                   11989 20.R1011
                  clt700042526.f1
5'-most EST
Seq. No.
                   266926
                   11991_1.R1011
Contig ID
5'-most EST
                   LIB3066-053-Q1-K1-C6
                   BLASTX
Method
NCBI GI
                   g3249106
BLAST score
                   171
E value
                   3.0e-17
Match length
                   148
                   34
% identity
NCBI Description (AC003114) T12M4.16 [Arabidopsis thaliana]
Seq. No.
                   266927
Contig ID
                   11993 1.R1011
                   LIB3079-006-Q1-K1-B8
5'-most EST
Method
                   BLASTX
NCBI GI
                   q541824
BLAST score
                   615
E value
                   3.0e-64
```

NCBI Description protein kinase - spinach >gi_457709_emb_CAA82991_ (Z30330)

137

Match length % identity

9.3 -



protein kinase [Spinacia oleracea]

Seq. No. 266928

Contig ID 11997 1.R1011 5'-most EST gct701178944.h1

Seq. No. 266929

Contig ID 11999_1.R1011 5'-most EST xyt700343714.h1

Method BLASTX
NCBI GI g3451075
BLAST score 1036
E value 1.0e-113
Match length 364
% identity 54

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 266930

Contig ID 12000 1.R1011

5'-most EST LIB3079-005-Q1-K1-H3

Method BLASTX
NCBI GI g1710598
BLAST score 370
E value 2.0e-35
Match length 144
% identity 51

NCBI Description MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L9 PRECURSOR (YML9)

>gi_279645_pir__R5BYL3 ribosomal protein L3 precursor,

mitochondrial - yeast (Saccharomyces cerevisiae)

>gi_886912_emb_CAA61168_ (X87941) ORF 269 [Saccharomyces
cerevisiae] >gi_1323396_emb_CAA97248_ (Z73004) ORF YGR220c

[Saccharomyces cerevisiae]

Seq. No. 266931

Contig ID 12001_1.R1011

5'-most EST LIB83-002-Q1-E1-E10

Seq. No. 266932

Contig ID 12003 1.R1011

5'-most EST LIB3158-004-Q1-K1-H6

Method BLASTX
NCBI GI g4039153
BLAST score 155
E value 4.0e-10
Match length 37
% identity 76

NCBI Description (AF104221) low temperature and salt responsive protein

LTI6A [Arabidopsis thaliana] >gi_4325217_gb_AAD17302_(AF122005) hydrophobic protein [Arabidopsis thaliana]

Seq. No. 266933

Contig ID 12007 1.R1011

5'-most EST LIB31 $\overline{5}$ 0-023-Q1-N1-E2

Seq. No. 266934

Contig ID 12013 1.R1011 5'-most EST qmh700028574.f1



Method BLASTX
NCBI GI g2995953
BLAST score 332
E value 9.0e-31
Match length 89
% identity 71

NCBI Description (AF053565) glutaredoxin I [Mesembryanthemum crystallinum]

Seq. No. 266935

Contig ID 12017_1.R1011 5'-most EST cjh700193015.h1

Seq. No. 266936

Contig ID 12018_1.R1011 5'-most EST xsy700208738.h1

Method BLASTX
NCBI GI g4587298
BLAST score 150
E value 3.0e-09
Match length 108
% identity 33

NCBI Description (AB023628) alpha(1,3) fucosyltransferase [Danio rerio]

Seq. No. 266937

Contig ID 12021_1.R1011

5'-most EST uC-zmflmo17266d08b1

Method BLASTX
NCBI GI g3309084
BLAST score 248
E value 6.0e-21
Match length 73
% identity 68

NCBI Description (AF076252) calcineurin B-like protein 2 [Arabidopsis

thaliana]

Seq. No. 266938

Contig ID 12021_2.R1011 5'-most EST ymt700222409.h1

Method BLASTX
NCBI GI g3309084
BLAST score 244
E value 1.0e-20
Match length 71
% identity 69

NCBI Description (AF076252) calcineurin B-like protein 2 [Arabidopsis

thaliana]

Seq. No. 266939

Contig ID 12022 1.R1011

5'-most EST LIB3079-005-Q1-K1-G3

Method BLASTX
NCBI GI g3024503
BLAST score 289
E value 6.0e-26
Match length 60
% identity 95

NCBI Description RAS-RELATED PROTEIN RAB11C >gi 623576 (L29268) putative



```
[Nicotiana tabacum]
                  266940
Seq. No.
                  12026 1.R1011
Contig ID
                  LIB3067-042-Q1-K1-D12
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2982243
                  183
BLAST score
                  3.0e-13
E value
Match length
                  101
% identity
                   41
                  (AF051204) hypothetical protein [Picea mariana]
NCBI Description
Seq. No.
                  266941
                  12028 1.R1011
Contig ID
5'-most EST
                  LIB3079-005-Q1-K1-H10
Method
                  BLASTN
                  g433706
NCBI GI
BLAST score
                   446
                   0.0e+00
E value
Match length
                   455
                   57
% identity
NCBI Description Z.mays PRP gene
                   266942
Seq. No.
Contig ID
                  12029 1.R1011
5'-most EST
                  LIB3079-005-Q1-K1-F5
                   266943
Seq. No.
                   12030 1.R1011
Contig ID
                  LIB3079-005-Q1-K1-D9
5'-most EST
                   266944
Seq. No.
Contig ID
                   12034 1.R1011
```

uC-zmflmo17187f03b1 5'-most EST

Seq. No. 266945

12034 3.R1011 Contig ID 5'-most EST nbm700469011.h1

Seq. No. 266946

Contig ID 12035 1.R1011

5'-most EST uC-zmflmo17344g09b1

Seq. No. 266947

Contig ID 12039_1.R1011

5'-most EST LIB3061-043-Q1-K1-E4

Method BLASTX NCBI GI g322870 BLAST score 2627 E value 0.0e+00Match length 541 95 % identity

glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) -NCBI Description

maize (fragment)

266948 Seq. No.

12039 5.R1011 Contig ID LIB3150-038-Q1-N1-B8 5'-most EST Method BLASTX NCBI GI q1707924 BLAST score 449 E value 1.0e-44Match length 110 85 % identity NCBI Description GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 1 PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) (SHRUNKEN-2) >gi_1947182 (M81603) shrunken-2 [Zea mays] >gi_444329_prf__1906378A ADP glucose pyrophosphorylase [Zea mays] 266949 Seq. No. 12039 11.R1011 Contig ID LIB3150-084-P2-N2-E12 5'-most EST Method BLASTN NCBI GI g168654 BLAST score 209 1.0e-114 E value 228 Match length 98 % identity NCBI Description Zea mays ADP glucose pyrophosphorylase (shrunken-2) gene, complete cds 266950 Seq. No. Contig ID 12040 1.R1011 LIB3069-053-Q1-K1-D8 5'-most EST Method BLASTX g2780365 NCBI GI BLAST score 260 2.0e-22 E value 92 Match length % identity 55 NCBI Description (AB007693) Elongin C [Drosophila melanogaster]

Seq. No. 266951

Contig ID 12041_1.R1011 5'-most EST LIB3079-005-Q1-K1-F1

Seq. No. 266952

Contig ID 12042 1.R1011 5'-most EST fdz701163705.h1

Method BLASTX
NCBI GI g4503325
BLAST score 861
E value 1.0e-92
Match length 224
% identity 71

NCBI Description deoxyhypusine synthase >gi_1352267_sp_P49366_DHYS_HUMAN DEOXYHYPUSINE SYNTHASE >gi_994715 (L39068) deoxyhypusine

synthase [Homo sapiens] >gi_1710220 (U79262) deoxyhypusine

synthase [Homo sapiens] >gi_3021398_emb_CAA04940_(AJ001701) deoxyhypusine synthase [Homo sapiens]



```
266953
Seq. No.
                  12043 1.R1011
Contig ID
                  LIB3079-005-Q1-K1-F4
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3935185
                  235
BLAST score
E value
                  1.0e-19
Match length
                  147
                   39
% identity
                  (AC004557) F17L21.28 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  266954
                  12044 1.R1011
Contig ID
                  rvt700550322.h1
5'-most EST
Seq. No.
                   266955
Contig ID
                  12045 1.R1011
                  uC-zmflb73193h09b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2832300
BLAST score
                  193
                  1.0e-14
E value
Match length
                   52
                   71
% identity
                  (AF044285) adenosine-5'-phosphosulfate-kinase [Catharanthus
NCBI Description
                   roseusl
                   266956
Seq. No.
                   12045 2.R1011
Contig ID
                   uC-zmflmo17103c04b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2832300
BLAST score
                   316
                   6.0e-29
E value
Match length
                   89
% identity
                  (AF044285) adenosine-5'-phosphosulfate-kinase [Catharanthus
NCBI Description
                   roseusl
Seq. No.
                   266957
Contig ID
                   12045 4.R1011
5'-most EST
                   dyk700102592.hl
Seq. No.
                   266958
                   12045 5.R1011
Contig ID
5'-most EST
                   LIB3061-030-Q1-K1-E1
Method
                   BLASTX
                   g2829133
NCBI GI
BLAST score
                   410
                   1.0e-39
E value
                   114
Match length
% identity
                   65
                  (AF043351) adenosine-5'-phosphosulfate-kinase [Arabidopsis
NCBI Description
                   thaliana] >gi_4490745_emb_CAB38907.1_ (AL035708)
```

Seq. No. 266959

adenosine-5'-phosphosulfate-kinase [Arabidopsis thaliana]



Contig ID 12054_1.R1011 5'-most EST xsy700211106.h1

Method BLASTX
NCBI GI g1103318
BLAST score 658
E value 1.0e-68
Match length 277
% identity 53

NCBI Description (X78818) casein kinase I [Arabidopsis thaliana] >gi 2244791 emb CAB10213.1 (Z97336) casein kinase I

[Arabidopsis thaliana]

Seq. No. 266960

Contig ID 12054_2.R1011 5'-most EST xjt700096879.h1

Seq. No. 266961

Contig ID 12056 1.R1011

5'-most EST LIB1 $4\overline{3}$ -051-Q1-E1-F12

Method BLASTX
NCBI GI g3015621
BLAST score 914
E value 1.0e-98
Match length 218
% identity 84

NCBI Description (AF035460) low molecular weight heat shock protein

precursor [Zea mays]

Seq. No. 266962

Contig ID 12060_1.R1011 5'-most EST uC-zmflB73009h07b1

Seq. No. 266963

Contig ID 12062_1.R1011

5'-most EST LIB3079-005-Q1-K1-B4

Seq. No. 266964

Contig ID 12067_1.R1011

5'-most EST LIB3069-048-Q1-K1-D10

Method BLASTX
NCBI GI g3492806
BLAST score 242
E value 2.0e-20
Match length 119
% identity 42

NCBI Description (AJ225045) adventitious rooting related oxygenase [Malus

domestica]

Seq. No. 266965

Contig ID 12071 1.R1011

5'-most EST LIB3069-005-Q1-K1-D4

Method BLASTX
NCBI GI g913445
BLAST score 600°
E value 4.0e-62
Match length 211
% identity 55



(S75487) alcohol dehydrogenase ADH=alcohol dehydrogenase NCBI Description homolog {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red cherry, Peptide, 389 aa] [Lycopersicon esculentum]

266966 Seq. No.

12071 2.R1011 Contig ID

LIB3066-001-Q1-K1-E8 5'-most EST

Method BLASTX NCBI GI g913445 BLAST score 409 E value 2.0e-45 Match length 277 % identity 51

(S75487) alcohol dehydrogenase ADH=alcohol dehydrogenase NCBI Description

homolog {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red cherry, Peptide, 389 aa] [Lycopersicon esculentum]

266967 Seq. No.

Contig ID 12072 1.R1011

5'-most EST LIB3070-005-Q1-N1-H4

Method BLASTX g1781299 NCBI GI BLAST score 173 E value 3.0e-12 Match length 49 65 % identity

NCBI Description (Y09506) transformer-SR ribonucleoprotein [Nicotiana

tabacum]

266968 Seq. No.

Contig ID 12076 1.R1011

5'-most EST uC-zmflmo17130d06b1

Method BLASTX NCBI GI g1350783 BLAST score 267 E value 2.0e-23 Match length 119 % identity 13

RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR NCBI Description

> >gi 282883 pir S27756 receptor-like protein kinase precursor - Arabidopsis thaliana >qi 166850 (M84660) receptor-like protein kinase [Arabidopsis thaliana]

>gi 2842492_emb_CAA16889 (AL021749) receptor-like protein kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. No. 266969

Contig ID 12084 1.R1011 qmh700027196.f1 5'-most EST

Method BLASTX NCBI GI q4191784 BLAST score 858 E value 6.0e-93 242 Match length % identity 69

(AC005917) putative WD-40 repeat protein [Arabidopsis NCBI Description

thaliana]

```
266970
Seq. No.
Contig ID
                  12085 1.R1011
5'-most EST
                  LIB3136-014-Q1-K2-C5
Method
                  BLASTX
NCBI GI
                  g1617274
BLAST score
                  1329
                  1.0e-147
E value
Match length
                  314
% identity
                  78
NCBI Description
                  (Z72152) AMP-binding protein [Brassica napus]
Seq. No.
                  266971
                  12085_2.R1011
Contig ID
                  LIB3079-004-Q1-K1-F1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1617274
BLAST score
                  372
                  3.0e-85
E value
                  201
Match length
% identity
                  83
NCBI Description
Seq. No.
                  266972
Contig ID
                  12087_1.R1011
```

(Z72152) AMP-binding protein [Brassica napus]

5'-most EST uC-zmflb73196h02b1 266973 Seq. No. 12088 1.R1011

Contig ID 5'-most EST LIB3159-011-Q1-K1-D3

Method BLASTX NCBI GI q2190992 BLAST score 583

E value 5.0e-60 Match length 221 % identity 52

(AF004358) glutathione S-transferase TSI-1 [Aegilops NCBI Description

tauschii]

Seq. No. 266974 Contig ID 12088 2.R1011

5'-most EST uC-zmflb73031h01b1

Method BLASTX NCBI GI q2190992 BLAST score 345 E value 3.0e - 32Match length 152 47 % identity

(AF004358) glutathione S-transferase TSI-1 [Aegilops NCBI Description

tauschii]

266975 Seq. No.

12091 1.R1011 Contig ID 5'-most EST fwa700099457.hl

Seq. No. 266976

12094 1.R1011 Contig ID

LIB3059-033-Q1-K1-H3 5'-most EST



Method BLASTX
NCBI GI g2435511
BLAST score 583
E value 4.0e-60
Match length 137
% identity 75

NCBI Description (AF024504) contains similarity to prolyl 4-hydroxylase

alpha subunit [Arabidopsis thaliana]

Seq. No. 266977

Contig ID 12095_1.R1011 5'-most EST wty700171467.h1

Seq. No. 266978

Contig ID 12095 2.R1011

5'-most EST uC-zmflmo17116h09b1

Method BLASTX
NCBI GI g4033467
BLAST score 635
E value 4.0e-66
Match length 213
% identity 57

NCBI Description ARGININE/SERINE-RICH SPLICING FACTOR RSP31

>gi_1707366_emb_CAA67798_ (X99435) splicing factor

[Arabidopsis thaliana]

Seq. No. 266979

Contig ID 12095_3.R1011 5'-most EST pmx700085051.h1

Method BLASTX
NCBI GI g4033467
BLAST score 188
E value 5.0e-14
Match length 59
% identity 59

NCBI Description ARGININE/SERINE-RICH SPLICING FACTOR RSP31

>gi_1707366_emb_CAA67798 (X99435) splicing factor

[Arabidopsis thaliana]

Seq. No. 266980

Contig ID 12095 7.R1011

5'-most EST uC-zmflmo17233b12a1

Seq. No. 266981

Contig ID 12098 1.R1011

5'-most EST LIB189-010-Q1-E1-H6

Method BLASTX
NCBI GI g1698582
BLAST score 150
E value 7.0e-19
Match length 58

% identity 91

NCBI Description (U60767) integral membrane protein OsNramp3 [Oryza sativa]

Seq. No. 266982

Contig ID 12099 1.R1011

5'-most EST LIB189-016-Q1-E1-D8



```
Seq. No.
                   266983
                   12102 1.R1011
Contig ID
                   LIB3079-004-Q1-K1-D11
5'-most EST
                   266984
Seq. No.
Contig ID
                   12104 1.R1011
                   ntr700072113.h1
5'-most EST
                   BLASTX
Method
                   g2245107
NCBI GI
BLAST score
                   783
                   3.0e-83
E value
                   278
Match length
                   36
% identity
NCBI Description (Z97343) thioesterase homolog [Arabidopsis thaliana]
Seq. No.
                   266985
Contig ID
                   12110 1.R1011
                   xmt70\overline{0}265711.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4530611
BLAST score
                   1667
E value
                   0.0e + 00
Match length
                   307
                   99
% identity
```

NCBI Description (AF134552) serine/threonine protein phosphatase PP2A-2 catalytic subunit [Oryza sativa subsp. indica]

Seq. No. 266986 12110 3.R1011 Contig ID uC-zmflmo17023h08a1 5'-most EST

266987 Seq. No.

Contig ID 12113 1.R1011 5'-most EST xjt700094694.hl

BLASTX Method NCBI GI q4056552 BLAST score 865 E value 1.0e-92 335 Match length 49 % identity

NCBI Description (AL034583) putative nucleotide binding protein

[Schizosaccharomyces pombe]

266988 Seq. No.

12113 2.R1011 Contig ID 5'-most EST uC-zmflMo17086c10b1

Seq. No. 266989

Contig ID 12113 3.R1011 5'-most EST LIB143-013-Q1-E1-F9

Seq. No. 266990

Contig ID 12113 6.R1011 5'-most EST wen700332494.h1

Method BLASTX NCBI GI q4056552

37128



```
BLAST score
                   151
E value
                    7.0e-10
Match length
                   37
% identity
                    73
                   (AL034583) putative nucleotide binding protein
NCBI Description
                    [Schizosaccharomyces pombe]
                   266991
Seq. No.
Contig ID
                   12114 1.R1011
5'-most EST
                   cyk70\overline{0}047332.f1
Method
                   BLASTX
NCBI GI
                   q2245009
```

96 % identity NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

266992 Seq. No. Contig ID 12115 1.R1011 LIB3061-028-Q1-K1-E2 5'-most EST Method BLASTX NCBI GI q2370595 BLAST score 618

154 4.0e-10

28

6.0e-64 E value Match length 299 % identity 43

BLAST score

E value Match length

(AJ001414) GTPase activating protein [Yarrowia lipolytica] NCBI Description

266993 Seq. No. Contig ID 12120 1.R1011 5'-most EST $xsy70\overline{0}208765.h1$ Method BLASTN NCBI GI g3821780 BLAST score 36

E value 3.0e-10Match length 36 % identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 266994 12123 1.R1011 Contig ID 5'-most EST

LIB3116-016-P1-K1-A7

Method BLASTX NCBI GI g3551954 BLAST score 796 E value 8.0e-85 Match length 268 % identity 54

(AF082030) senescence-associated protein 5 [Hemerocallis NCBI Description

hybrid cultivar]

Seq. No. 266995

Contig ID 12124 1.R1011

5'-most EST LIB3079-003-Q1-K1-G4

Seq. No. 266996



Contig ID 12126 1.R1011

5'-most EST LIB3066-021-Q1-K1-A4

BLASTX Method NCBI GI q4008555 BLAST score 165 9.0e-11 E value 120 Match length 34 % identity

(AL034490) putative PHD-type zinc finger NCBI Description

[Schizosaccharomyces pombe]

266997 Seq. No.

Contig ID 12129 1.R1011

5'-most EST uC-zmflmo17309f07b1

BLASTX Method g4559342 NCBI GI BLAST score 2446 0.0e + 00E value Match length 524 % identity 85

(AC007087) putative copper methylamine oxidase [Arabidopsis NCBI Description

thaliana]

266998 Seq. No.

12129 2.R1011 Contig ID

5'-most EST LIB3059-028-Q1-K1-F1

Method BLASTX g4559342 NCBI GI 160 BLAST score 1.0e-10 E value Match length 42

% identity 71

(AC007087) putative copper methylamine oxidase [Arabidopsis NCBI Description

thaliana]

266999 Seq. No.

Contig ID 12129 3.R1011 5'-most EST ntr700072791.h1

267000 Seq. No.

12129 4.R1011 Contig ID 5'-most EST qmh700025753.f1

Method BLASTX NCBI GI q1705812 BLAST score 160 E value 2.0e-10 Match length 56 % identity 57

NCBI Description ACIDIC CHITINASE PRECURSOR >gi 1150686 emb CAA92207

(Z68123) acidic chitinase [Vitis vinifera]

Seq. No. 267001

12129 5.R1011 Contig ID 5'-most EST fC-zmf1700337055a5

267002 Seq. No.

Contig ID 12129 6.R1011



5'-most EST qmh700025905.f1 Method BLASTX NCBI GI g1705812 BLAST score 177 1.0e-12 E value Match length 59 58 % identity ACIDIC CHITINASE PRECURSOR >gi_1150686_emb_CAA92207_ NCBI Description (Z68123) acidic chitinase [Vitis vinifera] Seq. No. 267003 12129 8.R1011 Contig ID uC-zmflb73078g09b2 5'-most EST Method BLASTX q4567319 NCBI GI BLAST score 166 3.0e-17 E value Match length 66 63 % identity NCBI Description (AC005956) putative copper amine oxidase [Arabidopsis thaliana] Seq. No. 267004 Contig ID 12129 9.R1011 wty700169865.hl 5'-most EST Method BLASTX g4567319 NCBI GI 213 BLAST score 8.0e-17 E value Match length 66 % identity 62 NCBI Description (AC005956) putative copper amine oxidase [Arabidopsis thaliana] Seq. No. 267005 Contig ID 12129 10.R1011 5'-most EST uC-zmflmo17286d11b1 267006 Seq. No. 12135 1.R1011 Contig ID 5'-most EST LIB3079-004-Q1-K1-A1 Method BLASTX NCBI GI g3892057 BLAST score 973 E value 1.0e-106 Match length 246 % identity 75 NCBI Description (AC002330) hypothetical protein [Arabidopsis thaliana] 267007 Seq. No. 12137 1.R1011 Contig ID LIB3079-004-Q1-K1-A12 5'-most EST

Seq. No. 267008

Contig ID 12141_1.R1011 5'-most EST afb700381679.h1

Method BLASTX



q3176726 NCBI GI 834 BLAST score E value 2.0e-89 Match length 269 % identity 59 (AC002392) putative serine proteinase [Arabidopsis NCBI Description thaliana] Seq. No. 267009

12141 2.R1011 Contig ID uC-zmflb73017h11a2 5'-most EST

267010 Seq. No.

12142 1.R1011 Contig ID

5'-most EST LIB3079-003-Q1-K1-F3

267011 Seq. No.

12150 1.R1011 Contig ID

LIB189-008-Q1-E1-D1 5'-most EST

Method BLASTX NCBI GI g1122317 BLAST score 505 8.0e-51 E value Match length 158 % identity 67

NCBI Description (X94193) heat shock protein 17.9 [Pennisetum glaucum]

267012 Seq. No.

Contig ID 12150 2.R1011

5'-most EST LIB143-040-Q1-E1-G1

Method BLASTX NCBI GI g1122317 BLAST score 551 E value 1.0e-56 Match length 123

% identity 88

(X94193) heat shock protein 17.9 [Pennisetum glaucum] NCBI Description

267013 Seq. No.

Contig ID 12150 3.R1011 5'-most EST uC-zmflm017026c01b1

Method BLASTN NCBI GI g1122316 BLAST score 124 E value 7.0e-63 Match length 389 % identity 87

NCBI Description P.glaucum mRNA for heat shock protein, HSP 17.9

267014 Seq. No.

Contig ID 12150 4.R1011 5'-most EST pwr700452443.h1

Method BLASTX NCBI GI g1122317 BLAST score 382 E value 9.0e-37 Match length 88



% identity NCBI Description (X94193) heat shock protein 17.9 [Pennisetum glaucum] 267015 Seq. No. 12150 7.R1011 Contig ID 5'-most EST LIB143-024-Q1-E1-C1 267016 Seq. No. Contig ID 12158_1.R1011 5'-most EST pmx700083217.h1 Method BLASTX g3309170 535

NCBI GI BLAST score E value 2.0e-54 Match length 207 % identity 54

NCBI Description (AF071314) COP9 complex subunit 4 [Mus musculus]

267017 Seq. No. Contig ID 12158 2.R1011

5'-most EST LIB3079-003-Q1-K1-E1

BLASTX Method NCBI GI g3309170 BLAST score 518 E value 5.0e-52 Match length 307 % identity 51

NCBI Description (AF071314) COP9 complex subunit 4 [Mus musculus]

Seq. No. 267018

Contig ID 12161 1.R1011 5'-most EST uC-zmflb73184f05a1

267019 Seq. No.

Contig ID 12164 1.R1011

5'-most EST LIB3150-032-Q1-N1-H9

Method BLASTX NCBI GI q2344894 BLAST score 151 E value 2.0e-09 Match length 199 % identity 29

NCBI Description (AC002388) hypothetical protein [Arabidopsis thaliana]

267020 Seq. No.

Contig ID 12165 1.R1011

5'-most EST LIB3079-003-Q1-K1-E8

Method BLASTX NCBI GI g2224695 BLAST score 325 E value 7.0e-30 221 Match length 38 -% identity

NCBI Description (AB002375) KIAA0377 [Homo sapiens]

Seq. No. 267021

Contig ID 12168 1.R1011



5'-most EST xjt700094656.h1

Method BLASTX
NCBI GI g1421730
BLAST score 894
E value 2.0e-96
Match length 276
% identity 59

NCBI Description (U43082) RF2 [Zea mays]

Seq. No. 267022

Contig ID 12172_1.R1011

5'-most EST LIB3066-009-Q1-K1-H5

Method BLASTX
NCBI GI g2245101
BLAST score 511
E value 1.0e-51
Match length 219
% identity 54

NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 267023

Contig ID 12172_2.R1011 5'-most EST uC-zmflb73064e06b1

Method BLASTX
NCBI GI g2245101
BLAST score 207
E value 6.0e-16
Match length 128
% identity 61

NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 267024

Contig ID 12173_1.R1011

5'-most EST LIB3079-003-Q1-K1-C3

Seq. No. 267025

Contig ID 12177_1.R1011 5'-most EST uC-zmflb73054a11b1

Seq. No. 267026

Contig ID 12177_2.R1011

5'-most EST uC-zmflmo17052b09b1

Seq. No. 267027

Contig ID 12177_3.R1011

5'-most EST uC-zmflmo17263g01b1

Seq. No. 267028

Contig ID 12177_5.R1011

5'-most EST uC-zmflmo17103g04b1

Seq. No. 267029

Contig ID 12177_6.R1011 5'-most EST tfd700573469.h2

Seq. No. 267030

Contig ID 12177 7.R1011



5'-most EST vux700158665.hl

Seq. No. 267031

Contig ID 12177_9.R1011 5'-most EST cyk700051416.f1

Seq. No. 267032

Contig ID 12178_1.R1011 5'-most EST cyk700049820.f1

Method BLASTX
NCBI GI g2435511
BLAST score 528
E value 1.0e-53
Match length 186
% identity 56

NCBI Description (AF024504) contains similarity to prolyl 4-hydroxylase

alpha subunit [Arabidopsis thaliana]

Seq. No. 267033

Contig ID 12178 2.R1011

5'-most EST LIB3067-060-Q1-K1-D11

Method BLASTX
NCBI GI g2980790
BLAST score 212
E value 1.0e-16
Match length 101
% identity 41

NCBI Description (AL022197) hypothetical protein [Arabidopsis thaliana]

Seq. No. 267034

Contig ID 12178_3.R1011 5'-most EST uC-zmflb73267b02a1

Seq. No. 267035

Contig ID 12179_1.R1011

5'-most EST uC-zmflmo17275g02a1

Seq. No. 267036

Contig ID 12179 2.R1011

5'-most EST LIB3079-053-Q1-K1-F2

Seq. No. 267037

Contig ID 12179_3.R1011

5'-most EST LIB3157-016-Q1-K1-B12

Seq. No. 267038

Contig ID 12180 1.R1011

5'-most EST LIB3069-036-Q1-K1-C6

Method BLASTX
NCBI GI 94033735
BLAST score 1548
E value 1.0e-173
Match length 342
% identity 87

NCBI Description (AF054284) spliceosomal protein SAP 155 [Homo sapiens]

Seq. No. 267039



```
Contig ID
                  12180 2.R1011
                  LIB189-029-Q1-E1-A3
5'-most EST
                  BLASTX
Method
                  g3387899
NCBI GI
                  291
BLAST score
                  6.0e-26
E value
                  89
Match length
                  61
% identity
                  (AF070540) putative nuclear protein [Homo sapiens]
NCBI Description
                  267040
Seq. No.
                  12180 3.R1011
                  uC-zmflb73053f02b2
```

Contig ID 5'-most EST

267041 Seq. No. 12180 4.R1011 Contig ID

uC-zmflmo17342f05a1 5'-most EST

267042 Seq. No.

12180 5.R1011 Contig ID

LIB3060-049-Q1-K1-H1 5'-most EST

267043 Seq. No. 12181 1.R1011 Contig ID rvt700552304.h1 5'-most EST

BLASTX Method g3193292 NCBI GI BLAST score 1458 1.0e-162

E value 363 Match length 78 % identity

(AF069298) similar to ATPases associated with various NCBI Description

cellular activites (Pfam: AAA.hmm, score: 230.91)

[Arabidopsis thaliana]

267044 Seq. No. Contig ID 12181 2.R1011

LIB3117-001-Q1-K1-B1 5'-most EST

267045 Seq. No.

12182 1.R1011 Contig ID 5'-most EST hvj700623889.h1

267046 Seq. No.

12187 1.R1011 Contig ID

5'-most EST fC-zmf1700550149f3

Method BLASTX NCBI GI q2979542 BLAST score 552 1.0e-56 E value Match length 154 % identity

(AC003680) putative Ser/Thr kinase [Arabidopsis thaliana] NCBI Description

267047 Seq. No.

12187 2.R1011 Contig ID 5'-most EST $xjt70\overline{0}093139.h1$

BLAST score

Match length

E value

259

85

4.0e-22



```
267048
Seq. No.
Contig ID
                   12188 1.R1011
5'-most EST
                  nbm700470737.hl
Method
                  BLASTX
NCBI GI
                  q3297891
BLAST score
                  170
                   6.0e-12
E value
Match length
                  42
                   74
% identity
NCBI Description
                  (AJ002990) nucleotide repair protein [Lilium longiflorum]
Seq. No.
                   267049
Contig ID
                  12190 1.R1011
5'-most EST
                   zla700379692.h1
Method
                  BLASTX
NCBI GI
                  q4538913
BLAST score
                   338
                   3.0e - 31
E value
Match length
                  192
                   42
% identity
NCBI Description
                  (AL049482) putative protein [Arabidopsis thaliana]
Seq. No.
                   267050
Contig ID
                   12192 1.R1011
5'-most EST
                  LIB3079-003-Q1-K1-B12
                   267051
Seq. No.
Contig ID
                  12196 1.R1011
5'-most EST
                  nbm700465222.h1
Method
                  BLASTX
NCBI GI
                   g4097340
BLAST score
                  825
E value
                   3.0e-88
Match length
                  170
% identity
                 (U57639) hydrophobic LEA-like protein [Oryza sativa]
NCBI Description
Seq. No.
                   267052
Contig ID
                   12198 1.R1011
                  LIB3079-002-Q1-K1-H1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g4235430
BLAST score
                   363
E value
                   1.0e-34
                   98
Match length
                   76
% identity
                  (AF098458) latex-abundant protein [Hevea brasiliensis]
NCBI Description
                   267053
Seq. No.
                   12200 1.R1011
Contig ID
5'-most EST
                  hbs701183505.h1
Method
                  BLASTX
NCBI GI
                   g729442
```

37137



% identity 54

NCBI Description PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR

>gi 166380 (M80235) glucose-regulated endoplasmic reticular

protein precursor [Medicago sativa]

Seq. No. 267054

Contig ID 12201_1.R1011

5'-most EST LIB3150-002-Q1-N1-D9

Method BLASTX
NCBI GI g3184100
BLAST score 262
E value 2.0e-22
Match length 85
% identity 54

NCBI Description (AL023777) rna binding protein [Schizosaccharomyces pombe]

Seq. No. 267055

Contig ID 12201_2.R1011 5'-most EST qmh700029536.f1

Method BLASTX
NCBI GI g3184100
BLAST score 310
E value 7.0e-28
Match length 154
% identity 38

NCBI Description (AL023777) rna binding protein [Schizosaccharomyces pombe]

Seq. No. 267056

Contig ID 12202 1.R1011

5'-most EST LIB3079-002-Q1-K1-H9

Method BLASTX
NCBI GI g4204281
BLAST score 230
E value 1.0e-18
Match length 201
% identity 31

NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 267057

Contig ID 12204 1.R1011

5'-most EST LIB3180-022-P2-M1-H11

Method BLASTX
NCBI GI g3395553
BLAST score 468
E value 1.0e-46
Match length 221
% identity 46

NCBI Description (AL031180) probable cation-transporting atpase

[Schizosaccharomyces pombe]

Seq. No. 267058

Contig ID 12206 1.R1011

5'-most EST LIB3079-002-Q1-K1-G5

Method BLASTX
NCBI GI g1706551
BLAST score 222
E value 6.0e-18



```
84
Match length
                  46
% identity
                  GLUCAN ENDO-1, 3-BETA-GLUCOSIDASE PRECURSOR
NCBI Description
                   ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                   (BETA-1, 3-ENDOGLUCANASE) >gi 924953 (U30323) beta
                  1,3-glucanase [Triticum aestivum]
                  267059
Seq. No.
                  12206_2.R1011
Contig ID
                  LIB3061-042-Q1-K1-E4
5'-most EST
                  BLASTX
Method
                  q4558591
NCBI GI
BLAST score
                  189
                  3.0e-14
E value
Match length
                  59
% identity
                  56
                  (AC006555) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                  thaliana]
                  267060
Seq. No.
                  12208 1.R1011
Contig ID
                  ntr700075062.h1
5'-most EST
                  267061
Seq. No.
Contig ID
                  12212_1.R1011
5'-most EST
                  wty700164475.hl
                   267062
Seq. No.
                  12213 1.R1011
Contig ID
                   xmt700265608.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4105683
BLAST score
                   430
E value
                   2.0e-49
Match length
                   124
% identity
                  (AF049892) unknown [Oryza sativa] >gi 4105692 (AF050155)
NCBI Description
                   embryo-specific protein [Oryza sativa subsp. indica]
Seq. No.
                   267063
                   12214 1.R1011
Contig ID
                   LIB3118-005-Q1-K1-C10
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3402675
BLAST score
                   198
E value
                   7.0e-15
Match length
                   118
                   36
% identity
NCBI Description (AC004697) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   267064
```

12218 1.R1011 Contig ID

LIB3079-002-Q1-K1-G12 5'-most EST

Method BLASTX NCBI GI g2660670 BLAST score 868 E value 1.0e-93



Match length 217 % identity 79

NCBI Description (AC002342) putative Cu2+-transporting ATPase [Arabidopsis

thaliana]

Seq. No. 267065

Contig ID 12219_1.R1011

5'-most EST LIB3066-036-Q1-K1-B3

Method BLASTX
NCBI GI g3021357
BLAST score 527
E value 1.0e-53
Match length 129
% identity 76

NCBI Description (AJ005082) UDP-galactose 4-epimerase [Cyamopsis

tetragonoloba]

Seq. No. 267066

Contig ID 12220_1.R1011

5'-most EST LIB3079-002-Q1-K1-G3

Seq. No. 267067

Contig ID 12223_1.R1011

5'-most EST uC-zmflmo17299b11b1

Method BLASTX
NCBI GI g4586260
BLAST score 385
E value 2.0e-36
Match length 215

% identity 42

NCBI Description (AL049640) putative protein [Arabidopsis thaliana]

Seq. No. 267068

Contig ID 12223_2.R1011 5'-most EST wyr700242578.h1

Seq. No. 267069

Contig ID 12223 3.R1011

5'-most EST uC-zmflmo17135f01a1

Seq. No. 267070

Contig ID 12225_1.R1011 5'-most EST pmx700084649.h1

Method BLASTX
NCBI GI g2832649
BLAST score 610
E value 2.0e-63
Match length 171
% identity 68

NCBI Description (AL021710) adenylosuccinate lyase - like protein

[Arabidopsis thaliana]

Seq. No. 267071

Contig ID 12225_2.R1011 5'-most EST uC-zmflb73155g08b2

Method BLASTX NCBI GI g2832649

E value

Match length % identity

2.0e-29 85

68



```
467
BLAST score
                  2.0e-46
E value
Match length
                  142
% identity
                  67
                  (AL021710) adenylosuccinate lyase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                  267072
Seq. No.
Contig ID
                  12225 3.R1011
                  LIB3079-002-Q1-K1-D9
5'-most EST
Method
                  BLASTX
                  g2832649
NCBI GI
                  404
BLAST score
                  2.0e-39
E value
Match length
                  129
% identity
                   61
                  (AL021710) adenylosuccinate lyase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  267073
                  12227 1.R1011
Contig ID
                  uC-zmflMo17063f09b1
5'-most EST
Method
                  BLASTX
                  q3319884
NCBI GI
                  698
BLAST score
                   2.0e-73
E value
Match length
                   310
% identity
                   46
                  (AJ224306) PRT1 [Arabidopsis thaliana]
NCBI Description
                   >gi 3319886 emb_CAA11892_ (AJ224307) PRT1 [Arabidopsis
                  thaliana]
                   267074
Seq. No.
                   12229 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17039g01b1
Method
                  BLASTX
NCBI GI
                  q2842704
BLAST score
                  143
E value
                   9.0e-09
Match length
                  120
                   36
% identity
                  HYPOTHETICAL 73.3 KD PROTEIN C6G9.14 IN CHROMOSOME I
NCBI Description
                   >gi 1644326_emb_CAB03616.1_ (Z81317) serine rich pumilio
                   family rna binding domain pr otein [Schizosaccharomyces
                  pombe]
                   267075
Seq. No.
                   12231 1.R1011
Contig ID
                  LIB3079-002-Q1-K1-E4
5'-most EST
                  BLASTX
Method
NCBI GI
                   g3461814
BLAST score
                   322
```

NCBI Description (AC004138) hypothetical protein [Arabidopsis thaliana]



267076 Seq. No.

Contig ID 12235 1.R1011

5'-most EST uC-zmflmo17277g03b1

267077 Seq. No.

12236 1.R1011 Contig ID

5'-most EST uC-zmroteosinte094g01b2

BLASTX Method NCBI GI q1168329 BLAST score 238 E value 2.0e-23 Match length 91

64 % identity

ACTIN-LIKE PROTEIN 3 (ACTIN-LIKE PROTEIN 66B) (ACTIN-2) NCBI Description

>gi_558568_emb_CAA50674_ (X71789) actin related protein
[Drosophila melanogaster] >gi_1096138_prf__2111232A

actin-related protein [Drosophila melanogaster]

267078 Seq. No.

Contig ID 12236 2.R1011

5'-most EST LIB143-019-Q1-E1-C12

Method BLASTX NCBI GI q1703143 BLAST score 676 E value 5.0e-71 Match length 213 60

% identity

NCBI Description ACTIN-LIKE PROTEIN 3 >qi 881635 (U29610) Arp3 [Acanthamoeba

castellanii]

Seq. No. 267079

12237 1.R1011 Contig ID

uC-zmflb73307h02b1 5'-most EST

267080 Seq. No.

12239 1.R1011 Contig ID ntr700077263.h1 5'-most EST

Method BLASTX NCBI GI q4337175 BLAST score 307 E value 1.0e-27 Match length 131 49 % identity

(AC006416) ESTs gb T20589, gb T04648, gb AA597906, NCBI Description

gb_T04111, gb_R841\overline{80}, gb_R654\overline{28}, gb_T444\overline{39}, gb_T76570, gb R90004, gb T45020, gb T42457, gb T20921, gb AA042762 and gb AA720210 come from this gene. [Arabidopsis thaliana]

267081 Seq. No.

Contig ID 12239 2.R1011 uC-zmflB73004h08b1 5'-most EST

BLASTX Method NCBI GI g4337175 BLAST score 247 E value 1.0e-20 Match length 119 % identity 45



NCBI Description (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No. 267082

Contig ID 12239 4.R1011

5'-most EST uC-zmflmo17157b12a1

Seq. No. 267083

Contig ID 12241_1.R1011

5'-most EST uC-zmflb73092e06b2

Seq. No. 267084

Contig ID 12242_1.R1011 5'-most EST dyk700105137.h1

Method BLASTX
NCBI GI g3420299
BLAST score 1253
E value 1.0e-138
Match length 275
% identity 86

NCBI Description (AF072849) jabl protein [Oryza sativa subsp. indica]

Seq. No. 267085

Contig ID 12244_1.R1011 5'-most EST xmt700265102.h1

Method BLASTX
NCBI GI g3183079
BLAST score 1567
E value 1.0e-175
Match length 349
% identity 89

NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR

>gi_1375075_dbj_BAA12870_ (D85763) glyoxysomal malate

dehydrogenase [Oryza sativa]

Seq. No. 267086

Contig ID 12248 1.R1011 5'-most EST wty700172649.h1

Seq. No. 267087

Contig ID 12249_1.R1011 5'-most EST xjt700095873.h1

Method BLASTX
NCBI GI g3176691
BLAST score 645
E value 2.0e-67
Match length 262
% identity 54

NCBI Description (AC003671) Contains homology to serine/threonine protein

kinase gb_X99618 from Mycobacterium tuberculosis. ESTs gb_F14403, gb_F14404, and gb_N96730 come from this gene.

[Arabidopsis thaliana]

Seq. No. 267088

Contig ID 12251 1.R1011



```
xyt700345285.h1
5'-most EST
                   BLASTX
Method
                   q4107099
NCBI GI
BLAST score
                   281
                   1.0e-24
E value
                   104
Match length
% identity
                   48
                   (AB015141) AHP1 [Arabidopsis thaliana]
NCBI Description
                   >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis
                   thaliana]
                   267089
Seq. No.
                   12252 1.R1011
Contig ID
                   LIB3079-002-Q1-K1-A4
5'-most EST
                   267090
Seq. No.
                   12257 1.R1011
Contig ID
                   uC-zm\overline{f}lmo17103h11b1
5'-most EST
                   267091
Seq. No.
                   12259 1.R1011
Contig ID
                   LIB143-025-Q1-E1-D11
5'-most EST
                   BLASTX
Method
                   q3935169
NCBI GI
                   172
BLAST score
                   3.0e-12
E value
                   66
Match length
% identity
                   56
                  (AC004557) F17L21.12 [Arabidopsis thaliana]
NCBI Description
                   267092
Seq. No.
                   12259 2.R1011
Contig ID
                   LIB3079-001-Q1-K1-H6
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3935169
BLAST score
                   172
E value
                   4.0e-12
                   66
Match length
                   56
% identity
NCBI Description (AC004557) F17L21.12 [Arabidopsis thaliana]
                   267093
Seq. No.
                   12261 1.R1011
Contig ID
                   nbm70\overline{04}67870.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4510385
BLAST score
                   1065
E value
                   1.0e-116
Match length
                   334
% identity
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
```

Seq. No. 267094

Contig ID 12262_1.R1011 5'-most EST hbs701181840.h1

Seq. No. 267095



Contig ID 12263 1.R1011 5'-most EST cjh700196351.h1 BLASTX Method g2213603 NCBI GI 154 BLAST score 5.0e-10 E value 70 Match length 41 % identity (AC000348) T7N9.23 [Arabidopsis thaliana] NCBI Description 267096 Seq. No. Contig ID 12263 2.R1011 ypc700805123.hl 5'-most EST 267097 Seq. No. Contig ID 12264 1.R1011 LIB3151-010-Q1-K1-G8 5'-most EST Method BLASTX q3982577 NCBI GI 656 BLAST score 1.0e-120 E value 272 Match length % identity 80 (AF023141) histidinol dehydrogenase [Thlaspi goesingense] NCBI Description 267098 Seq. No. 12269 1.R1011 Contig ID uC-zmflmo17269a06b1 5'-most EST BLASTX Method q2065531 NCBI GI 1670 BLAST score 0.0e+00E value 409 Match length 73 % identity (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum] NCBI Description Seq. No. 267099 Contig ID 12269 2.R1011 uC-zmflb73238e05b2 5'-most EST BLASTX Method NCBI GI q2065531 BLAST score 943 1.0e-116 E value Match length 328 65 % identity NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum] Seq. No. 267100 Contig ID 12269 3.R1011 uC-zmflb73411c02a1 5'-most EST

Seq. No. 267101

Contig ID 12269_6.R1011 5'-most EST uC-zmflb73116e03b2

Method BLASTX NCBI GI g2065531 BLAST score 341

Seq. No.

267107



```
6.0e-32
E value
                   125
Match length
% identity
                   58
                  (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
NCBI Description
                   267102
Seq. No.
                   12269 7.R1011
Contig ID
                   gw1700612427.h1
5'-most EST
                   BLASTX
Method
                   g3341677
NCBI GI
                   163
BLAST score
                   8.0e-12
E value
                   39
Match length
                   74
% identity
                   (AC003672) putative glycosyl hydrolase [Arabidopsis
NCBI Description
                   thaliana]
                   267103
Seq. No.
                   12275 1.R1011
Contig ID
                   xsy700214077.h1
5'-most EST
Method
                   BLASTX
                   q1770515
NCBI GI
BLAST score
                   402
                   1.0e-38
E value
                   157
Match length
                   49
% identity
                   (X99459) sigma 3 protein [Homo sapiens] >gi_1923272
NCBI Description
                   (U91933) AP-3 complex sigma3B subunit [Mus musculus]
                   267104
Seq. No.
                   12275 3.R1011
Contig ID
5'-most EST
                   uC-zmflB73004g11b1
                   267105
Seq. No.
                   12276_1.R1011
Contig ID
                   LIB3079-001-Q1-K1-F12
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3513451
                   177
BLAST score
                   9.0e-13
E value
                   145
Match length
% identity
                  (U78090) potassium channel regulator 1 [Rattus norvegicus]
NCBI Description
                   267106
Seq. No.
                   12278 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73056f11b1
Method
                   BLASTX
NCBI GI
                   q337767
BLAST score
                   165
                   8.0e-11
E value
                   186
Match length
% identity
                   25
                   (M60258) cerebroside sulfate activator protein [Homo
NCBI Description
                   sapiens]
```

37146



Contig ID 12278_6.R1011 5'-most EST wyr700238905.h1

 Seq. No.
 267110

 Contig ID
 12279_1.R1011

 5'-most EST
 uC-zmflmo17310c06b1

 Method
 BLASTX

 NCBI GI
 g3618316

 BLAST score
 725

BLAST score 725
E value 1.0e-76
Match length 219
% identity 67

NCBI Description (AB001886) zinc finger protein [Oryza sativa]

 Seq. No.
 267111

 Contig ID
 12279_2.R1011

 5'-most EST
 LIB3079-001-Q1-K1-F5

 Method
 BLASTX

NCBI GI g3618316
BLAST score 315
E value 5.0e-29
Match length 79
% identity 77

NCBI Description (AB001886) zinc finger protein [Oryza sativa]

 Seq. No.
 267112

 Contig ID
 12280_1.R1011

 5'-most EST
 uC-zmflmo17428c11a1

 Method
 BLASTX

Method BLASTX
NCBI GI g1173630
BLAST score 979
E value 1.0e-106
Match length 268
% identity 69

NCBI Description (U34747) cysteine proteinase [Phalaenopsis sp. 'hybrid

SM9108']

Seq. No. 267113 Contig ID 12282_1.R1011

5'-most EST uC-zmflmo17174h06a1

Seq. No. 267114

Contig ID 12282_2.R1011 5'-most EST uC-zmflmo17064q03a1

Seq. No. 267115

Contig ID 12282_3.R1011

5'-most EST LIB3079-001-Q1-K1-F9

Method BLASTX



```
g4567201
NCBI GI
BLAST score
                  902
                  2.0e-97
E value
Match length
                  258
                  68
% identity
                  (AC007168) putative aspartate aminotransferase [Arabidopsis
NCBI Description
                  thaliana]
                  267116
Seq. No.
                  12282 4.R1011
Contig ID
                  uC-zmflmo17019b06a1
5'-most EST
                  267117
Seq. No.
                  12284 1.R1011
Contig ID
                  LIB3180-047-P2-F1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3282674
                  340
BLAST score
                  6.0e-32
E value
                  98
Match length
                   67
% identity
                  (AF036684) CCAAT-box binding factor HAP3 homolog
NCBI Description
                   [Arabidopsis thaliana]
                  267118
Seq. No.
                  12287 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73219b07b2
                  267119
Seq. No.
                  12288 1.R1011
Contig ID
                  LIB3079-001-Q1-K1-D4
5'-most EST
                  BLASTX
Method
                   g3746060
NCBI GI
                   175
BLAST score
E value
                   1.0e-12
Match length
                   37
% identity
                   84
NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]
                   267120
Seq. No.
                   12292 1.R1011
Contig ID
5'-most EST
                   LIB3079-001-Q1-K1-E11
                   267121
Seq. No.
                   12293 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73180b09b1
Method
                   BLASTX
NCBI GI
                   q2792155
BLAST score
                   822
                   6.0e-88
E value
```

267122 Seq. No.

Match length % identity

12293 2.R1011 Contig ID

LIB3059-044-Q1-K1-H2 5'-most EST

275

NCBI Description (AJ223291) chalcone reductase [Sesbania rostrata]



BLASTX Method q4249390 NCBI GI 486 BLAST score 8.0e-49E value 155 Match length 57 % identity

(AC005966) Similar to gb_AF039182 probable aldo-keto NCBI Description reductase from Fragaria x ananassa. This gene may be cut off. EST gb U74151 comes from this gene. [Arabidopsis

thaliana]

267123 Seq. No.

12294 1.R1011 Contig ID

LIB3069-036-Q1-K1-B11 5'-most EST

BLASTX Method g3367568 NCBI GI 353 BLAST score 3.0e - 33E value 100 Match length 61 % identity

(ALO31135) protein kinase - like protein [Arabidopsis NCBI Description

thaliana]

267124 Seq. No.

12295 1.R1011 Contig ID

LIB3069-010-Q1-K1-B5 5'-most EST

BLASTX Method g3643603 NCBI GI 2093 BLAST score 0.0e + 00E value 628 Match length 64 % identity

(AC005395) unknown protein [Arabidopsis thaliana] NCBI Description

267125 Seq. No.

12295 2.R1011 Contig ID 5'-most EST uC-zmflmo17118b07a1

267126

Seq. No. Contig ID 12296 1.R1011 uC-zmflb73091f01b2 5'-most EST

Method BLASTX q2190551 NCBI GI 250 BLAST score 5.0e-21 E value 96 Match length 51 % identity

(AC001229) Similar to C. elegans hypothetical protein NCBI Description

K07C5.6 (gb_Z71181). ESTs gb_H36844,gb_AA394956 come from

this gene. [Arabidopsis thaliana]

267127 Seq. No.

12296 3.R1011 Contiq ID nbm700464947.h1 5'-most EST

BLASTX Method g2190551 NCBI GI BLAST score 852



E value 1.0e-91 Match length 229 70

NCBI Description (AC001229) Similar to C. elegans hypothetical protein K07C5.6 (gb_Z71181). ESTs gb_H36844,gb_AA394956 come from

this gene. [Arabidopsis thaliana]

Seq. No. 267128

Contig ID 12309_2.R1011 5'-most EST uer700583805.h1

Seq. No. 267129

Contig ID 12315 1.R1011

5'-most EST LIB3079-001-Q1-K1-A9

Seq. No. 267130

Contig ID 12318_1.R1011

5'-most EST uC-zmflmo17071g11b1

Method BLASTX
NCBI GI 9602076
BLAST score 1435
E value 1.0e-160
Match length 291
% identity 52

NCBI Description (X77456) pentameric polyubiquitin [Nicotiana tabacum]

Seq. No. 267131

Contig ID 12319_1.R1011

5'-most EST LIB3079-001-Q1-K1-B12

Method BLASTX
NCBI GI 94176420
BLAST score 668
E value 5.0e-70
Match length 232
% identity 56

NCBI Description (AB008097) cytochrome P450 [Arabidopsis thaliana]

Seq. No. 267132

Contig ID 12320_1.R1011 5'-most EST ymt700221523.h1

Method BLASTX
NCBI GI g3413511
BLAST score 2287
E value 0.0e+00
Match length 537
% identity 80

NCBI Description (AJ000265) glucose-6-phosphate isomerase [Spinacia

oleracea]

Seq. No. 267133

Contig ID 12320_2.R1011

5'-most EST uC-zmflmo17076a03b1

Method BLASTX
NCBI GI g282994
BLAST score 3249
E value 0.0e+00
Match length 758



% identity Sip1 protein - barley >gi_167100 (M77475) seed imbibition NCBI Description protein [Hordeum vulgare] Seq. No. 267134 12320 4.R1011 Contig ID LIB3156-021-Q1-K1-B12 5'-most EST Method BLASTX q3413511 NCBI GI 247 BLAST score 5.0e-21 E value 53 Match length % identity 77 (AJ000265) glucose-6-phosphate isomerase [Spinacia NCBI Description oleracea] Seq. No. 267135 12320 6.R1011 Contig ID LIB143-031-Q1-E1-B8 5'-most EST BLASTX Method NCBI GI q282994 BLAST score 152 6.0e-10 E value Match length 46 57 % identity Sip1 protein - barley >gi_167100 (M77475) seed imbibition NCBI Description protein [Hordeum vulgare] Seq. No. 267136 12320 7.R1011 Contig ID hvj700620261.hl 5'-most EST 267137 Seq. No. 12322 1.R1011 Contig ID uC-zmroteosinte088c06b1 5'-most EST BLASTX Method g2129742 NCBI GI BLAST score 277 3.0e-24E value Match length 74 68 % identity stress-induced protein OZI1 precursor - Arabidopsis NCBI Description

thaliana >gi_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No definition line found [Arabidopsis thaliana]

267138 Seq. No. Contig ID 12324 1.R1011 nbm700471675.h1 5'-most EST Method BLASTX NCBI GI q3218410 BLAST score 1348 1.0e-149 E value Match length 479

% identity

55

37151



NCBI Description (AL023859) putative prolyl-trna synthetase [Schizosaccharomyces pombe]

Seq. No. 267139

Contig ID 12324_2.R1011

5'-most EST LIB3059-011-Q1-K1-A2

Method BLASTX
NCBI GI 9731640
BLAST score 176
E value 2.0e-12
Match length 100
% identity 43

NCBI Description PUTATIVE PROLYL-TRNA SYNTHETASE YHRO20W (PROLINE--TRNA

LIGASE) (PRORS) >gi_626755_pir___S46774 multifunctional amino acid--tRNA ligase homolog - yeast (Saccharomyces cerevisiae) >gi_500692 (U10399) Yhr020wp [Saccharomyces

cerevisiae]

Seq. No. 267140

Contig ID 12326_1.R1011

5'-most EST LIB3279-012-P1-K1-B8

Method BLASTX
NCBI GI 94337206
BLAST score 169
E value 1.0e-11
Match length 126
% identity 32

NCBI Description (AC006403) putative replication factor-A protein

[Arabidopsis thaliana]

Seq. No. 267141

Contig ID 12328 1.R1011 5'-most EST fC-zmf1700381538a1

Method BLASTX
NCBI GI g3367517
BLAST score 1274
E value 1.0e-141

Match length 436 % identity 52

NCBI Description (AC004392) Similar to F4I1.26 putative beta-glucosidase

gi_3128187 from A. thaliana BAC gb_AC004521. ESTs gb_N97083, gb_F19868 and gb_F15482 come from this gene.

[Arabidopsis thaliana]

Seq. No. 267142

Contig ID 12328_2.R1011 5'-most EST uC-zmflb73056g07b1

Method BLASTX
NCBI GI g4455284
BLAST score 192
E value 3.0e-18
Match length 96

Match length 96 % identity 48

NCBI Description (AL035527) beta-glucosidase-like protein [Arabidopsis

thaliana]

Seq. No. 267143



```
12329 1.R1011
Contig ID
                  LIB3079-059-Q1-K1-C9
5'-most EST
                   267144
Seq. No.
                   12332 1.R1011
Contig ID
                   uC-zm\overline{f}1B73045a06b1
5'-most EST
                   BLASTX
Method
                   q2995384
NCBI GI
                   249
BLAST score
                   2.0e-21
E value
                   55
Match length
                   91
% identity
                  (AJ004810) cytochrome P450 monooxygenase [Zea mays]
NCBI Description
                   267145
Seq. No.
Contig ID
                   12333 1.R1011
                   LIB83-006-Q1-E1-C5
5'-most EST
                   BLASTX
Method
                   g4056457
NCBI GI
                   431
BLAST score
                   3.0e-42
E value
                   137
Match length
                   64
% identity
                   (AC005990) ESTs gb 234051 and gb F13722 come from this
NCBI Description
                   gene. [Arabidopsis thaliana]
Seq. No.
                   267146
                   12333 2.R1011
Contig ID
5'-most EST
                   xmt700267388.hl
                   267147
Seq. No.
                   12339 1.R1011
Contig ID
                   uC-zmflb73292f12b1
5'-most EST
                   267148
Seq. No.
Contig ID
                   12341_1.R1011
5'-most EST
                   xjt700093407.h1
                   BLASTX
Method
NCBI GI
                   q3426045
BLAST score
                   322
                   2.0e-29
E value
Match length
                   187
                   42
% identity
                  (AC005168) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   267149
Seq. No.
                   12345 1.R1011
Contig ID
                   LIB3062-002-Q1-K2-E5
5'-most EST
Method
                   BLASTX
                   q3928150
NCBI GI
BLAST score
                   961
E value
                   1.0e-104
                   255
Match length
 % identity
                   (AJ131049) hypothetical protein [Cicer arietinum]
NCBI Description
```

37153

267150

Seq. No.



Contig ID 12348_1.R1011 5'-most EST uC-zmflb73152a09b1

Method BLASTX
NCBI GI g4572671
BLAST score 1634
E value 0.0e+00
Match length 501
% identity 62

NCBI Description (AC006954) putative cyclic nucleotide regulated ion channel

[Arabidopsis thaliana]

Seq. No. 267151

Contig ID 12350_1.R1011

5'-most EST LIB3079-059-Q1-K1-C12

Seq. No. 267152

Contig ID 12350_2.R1011

5'-most EST LIB3136-034-Q1-K1-D3

Seq. No. 267153

Contig ID 12356 1.R1011

5'-most EST LIB3079-058-Q1-K1-F3

Seq. No. 267154

Contig ID 12367_1.R1011

5'-most EST uC-zmf1B73022b06b1

Seq. No. 267155

Contig ID 12367 2.R1011

5'-most EST uC-zmflmo17118f10b1

Seq. No. 267156

Contig ID 12367_3.R1011 5'-most EST nbm700469682.h1

Seq. No. 267157

Contig ID 12368_1.R1011 5'-most EST hvj700623850.h1

Seq. No. 267158

Contig ID 12374_1.R1011

5'-most EST uC-zmflm017214d09b1

Method BLASTX
NCBI GI g2829911
BLAST score 685
E value 6.0e-72
Match length 175
% identity 73

NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No. 267159

Contig ID 12375_1.R1011 5'-most EST uC-zmflb73049c06b1

Seq. No. 267160

Contig ID 12376_1.R1011 5'-most EST wty700169543.h1



BLASTX Method q2462762 NCBI GI 862 BLAST score 2.0e-92 E value Match length 337 53 % identity (AC002292) Highly similar to auxin-induced protein NCBI Description (aldo/keto reductase family) [Arabidopsis thaliana] 267161 Seq. No. 12376_2.R1011 Contig ID $dyk70\overline{0}102202.h1$ 5'-most EST BLASTX

Method g2462741 NCBI GI 690 BLAST score 1.0e-72 E value 208 Match length 66 % identity

(AC002292) Highly similar to auxin-induced protein NCBI Description (aldo/keto reductase family) [Arabidopsis thaliana]

267162 Seq. No. 12376 3.R1011

Contig ID LIB3088-004-Q1-K1-F5

5'-most EST

BLASTX Method g2462761 NCBI GI BLAST score 206 3.0e-16 E value 84 Match length 51 % identity

(AC002292) Highly similar to auxin-induced protein NCBI Description (aldo/keto reductase family) [Arabidopsis thaliana]

267163 Seq. No.

12382 1.R1011 Contig ID

5'-most EST LIB3066-043-Q1-K1-B7

Method BLASTN q3821780 NCBI GI 35 BLAST score 1.0e-09 E value 35 Match length % identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

267164 Seq. No.

12385 1.R1011 Contig ID

LIB143-001-Q1-E1-A3 5'-most EST

267165 Seq. No.

12390 1.R1011 Contia ID

LIB3079-056-Q1-K1-F2 5'-most EST

267166 Seq. No.

12400 1.R1011 Contig ID

LIB3079-056-Q1-K1-E12 5'-most EST

BLASTX Method g4115934 NCBI GI

37155



595 BLAST score 2.0e-61 E value Match length 127 % identity 81

(AF118223) contains similarity to Methanobacterium NCBI Description

thermoautotrophicum transcriptional regulator (GB:AE000850)

[Arabidopsis thaliana]

267167 Seq. No.

12400 2.R1011 Contig ID

uC-zmflmo17268d11b1 5'-most EST

267168 Seq. No.

12400 3.R1011 Contig ID mwy700442817.hl 5'-most EST

BLASTX Method q4115934 NCBI GI BLAST score 445 5.0e-44E value 91 Match length 82 % identity

(AF118223) contains similarity to Methanobacterium NCBI Description

thermoautotrophicum transcriptional regulator (GB:AE000850)

[Arabidopsis thaliana]

267169 Seq. No.

12408 1.R1011 Contig ID

LIB3079-056-Q1-K1-E10 5'-most EST

267170 Seq. No.

12413 1.R1011 Contig ID

uC-zmflmo17092c10a1 5'-most EST

267171 Seq. No.

12417 1.R1011 Contig ID rvt700550577.h1 5'-most EST

BLASTX Method g399940 NCBI GI 1998 BLAST score 0.0e + 00E value 505 Match length 83 % identity

MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR NCBI Description

>gi_100004_pir__S25005 heat shock protein, 70K - kidney bean >gi_22636_emb_CAA47345_ (X66874) 70 kDa heat shock protein [Phaseolus vulgaris]

267172 Seq. No.

12417 3.R1011 Contig ID vmt700219168.hl 5'-most EST

BLASTX Method q399940 NCBI GI BLAST score 756 2.0e-80 · E value Match length 178 % identity

NCBI Description MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR



>gi_100004_pir__S25005 heat shock protein, 70K - kidney bean >gi_22636_emb_CAA47345_ (X66874) 70 kDa heat shock protein [Phaseolus vulgaris]

Seq. No. 267173

Contig ID 12417_5.R1011

5'-most EST LIB3079-053-Q1-K1-C9

Method BLASTX
NCBI GI g585272
BLAST score 150
E value 2.0e-09
Match length 118
% identity 36

NCBI Description MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR

>gi_20835_emb_CAA38536_ (X54739) HSP70 [Pisum sativum]

Seq. No. 267174

Contig ID 12420_1.R1011 5'-most EST qmh700029667.f1

Seq. No. 267175

Contig ID 12420 2.R1011

5'-most EST LIB31 $\overline{5}$ 1-007-Q1-K1-F7

Seq. No. 267176

Contig ID 12420 3.R1011

5'-most EST LIB3180-015-P2-M1-H10

Seq. No. 267177

Contig ID 12424 1.R1011

5'-most EST LIB3067-044-Q1-K1-C5

Method BLASTX
NCBI GI g2290202
BLAST score 347
E value 2.0e-32
Match length 134

Match length 134 % identity 54

NCBI Description (U87148) nucellin [Hordeum vulgare] >gi_2290204 (U87149)

nucellin [Hordeum vulgare]

Seq. No. 267178

Contig ID 12424_2.R1011

5'-most EST uC-zmflmo17187b07b1

Method BLASTX
NCBI GI 9465740
BLAST score 245
E value 2.0e-20
Match length 220
% identity 15

NCBI Description HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III

>gi_630513_pir__S44609 hypothetical protein C02F5.7 Caenorhabditis elegans >gi_289614 (L14745) homology with
glucose induced repressor, GRR1; putative [Caenorhabditis

elegans]

Seq. No. 267179

Contig ID 12426 1.R1011



```
LIB3137-005-Q1-K1-A5
5'-most EST
                  BLASTX
Method
                  q3236237
NCBI GI
                  928
BLAST score
                  1.0e-100
E value
                  318
Match length
                  56
% identity
                  (AC004684) putative ribotol dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
                   267180
Seq. No.
                  12426 2.R1011
Contig ID
                  LIB189-015-Q1-E1-A8
5'-most EST
                  BLASTX
Method
                  q629592
NCBI GI
                   209
BLAST score
                   2.0e-16
E value
                   67
Match length
                   60
% identity
NCBI Description hypothetical protein - rape
                   267181
Seq. No.
                   12426 4.R1011
Contig ID
                   clt70\overline{0}042660.f1
5'-most EST
                   267182
Seq. No.
                   12434 1.R1011
Contig ID
                   LIB3079-055-Q1-K1-F7
5'-most EST
                   BLASTX
Method
                   q4559368
NCBI GI
                   273
BLAST score
                   7.0e-24
E value
                   178
Match length
                   38
% identity
NCBI Description (AC006585) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   267183
                   12443 1.R1011
Contig ID
5'-most EST
                   LIB3180-034-P2-M2-C5
                   BLASTX
Method
                   g1019946
NCBI GI
BLAST score
                   1082
                   1.0e-118
E value
Match length
                   274
 % identity
                   75
NCBI Description (U37060) ascorbate peroxidase [Gossypium hirsutum]
 Seq. No.
                   267184
                   12445 1.R1011
 Contig ID
                   pmx700086685.h1
 5'-most EST
                   BLASTX
 Method
 NCBI GI
                   g1749546
                   219
 BLAST score
                   4.0e-17
 E value
                   97
 Match length
                   51
 % identity
```

NCBI Description (D89169) similar to Saccharomyces cerevisiae SCD6 protein,



SWISS-PROT Accession Number P45978 [Schizosaccharomyces pombe]

267185 Seq. No.

12446 1.R1011 Contig ID

uC-zmflmo17011d03b1 5'-most EST

267186 Seq. No.

12451_1.R1011 Contig ID

LIB3079-038-Q1-K1-G8 5'-most EST

267187 Seq. No.

12453 1.R1011 Contig ID

LIB3150-037-Q1-N1-E11 5'-most EST

BLASTX Method g1620753 NCBI GI 227 BLAST score 2.0e-18 E value 60 Match length

65 % identity

(U72942) proteinase inhibitor [Oryza sativa] NCBI Description

>gi 2829212 gb_AAC00503_ (AF044059) proteinase inhibitor

[Oryza sativa]

267188 Seq. No.

12453 2.R1011 Contig ID

LIB3059-001-Q1-K2-D3 5'-most EST

BLASTX Method g1620753 NCBI GI 182 BLAST score 4.0e-13 E value Match length 50 64 % identity

(U72942) proteinase inhibitor [Oryza sativa] NCBI Description

>gi_2829212_gb_AAC00503_ (AF044059) proteinase inhibitor

[Oryza sativa]

267189 Seq. No.

12453 4.R1011 Contig ID xmt700262222.hl 5'-most EST

BLASTX Method NCBI GI g1620753 BLAST score 223 6.0e-18 E value 63 Match length 62 % identity

(U72942) proteinase inhibitor [Oryza sativa] NCBI Description

>gi 2829212 gb_AAC00503_ (AF044059) proteinase inhibitor

[Oryza sativa]

267190 Seq. No.

Contig ID 12454 1.R1011

LIB3079-055-Q1-K1-C8 5'-most EST

267191 Seq. No.

12455 1.R1011 Contig ID

LIB3060-036-Q1-K1-D12 5'-most EST



```
BLASTX
Method
                  g4249733
NCBI GI
BLAST score
                  207
                   1.0e-15
E value
Match length
                   265
% identity
                  (AF109377) ldlBp [Mus musculus]
NCBI Description
                   267192
Seq. No.
                   12456 1.R1011
Contig ID
                   uC-zmflmo17101b04b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4262167
                   1113
BLAST score
                   1.0e-121
E value
                   674
Match length
                   41
% identity
                   (AC005275) putative LRR receptor-linked protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   267193
Seq. No.
                   12459 1.R1011
Contig ID
                   LIB3137-011-Q1-K1-G2
5'-most EST
                   267194
Seq. No.
                   12466 1.R1011
Contig ID
                   hvj700620965.h1
5'-most EST
                   BLASTX
Method
                   g1931654
NCBI GI
BLAST score
                   403
                   1.0e-39
E value
                   185
Match length
                   48
 % identity
                   (U95973) BRCA1-associated RING domain protein isolog
NCBI Description
                    [Arabidopsis thaliana]
                   267195
 Seq. No.
                   12469 1.R1011
 Contig ID
                   LIB3079-055-Q1-K1-B5
 5'-most EST
 Method
                   BLASTX
                    q4512348
 NCBI GI
                    836
 BLAST score
                    2.0e-89
 E value
                    302
 Match length
                    55
 % identity
                   (AB011836) similar to B.subtilis yerM gene(84%-identity)
 NCBI Description
                    [Bacillus halodurans]
                    267196
 Seq. No.
                    12470_1.R1011
 Contig ID
                    LIB143-068-Q1-E1-B3
 5'-most EST
                    BLASTX
 Method
                    g3850999
 NCBI GI
                    1773
 BLAST score
                    0.0e+00
 E value
```

37160

373

94

Match length

% identity



NCBI Description (AF069908) pyruvate dehydrogenase E1 beta subunit isoform 1 [Zea mays]

Seq. No. 267197

Contig ID 12472_1.R1011 5'-most EST zuv700354842.h1

Method BLASTX
NCBI GI g3023522
BLAST score 1137
E value 1.0e-124
Match length 448
% identity 50

NCBI Description COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)

(P102) >gi_2454309 (AF002705) beta prime COP [Rattus

norvegicus]

Seq. No. 267198

Contig ID 12472_2.R1011

5'-most EST LIB3067-019-Q1-K1-C2

Seq. No. 267199

Contig ID 12472 3.R1011 5'-most EST gwl700614289.h1

Seq. No. 267200

Contig ID 12472_4.R1011

5'-most EST LIB3115-038-P1-K2-H4

Seq. No. 267201

Contig ID 12472_7.R1011 5'-most EST ymt700222939.h1

Seq. No. 267202

Contig ID 12474 1.R1011

5'-most EST LIB3150-100-P1-N1-E2

Seq. No. 267203

Contig ID 12476_1.R1011 5'-most EST wyr700241578.h1

Method BLASTX
NCBI GI g3548803
BLAST score 1264
E value 1.0e-140
Match length 313
% identity 78

NCBI Description (AC005313) putative DNA-binding protein [Arabidopsis

thaliana] >gi_4335770_gb_AAD17447_ (AC006284) putative SMUBP-2 [mouse] DNA-binding protein [Arabidopsis thaliana]

Seq. No. 267204

Contig ID 12477_1.R1011

5'-most EST LIB3079-054-Q1-K1-H10

Method BLASTX
NCBI GI g3935184
BLAST score 367
E value 4.0e-35
Match length 124

37161



% identity 56 (AC004557) F17L21.27 [Arabidopsis thaliana] NCBI Description 267205 Seq. No. 12479 1.R1011 Contig ID qw1700612939.h1 5'-most EST BLASTX Method g1176485

NCBI GI 147 BLAST score 7.0e-09 E value 103 Match length 40 % identity

HYPOTHETICAL 16.2 KD PROTEIN IN IME2-MEF2 INTERGENIC REGION NCBI Description >gi_1078244_pir__S53383 probable membrane protein YJL104w -

yeast (Saccharomyces cerevisiae) >gi_728706_emb_CAA59390_

(X85021) orf 8 [Saccharomyces cerevisiae] >qi 1009450 emb CAA89399_ (Z49379) ORF YJL104w

[Saccharomyces cerevisiae]

267206 Seq. No.

12480 1.R1011 Contig ID

LIB3079-054-Q1-K1-H3 5'-most EST

BLASTN Method g2104711 NCBI GI 538 BLAST score 0.0e+00E value 584 Match length % identity 98

Zea mays endosperm specific protein mRNA, complete cds NCBI Description

267207 Seq. No.

12481 1.R1011 Contig ID

LIB3079-054-Q1-K1-H4 5'-most EST

267208 Seq. No.

12486 1.R1011 Contig ID 5'-most EST dyk700104148.h1

267209 Seq. No.

12489 1.R1011 Contig ID

5'-most EST LIB3115-016-P1-K1-H7

BLASTX Method q560610 NCBI GI 180 BLAST score 3.0e-13E value 58 Match length 52 % identity

NCBI Description trypsin inhibitor, WTI [Triticum aestivum=wheat, variety

San Pastore, endosperm, Peptide, 71 aa]

267210 Seq. No.

12490 1.R1011 Contig ID $uC-zm\overline{f}lmo17074g11b1$ 5'-most EST

BLASTX Method NCBI GI g4006926 BLAST score 636 E value 4.0e-66



```
Match length
                  227
% identity
                  (Z99708) putative protein (fragment) [Arabidopsis thaliana]
NCBI Description
                  267211
Seq. No.
                  12491 1.R1011
Contig ID
                  LIB30\overline{7}9-054-Q1-K1-F3
5'-most EST
                   BLASTX
Method
                   g3650037
NCBI GI
                   391
BLAST score
                   9.0e-38
E value
                   104
Match length
                   75
% identity
                   (ACO05396) auxin-responsive GH3-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   267212
Seq. No.
                   12498 1.R1011
Contig ID
                   wty700166246.hl
5'-most EST
                   BLASTX
Method
                   q1256771
NCBI GI
                   580
BLAST score
                   1.0e-59
E value
Match length
                   196
                   54
% identity
                   (U51270) COP9 [Spinacia oleracea]
NCBI Description
Seq. No.
                   267213
                   12499 1.R1011
Contig ID
                   tbg700930453.hl
5'-most EST
                   267214
Seq. No.
                   12500 1.R1011
Contig ID
                   LIB3079-054-Q1-K1-G2
5'-most EST
                   267215
Seq. No.
                   12503_1.R1011
Contig ID
                   xjt700096753.hl
 5'-most EST
Method
                   BLASTX
                   g2293332
NCBI GI
                    307
BLAST score
                   2.0e-27
E value
                   206
Match length
                    37
 % identity
NCBI Description (AF011338) unknown [Dictyostelium discoideum]
                    267216
 Seq. No.
                    12509 1.R1011
 Contig ID
                    uC-zmflb73137h07b1
 5'-most EST
                    BLASTX
 Method
                    g4263820
 NCBI GI
                    168
 BLAST score
                    1.0e-11
 E value
                    87
 Match length
```

NCBI Description (AC006067) hypothetical protein [Arabidopsis thaliana]

41

% identity



 Seq. No.
 267217

 Contig ID
 12510_1.R1011

 5'-most EST
 yyf700352579.h1

Seq. No. 267218

Contig ID 12512_1.R1011

5'-most EST LIB3079-054-Q1-K1-E6

Seq. No. 267219

Contig ID 12515_1.R1011 5'-most EST uC-zmflb73061c08b1

Method BLASTX
NCBI GI g1350680
BLAST score 1338
E value 1.0e-148
Match length 397

% identity 64

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 267220

Contig ID 12515 2.R1011 5'-most EST tfd700571112.h1

Method BLASTX
NCBI GI g1350680
BLAST score 378
E value 5.0e-36
Match length 132
% identity 56

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 267221

Contig ID 12515_3.R1011

5'-most EST LIB3069-017-Q1-K1-H9

Method BLASTX
NCBI GI g1350680
BLAST score 493
E value 1.0e-49
Match length 119

% identity 75

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 267222

Contig ID 12515_4.R1011

5'-most EST LIB3059-028-Q1-K1-A3

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 48
% identity 67

% identity 67 NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 267223

Contig ID 12515_5.R1011 5'-most EST zuv700355311.h1

Method BLASTX NCBI GI g1350680



```
BLAST score
                   246
                   8.0e-23
E value
                   70
Match length
                   80
% identity
                   60S RIBOSOMAL PROTEIN L1
NCBI Description
                   267224
Seq. No.
                   12516 1.R1011
Contig ID
                   uC-zm\overline{f}lMo17019e12b1
5'-most EST
                   BLASTX
Method
                   g4559339
NCBI GI
BLAST score
                   813
                   9.0e-87
E value
                   182
Match length
                   87
% identity
                   (AC007087) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                   thaliana]
                   267225
Seq. No.
                   12518 1.R1011
Contig ID
                   hbs701184605.h1
5'-most EST
                   BLASTX
Method
                   g4567275
NCBI GI
BLAST score
                   154
                   4.0e-10
E value
                   118
Match length
                   36
% identity
                   (AC006841) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   267226
                   12520 1.R1011
Contig ID
                   ntr700075216.hl
5'-most EST
                   267227
Seq. No.
                   12523_1.R1011
Contig ID
                   xsy700212447.h1
5'-most EST
                   BLASTX
Method
                   g1244716
NCBI GI
                   787
BLAST score
                   1.0e-87
E value
                   214
Match length
                   78
% identity
                  (U42336) ACC synthase [Triticum aestivum]
NCBI Description
                   267228
Seq. No.
                    12524 1.R1011
Contig ID
                   uC-zm\overline{f}1b73164h05b2
5'-most EST
                   BLASTX
Method
                    q2494034
NCBI GI
BLAST score
                    1123
                    1.0e-157
E value
                    407
Match length
 % identity
                    66
                   DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG
NCBI Description
```

diacylglycerol kinase [Arabidopsis thaliana]

KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase - Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787)

E value

Match length % identity

5.0e-61 229

49



```
267229
Seq. No.
Contig ID
                  12528 1.R1011
5'-most EST
                  cat700020295.r1
                  BLASTX
Method
NCBI GI
                  g2827477
                  223
BLAST score
                  4.0e-18
E value
                  127
Match length
% identity
                  26
NCBI Description (AL009147) EG:171D11.3 [Drosophila melanogaster]
Seq. No.
                  267230
                  12528 2.R1011
Contig ID
5'-most EST
                  uC-zmroteosinte067g04b1
                  BLASTX
Method
NCBI GI
                  q4503007
BLAST score
                  157
                  2.0e-10
E value
Match length
                  144
% identity
                  28
NCBI Description carboxypeptidase D >gi 2462777 (U65090) carboxypeptidase D
                  [Homo sapiens]
                  267231
Seq. No.
Contig ID
                  12529 1.R1011
5'-most EST
                  pwr700450235.hl
                  BLASTX
Method
                  q4185140
NCBI GI
BLAST score
                  411
E value
                  5.0e-40
Match length
                  88
% identity
                  91
NCBI Description (AC005724) putative small nuclear ribonucleoprotein E
                  (snRNP-E) [Arabidopsis thaliana]
                  267232
Seq. No.
                  12529 2.R1011
Contig ID
5'-most EST
                  wyr700236247.hl
                  BLASTX
Method
NCBI GI
                  q4185140
BLAST score
                  393
E value
                  6.0e-38
Match length
                  84
% identity
NCBI Description (AC005724) putative small nuclear ribonucleoprotein E
                  (snRNP-E) [Arabidopsis thaliana]
Seq. No.
                  267233
Contig ID
                  12530 1.R1011
5'-most EST
                  ntr700073973.hl
                  BLASTX
Method
NCBI GI
                  q4140326
                  592
BLAST score
```



(AL031282) dJ283E3.6.1 (PUTATIVE novel protein similar to NCBI Description many (archae) bacterial, worm and yeast hypothetical proteins) [Homo sapiens] 267234 Seq. No. 12530 2.R1011 Contig ID uC-zmflmo17205b01a1 5'-most EST 267235 Seq. No. 12531 1.R1011 Contig ID LIB3279-016-P1-K1-D10 5'-most EST BLASTX Method g3024430 NCBI GI 880 BLAST score 1.0e-94 E value 265 Match length 68 % identity PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) NCBI Description >gi_1928962 (U92287) pyrroline-5-carboxylate reductase [Actinidia deliciosa] 267236 Seq. No. 12536 1.R1011 Contig ID LIB3079-054-Q1-K1-A9 5'-most EST BLASTX Method q4490325 NCBI GI 479 BLAST score 7.0e-48E value 137 Match length 62 % identity (AL035656) hypothetical protein [Arabidopsis thaliana] NCBI Description 267237 Seq. No. 12542 1.R1011 Contig ID LIB3079-054-Q1-K1-B6 5'-most EST BLASTX Method NCBI GI q1173137 851 BLAST score 2.0e-91 E value 173 Match length 92 % identity NCBI Description DNA-DIRECTED RNA POLYMERASE II 19 KD POLYPEPTIDE (RNA POLYMERASE II SUBUNIT 5) >gi 322700 pir B44457 RNA polymerase II fifth largest subunit - Glycine max=soybeans >gi 170052 (M90504) RNA polymerase II [Glycine max] 267238 Seq. No. 12545 1.R1011

Contig ID

LIB3079-053-Q1-K1-G11 5'-most EST

BLASTX Method q4335761 NCBI GI 414 BLAST score E value 3.0e-40282 Match length 34 % identity

NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]



```
267239
Seq. No.
                  12550 1.R1011
Contig ID
5'-most EST
                  LIB3069-004-Q1-K1-E5
                  267240
Seq. No.
                  12550 2.R1011
Contig ID
5'-most EST
                  uer700583407.hl
Seq. No.
                  267241
                  12559 1.R1011
Contig ID
                  hbs701183253.hl
5'-most EST
                  BLASTX
Method
                  g3414809
NCBI GI
                  206
BLAST score
                  7.0e-16
E value
                  151
Match length
% identity
                  6
NCBI Description (AF061529) rjs [Mus musculus]
Seg. No.
                  267242
Contig ID
                  12563 1.R1011
5'-most EST
                  LIB3069-017-Q1-K1-H3
Method
                  BLASTX
NCBI GI
                  g3953478
BLAST score
                  189
                  6.0e-26
E value
Match length
                  90
% identity
                  73
NCBI Description (AC002328) F2202.23 [Arabidopsis thaliana]
Seq. No.
                  267243
Contig ID
                  12565 1.R1011
5'-most EST
                  LIB3079-053-Q1-K1-D3
                  BLASTX
Method
NCBI GI
                  g2652938
BLAST score
                  319
E value
                  1.0e-29
Match length
                  75
                  80
% identity
NCBI Description (Z47554) orf [Zea mays]
                  267244
Seq. No.
                  12569 1.R1011
Contig ID
5'-most EST
                  ymt700221747.hl
Method
                  BLASTX
                  q4584358
NCBI GI
BLAST score
                  728
E value
                  5.0e-77
Match length
                  213
% identity
                  74
NCBI Description (AC006420) unknown protein [Arabidopsis thaliana]
Seq. No.
                  267245
```

12579 1.R1011 Contig ID 5'-most EST wyr700242764.hl

Method BLASTX NCBI GI g3128234



BLAST score 364
E value 2.0e-49
Match length 179
% identity 59

NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana]

Seq. No. 267246

Contig ID 12585 1.R1011

5'-most EST LIB3079-053-Q1-K1-A7

Seq. No. 267247

Contig ID 12587 2.R1011 5'-most EST uC-zmrob73012g01b1

Method BLASTX
NCBI GI g4574320
BLAST score 177
E value 1.0e-12
Match length 81
% identity 56

NCBI Description (AF117224) wound-induced protein WI12 [Mesembryanthemum

crystallinum]

Seq. No. 267248

Contig ID 12590_1.R1011 5'-most EST cyk700047474.f1

Method BLASTX
NCBI GI g3413700
BLAST score 1241
E value 1.0e-137
Match length 326
% identity 75

NCBI Description (AC004747) putative YME1 protein [Arabidopsis thaliana]

Seq. No. 267249

Contig ID 12590_2.R1011

5'-most EST LIB3115-012-Q1-K1-E12

Seq. No. 267250

Contig ID 12593_1.R1011 5'-most EST yyf700351496.h1

Method BLASTX
NCBI GI g3341692
BLAST score 415
E value 6.0e-40
Match length 161
% identity 55

NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 267251

Contig ID 12595_1.R1011

5'-most EST LIB3079-052-Q1-K1-G3

Seq. No. 267252

Contig ID 12602_1.R1011 5'-most EST cyk700052080.f1

Method BLASTX NCBI GI g4507857



BLAST score 206 E value 1.0e-15 Match length 302 % identity 27

NCBI Description Herpes virus-associated ubiquitin-specific protease >gi 2501460 sp Q93009 UBPH HUMAN PROBABLE UBIQUITIN

CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) >gi_1545952_emb_CAA96580_

(Z72499) herpesvirus associated ubiquitin-specific protease

(HAUSP) [Homo sapiens]

Seq. No. 267253

Contig ID 12602 2.R1011

5'-most EST LIB3137-008-Q1-K1-C2

Method BLASTX
NCBI GI g3395938
BLAST score 313
E value 9.0e-29
Match length 92
% identity 35

NCBI Description (AF076924) polypyrimidine tract-binding protein homolog

[Arabidopsis thaliana]

Seq. No. 267254

Contig ID 12602_3.R1011

5'-most EST uC-zmflmo17066b12b1

Method BLASTX
NCBI GI g3860998
BLAST score 270
E value 6.0e-23
Match length 159
% identity 33

NCBI Description (AJ235271) unknown [Rickettsia prowazekii]

Seq. No. 267255

Contig ID 12602_4.R1011 5'-most EST uC-zmflb73124h02b1

Method BLASTX
NCBI GI g1730878
BLAST score 359
E value 2.0e-34
Match length 211
% identity 40

NCBI Description HYPOTHETICAL 69.1 KD PROTEIN (ORF4)

>gi_1200047_emb_CAA64951_ (X95649) function unknown

[Corynebacterium glutamicum]

Seq. No. 267256

Contig ID 12602_5.R1011 5'-most EST rvt700550945.h1

Method BLASTX
NCBI GI g3395938
BLAST score 430
E value 2.0e-42
Match length 104



% identity 39

(AF076924) polypyrimidine tract-binding protein homolog NCBI Description [Arabidopsis thaliana]

267257 Seq. No.

12602 6.R1011 Contig ID

LIB3069-026-Q1-K1-H9 5'-most EST

BLASTX Method g3395938 NCBI GI 210 BLAST score 2.0e-16 E value 58 Match length 71 % identity

(AF076924) polypyrimidine tract-binding protein homolog NCBI Description

[Arabidopsis thaliana]

267258 Seq. No.

12603 1.R1011 Contig ID

LIB3137-030-Q1-K1-H3 5'-most EST

BLASTX Method NCBI GI g113220 BLAST score 1915 E value 0.0e+00376 Match length % identity 98

ACTIN 1 >gi 71640 pir ATZM1 actin - maize NCBI Description

Seq. No. 267259

12603 2.R1011 Contig ID

LIB3279-010-P1-K1-C3 5'-most EST

BLASTX Method NCBI GI g1703108 BLAST score 433 2.0e-42 E value 88 Match length 93 % identity

NCBI Description

ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis

thaliana]

267260 Seq. No.

12603 3.R1011 Contig ID uC-zmflb73201a09b1 5'-most EST

Method BLASTX NCBI GI g1531674 BLAST score 687 E value 2.0e-72 Match length 134 % identity

NCBI Description (U68462) actin [Striga asiatica]

267261 Seq. No.

Contig ID 12603 7.R1011 uC-zmflb73226a05b1 5'-most EST

Method BLASTX



NCBI GI g1498384 488 BLAST score 1.0e-54 E value Match length 126 90 % identity

(U60508) actin [Zea mays] NCBI Description

Seq. No. 267262

12603 8.R1011 Contig ID 5'-most EST uC-zmflb73350d11a1

Seq. No. 267263

12604 1.R1011 Contig ID

LIB143-002-Q1-E1-B12 5'-most EST

Method BLASTX NCBI GI g3860319 BLAST score 1481 E value 1.0e-165 Match length 369

% identity 80

(AJ012686) nucleolar protein [Cicer arietinum] NCBI Description

Seq. No. 267264

Contig ID 12604 3.R1011

LIB3067-045-Q1-K1-C12 5'-most EST

Method BLASTX NCBI GI g3860319 BLAST score 193 E value 2.0e-14 57 Match length 65 % identity

(AJ012686) nucleolar protein [Cicer arietinum] NCBI Description

267265 Seq. No.

12604 4.R1011 Contig ID 5'-most EST hvj700623109.h1

Seq. No. 267266

12604 5.R1011 Contig ID 5'-most EST yyf700348129.h1

BLASTX Method NCBI GI g3860319 BLAST score 327 E value 1.0e-30 Match length 86 % identity 76

NCBI Description (AJ012686) nucleolar protein [Cicer arietinum]

267267 Seq. No.

12604_6.R1011 Contig ID

5'-most EST LIB3067-018-Q1-K1-G6

BLASTX Method NCBI GI q4160346 BLAST score 262 E value 1.0e-22 Match length 119 % identity 48

% identity

62



```
(AL035216) nucleolar protein involved in pre-rRNA
NCBI Description
                  processing [Schizosaccharomyces pombe]
                  267268
Seq. No.
                  12604 7.R1011
Contig ID
                  uC-zmflb73255f04b1
5'-most EST
                  BLASTX
Method
                  g3860319
NCBI GI
BLAST score
                  392
                  7.0e-38
E value
                  114
Match length
                  72
% identity
NCBI Description (AJ012686) nucleolar protein [Cicer arietinum]
                  267269
Seq. No.
                  12604 9.R1011
Contig ID
                  tzu70\overline{0}204175.h1
5'-most EST
                  BLASTX
Method
                   g2811001
NCBI GI
BLAST score
                   174
                   6.0e-19
E value
Match length
                   66
                   69
% identity
                  NUCLEOLAR PROTEIN NOP56 >gi 2230878_emb_CAA72789_ (Y12065)
NCBI Description
                  hNop56 [Homo sapiens]
Seq. No.
                   267270
                   12605 1.R1011
Contig ID
                  LIB3068-005-Q1-K1-G5
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3024894
BLAST score
                   229
                   2.0e-18
E value
Match length
                   164
                   37
% identity
NCBI Description HYPOTHETICAL 54.8 KD PROTEIN CY20H10.28C
Seq. No.
                   267271
                   12605 2.R1011
Contig ID
5'-most EST
                   LIB3115-025-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   g3024894
BLAST score
                   207
E value
                   3.0e-16
Match length
                   154
% identity
NCBI Description HYPOTHETICAL 54.8 KD PROTEIN CY20H10.28C
Seq. No.
                   267272
                   12606 1.R1011
Contig ID
                   wyr700239551.h1
5'-most EST
Method
                   BLASTX
                   g4220527
NCBI GI
BLAST score
                   872
                   1.0e-93
E value
Match length
                   256
```



```
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
                  267273
Seq. No.
                  12614 1.R1011
Contig ID
                  LIB143-039-Q1-E1-D7
5'-most EST
                   267274
Seq. No.
                   12620 1.R1011
Contig ID
                  LIB3079-052-Q1-K1-B8
5'-most EST
                   BLASTX
Method
                   g2979553
NCBI GI
BLAST score
                   371
                   2.0e-35
E value
                   156
Match length
                   48
% identity
                  (AC003680) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   267275
Seq. No.
                   12624 1.R1011
Contig ID
                   xdb700339376.h1
5'-most EST
                   267276
Seq. No.
                   12625 1.R1011
Contig ID
                   yyf70\overline{0}350921.h1
5'-most EST
                   BLASTX
Method
                   q1084952
NCBI GI
BLAST score
                   258
                   2.0e-21
E value
                   209
Match length
                   31
% identity
                   hypothetical protein YPR031w - yeast (Saccharomyces
NCBI Description
                   cerevisiae) >gi_809596_emb_CAA89285_ (Z49274) unknown
                   [Saccharomyces cerevisiae] > gi 1314105_emb_CAA95027_
                   (Z71255) unknown [Saccharomyces cerevisiae]
Seq. No.
                   267277
                   12630 1.R1011
Contig ID
5'-most EST
                   uC-zmroB73015c04b1
                   BLASTX
Method
NCBI GI
                   q1362051
BLAST score
                   1255
E value
                   1.0e-139
                   273
Match length
                   85
% identity
                   protein kinase 3 - soybean >gi 310582 (L19361) protein
NCBI Description
                   kinase 3 [Glycine max]
                   267278
Seq. No.
                   12630 2.R1011
Contig ID
                   LIB3150-050-Q1-N1-E9
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2129803
                   353
BLAST score
                   5.0e-33
E value
                   101
Match length
                   66
% identity
```

NCBI Description probable serine/threonine-specific protein kinase (EC



2.7.1.-) BSK2 - rape >gi_289374 (L12394) serine/threonine protein kinase [Brassica napus] >gi_1097354_prf__2113401B protein kinase [Brassica napus]

Seq. No. 267279

Contig ID 12634 1.R1011

5'-most EST LIB3079-052-Q1-K1-A12

Seq. No. 267280

Contig ID 12638_1.R1011 5'-most EST xmt700260417.h1

Method BLASTX
NCBI GI g3116020
BLAST score 735
E value 7.0e-78
Match length 207
% identity 72

NCBI Description (Y15383) FtsZ protein [Pisum sativum]

Seq. No. 267281

Contig ID 12638_3.R1011 5'-most EST pwr700452565.h1

Method BLASTX
NCBI GI g3116020
BLAST score 318
E value 3.0e-29
Match length 79
% identity 85

NCBI Description (Y15383) FtsZ protein [Pisum sativum]

Seq. No. 267282

Contig ID 12641_1.R1011 5'-most EST uC-zmrob73012g07b1

Method BLASTX
NCBI GI g2245087
BLAST score 161
E value 4.0e-11
Match length 80
% identity 40

NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No. 267283

Contig ID 12644_1.R1011

5'-most EST LIB3069-035-Q1-K1-B7

Method BLASTX
NCBI GI g1169546
BLAST score 186
E value 1.0e-13
Match length 150
% identity 33

NCBI Description PUTATIVE ER LUMEN PROTEIN RETAINING RECEPTOR C28H8.4

>gi_669010 (U20861) similar to endoplasmic reticulum lumen

protein retaining receptor [Caenorhabditis elegans]

Seq. No. 267284

Contig ID 12644 2.R1011

5'-most EST LIB3067-060-Q1-K1-H11



Method BLASTX
NCBI GI g4105782
BLAST score 181
E value 6.0e-13
Match length 118
% identity 36

NCBI Description (AF049922) PGP169-12 [Petunia x hybrida]

Seq. No. 267285

Contig ID 12644 3.R1011

5'-most EST uC-zmroteosinte092f05b2

Method BLASTX
NCBI GI g4490331
BLAST score 443
E value 6.0e-44
Match length 117
% identity 75

NCBI Description (AL035656) hypothetical protein [Arabidopsis thaliana]

Seq. No. 267286

Contig ID 12657_1.R1011 5'-most EST tfd700572330.h1

Seq. No. 267287

Contig ID 12662_1.R1011

5'-most EST LIB3079-051-Q1-K1-B12

Seq. No. 267288

Contig ID 12663_1.R1011 5'-most EST cat700018563.r1

Method BLASTN
NCBI GI g2586142
BLAST score 46
E value 2.0e-16
Match length 54
% identity 96

NCBI Description Musa acuminata ripening-associated protein mRNA, partial

cds

Seq. No. 267289

Contig ID 12663_2.R1011

5'-most EST LIB3069-027-Q1-K1-B10

Seq. No. 267290

Contig ID 12663_4.R1011 5'-most EST nwy700443818.h1

Seq. No. 267291

Contig ID 12673_1.R1011

5'-most EST LIB3079-050-Q1-K1-F6

Method BLASTX
NCBI GI g2429483
BLAST score 155
E value 8.0e-10
Match length 151
% identity 27

NCBI Description (AF025464) No definition line found [Caenorhabditis



elegans]

267292 Seq. No. 12674 1.R1011 Contig ID LIB3079-050-Q1-K1-C5 5'-most EST BLASTX Method g3643610 NCBI GI 803 BLAST score 5.0e-86 E value 168

88 % identity (AC005395) putative serine/threonine protein kinase NCBI Description

[Arabidopsis thaliana]

267293 Seq. No.

Match length

12681 1.R1011 Contig ID

LIB3079-049-Q1-K1-H5 5'-most EST

BLASTX Method q4200249 NCBI GI BLAST score 221 1.0e-17 E value 158 Match length 34 % identity

NCBI Description (AL035297) hypothetical protein [Homo sapiens]

267294 Seq. No.

12682 1.R1011 Contig ID

uC-zmflmo17332e03a1 5'-most EST

267295 Seq. No.

12682 2,R1011 Contig ID

LIB3088-011-Q1-K1-B5 5'-most EST

267296 Seq. No.

12683 1.R1011 Contig ID

uC-zmflmo17342g04b1 5'-most EST

BLASTX Method q4582436 NCBI GI 440 BLAST score E value 6.0e-43381 Match length 50 % identity

(AC007196) unknown protein [Arabidopsis thaliana] NCBI Description

267297 Seq. No.

12683 2.R1011 Contig ID

uC-zmflmo17310a02b1 5'-most EST

267298 Seq. No.

Contig ID 12683 4.R1011 qmh700028524.f1 5'-most EST

BLASTX Method q4582436 NCBI GI 191 BLAST score 3.0e-14E value 121 Match length 44 % identity



```
NCBI Description (AC007196) unknown protein [Arabidopsis thaliana]
                   267299
Seq. No.
                   12686 1.R1011
Contig ID
                   uC-zmroteosinte027e12b1
5'-most EST
                   BLASTX
Method
                   q2384696
NCBI GI
BLAST score
                   730
                   7.0e-77
E value
                   418
Match length
                   41
% identity
NCBI Description (AF013216) acyl-CoA oxidase [Myxococcus xanthus]
                   267300
Seq. No.
                   12692 1.R1011
Contig ID
                   ceu70\overline{0}431182.h1
5'-most EST
                   BLASTX
Method
                   q3608155
NCBI GI
BLAST score
                   506
                   5.0e-51
E value
                   127
Match length
                   69
% identity
NCBI Description (AC005314) putative RNA helicase [Arabidopsis thaliana]
                   267301
Seq. No.
                   12693 1.R1011
Contig ID
                   LIB3137-039-Q1-K1-C5
5'-most EST
                   267302
Seq. No.
Contig ID
                   12693 2.R1011
                   tfd700571057.hl
5'-most EST
                   267303
Seq. No.
                   12697 1.R1011
Contig ID
                   uC-zmflmo17363c06a1
5'-most EST
                   267304
Seq. No.
                   12699 1.R1011
Contig ID
5'-most EST
                   LIB3079-049-Q1-K1-F4
                   267305
Seq. No.
                   12712 1.R1011
Contig ID
                   uC-zm\overline{f}lb73290b02b1
5'-most EST
                   267306
Seq. No.
                   12712 2.R1011
Contig ID
                   LIB3180-018-P2-M1-B5
5'-most EST
                    267307
Seq. No.
                    12723 1.R1011
Contig ID
                   uC-zm\overline{f}1b73257g01b3
5'-most EST
                    BLASTX
Method
                    g1350548
NCBI GI
                    205
BLAST score
                    2.0e-15
E value
                    119
Match length
```

40

% identity



```
(L47609) heat shock-like protein [Picea glauca]
NCBI Description
                   267308
Seq. No.
                   12723 2.R1011
Contig ID
                   uC-zm\overline{f}lMo17005c07b1
5'-most EST
                   BLASTX
Method
                   g1350548
NCBI GI
                   153
BLAST score
                   2.0e-09
E value
                   58
Match length
                   55
% identity
                  (L47609) heat shock-like protein [Picea glauca]
NCBI Description
                   267309
Seq. No.
                   12723 3.R1011
Contig ID
                   uC-zm\overline{f}lmo17126h11b1
5'-most EST
                   BLASTX
Method
                   q1350548
NCBI GI
                   151
BLAST score
                   2.0e-15
E value
                   122
Match length
                   43
% identity
                  (L47609) heat shock-like protein [Picea glauca]
NCBI Description
                   267310
Seq. No.
                   12723 4.R1011
Contig ID
5'-most EST
                   xjt700093334.h1
                   267311
Seq. No.
                   12726 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73062b07a1
                   267312
Seq. No.
                   12729 1.R1011
Contig ID
                   fC-zmst700457169f1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2499488
                   981
BLAST score
                   1.0e-106
E value
                   276
Match length
% identity
                   67
                   PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
NCBI Description
                   ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                   (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                    (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849)
                   pyrophosphate-dependent phosphofructokinase alpha subunit
                    [Ricinus communis]
Seq. No.
                   267313
                   12729 2.R1011
Contig ID
5'-most EST
                   LIB3061-026-Q1-K1-C2
Method
                   BLASTX
                   g129881
NCBI GI
BLAST score
                   150
                   2.0e-16
E value
```

76

72

Match length

% identity



NCBI Description PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE

ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))

(PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)

(PPI-PFK) >gi 482294 pir A36094

pyrophosphate--fructose-6-phosphate 1-phosphotransferase

(EC 2.7.1.90) alpha chain - potato (cv. Kennebec)

>gi_169538 (M55190) pyrophosphate-fructose 6-phosphate
1-phosphotransferase alpha-subunit [Solanum tuberosum]

Seq. No. 267314

Contig ID 12734 1.R1011

5'-most EST LIB3152-014-P1-K1-F6

Method BLASTX
NCBI GI g1143427
BLAST score 1793
E value 0.0e+00
Match length 453
% identity 79

NCBI Description (X73961) heat shock protein 70 [Cucumis sativus]

Seq. No. 267315

Contig ID 12734 4.R1011

5'-most EST uC-zmflMo17018b08b1

Seq. No. 267316

Contig ID 12738 1.R1011

5'-most EST LIB3079-048-Q1-K1-F12

Seq. No. 267317

Contig ID 12741 1.R1011

5'-most EST LIB3061-022-Q1-K1-B11

Method BLASTX
NCBI GI g3193310
BLAST score 166
E value 2.0e-11
Match length 112
% identity 36

NCBI Description (AF069300) contains similarity to Nicotiana tabacum hin1

(GB:Y07563) [Arabidopsis thaliana]

Seq. No. 267318

Contig ID 12743_1.R1011 5'-most EST uC-zmflb73196c07b1

Method BLASTX
NCBI GI g2827709
BLAST score 213
E value 3.0e-16
Match length 171
% identity 33

NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

Seq. No. 267319

Contig ID 12747_1.R1011 5'-most EST uC-zmflb73233d11b1

Method BLASTX NCBI GI g3176686 BLAST score 990



E value 1.0e-107 Match length 313 % identity 62

NCBI Description (AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No. 267320

Contig ID 12747 2.R1011

5'-most EST uC-zmflmo17045d08b1

Method BLASTX
NCBI GI g3176686
BLAST score 895
E value 1.0e-96
Match length 230
% identity 73

NCBI Description (AC003671) Similar to high affinity potassium transporter,

HAK1 protein gb U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No. 267321

Contig ID 12748_1.R1011 5'-most EST ymt700221318.h1

Method BLASTX
NCBI GI 94508079
BLAST score 958
E value 1.0e-104
Match length 309
% identity 60

NCBI Description (AC005882) 66284 [Arabidopsis thaliana]

Seq. No. 267322

Contig ID 12749_1.R1011

5'-most EST uC-zm \overline{f} lb73194h01b2

Method BLASTX
NCBI GI g3763934
BLAST score 408
E value 1.0e-39
Match length 214
% identity 39

NCBI Description (AC004450) hypothetical protein [Arabidopsis thaliana]

Seq. No. 267323

Contig ID 12752 1.R1011

5'-most EST LIB3059-046-Q1-K1-F3

Seq. No. 267324

Contig ID 12758_1.R1011

5'-most EST LIB3079-048-Q1-K1-C9

Seq. No. 267325

Contig ID 12758_2.R1011 5'-most EST uC-zmflb73354a07a1

Seq. No. 267326

Contig ID 12760 1.R1011

5'-most EST uC-zmflMo17065b01b1



Seq. No. 267327

Contig ID 12775_1.R1011 5'-most EST rvt700548531.h1

Method BLASTX
NCBI GI g3057120
BLAST score 446
E value 2.0e-60
Match length 148
% identity 76

NCBI Description (AF023159) starch synthase DULL1 [Zea mays]

Seq. No. 267328

Contig ID 12776_1.R1011

5'-most EST LIB3136-014-Q1-K1-B9

Method BLASTX
NCBI GI g1353013
BLAST score 190
E value 1.0e-13
Match length 344
% identity 26

NCBI Description HYPOTHETICAL 47.4 KD PROTEIN IN RPS25B-MRS3 INTERGENIC

REGION >gi_1077836_pir__ S55178 hypothetical protein YJL134w - yeast (Saccharomyces cerevisiae) >gi_854562_emb_CAA60821_(X87371) ORF21; homologous to ORF YKR053c [Saccharomyces cerevisiae] >gi_1008341_emb_CAA89430_(Z49410) ORF YJL134w

[Saccharomyces cerevisiae]

Seq. No. 267329

Contig ID 12779_2.R1011 5'-most EST uC-zmroB73070f05b1

Seq. No. 267330

Contig ID 12780_1.R1011

5'-most EST LIB189-026-Q1-E1-F1

Seq. No. 267331

Contig ID 12802_1.R1011 5'-most EST ceu700426869.h1

Seq. No. 267332

Contig ID 12806 1.R1011

5'-most EST uC-zmflb73091a07b2

Method BLASTX
NCBI GI g2651303
BLAST score 1073
E value 1.0e-117
Match length 269

% identity 74

NCBI Description (AC002336) putative potassium transporter [Arabidopsis

thaliana]

Seq. No. 267333

Contig ID 12807_1.R1011

5'-most EST LIB3150-107-P1-N1-E2

Seq. No. 267334



Contig ID 12808_1.R1011 5'-most EST pwr700451402.h1

Seq. No. 267335

Contig ID 12808_5.R1011 5'-most EST zla700380778.h1

Seq. No. 267336

Contig ID 12809_1.R1011

5'-most EST uC-zmflB73007b02b1

Seq. No. 267337

Contig ID 12810 1.R1011

5'-most EST uC-zmflmo17150a12b1

Seq. No. 267338

Contig ID 12810 2.R1011

5'-most EST LIB3079-046-Q1-K1-G6

Seq. No. 267339

Contig ID 12810 4.R1011 5'-most EST xjt700093734.h1

Seq. No. 267340

Contig ID 12817 1.R1011

5'-most EST uC-zmroteosinte023h05b2

Method BLASTX
NCBI GI g4262600
BLAST score 156
E value 5.0e-10
Match length 119
% identity 36

NCBI Description (AF125956) similar to vertebrate galactoside-binding

lectins (Pfam: PF00337, Score=76.8, E=1.5e-21, N=1)

[Caenorhabditis elegans]

Seq. No. 267341

Contig ID 12817_2.R1011 5'-most EST xdb700341120.h1

Seq. No. 267342

Contig ID 12817 3.R1011

5'-most EST uC-zmflmo17297d06b1

Seq. No. 267343

Contig ID 12829 1.R1011 5'-most EST rvt700551971.h1

Method BLASTX
NCBI GI g2865416
BLAST score 1194
E value 1.0e-131
Match length 410
% identity 58

NCBI Description (AF039367) chromomethylase [Arabidopsis thaliana]

Seq. No. 267344

Contig ID 12851_1.R1011



```
5'-most EST
                  LIB3062-012-Q1-K1-H1
                  BLASTX
Method
NCBI GI
                  g4510346
BLAST score
                  529
E value
                  1.0e-53
Match length
                  212
% identity
                  52
NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]
                  267345
Seq. No.
Contig ID
                  12853 1.R1011
5'-most EST
                  xmt700259159.h2
Method
                  BLASTX
NCBI GI
                  q4309700
BLAST score
                  245
E value
                  2.0e-20
Match length
                  141
% identity
                  38
NCBI Description (AC006266) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  267346
                  12859 1.R1011
Contig ID
5'-most EST
                  LIB3115-022-P1-K1-F12
                  BLASTX
Method
                  g3241945
NCBI GI
BLAST score
                  221
E value
                  5.0e-18
Match length
                  93
% identity
                  48
NCBI Description (AC004625) unknown protein [Arabidopsis thaliana]
Seq. No.
                  267347
                  12861 1.R1011
Contig ID
5'-most EST
                  LIB3066-023-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                  g3738316
BLAST score
                  371
                  2.0e-35
E value
Match length
                  120
                  59
% identity
NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]
Seq. No.
                  267348
Contig ID
                  12861 2.R1011
5'-most EST
                  uC-zmflmo17158f05b1
Method
                  BLASTX
NCBI GI
                  q3193330
BLAST score
                  341
E value
                  1.0e-31
Match length
                  175
% identity
                  46
NCBI Description (AF069299) contains similarity to Medicago sativa corC
                  (GB:L22305) [Arabidopsis thaliana]
```

Seq. No. 267349

Contig ID 12861_3.R1011

5'-most EST uC-zmflmo17344h07b1



Method BLASTX
NCBI GI g3063471
BLAST score 302
E value 3.0e-27
Match length 126
% identity 50

NCBI Description (AC003981) F22013.33 [Arabidopsis thaliana]

1

Seq. No. 267350

Contig ID 12865_1.R1011 5'-most FST UC-zmflmo1711

5'-most EST uC-zmflmo17118h08b1

Seq. No. 267351

Contig ID 12869 1.R1011

5'-most EST LIB3150-097-P1-N1-D8

Seq. No. 267352

Contig ID 12874 1.R1011

5'-most EST uC-zmroteosinte003h03b1

Method BLASTX
NCBI GI g1097875
BLAST score 678
E value 2.0e-71
Match length 163
% identity 80

NCBI Description peroxidase: ISOTYPE=RPA [Oryza sativa]

Seq. No. 267353

Contig ID 12881 1.R1011

5'-most EST LIB3067-023-Q1-K1-C3

Seq. No. 267354

Contig ID 12883 1.R1011

5'-most EST LIB3079-043-Q1-K1-G7

Seq. No. 267355

Contig ID 12884 1.R1011

5'-most EST LIB3079-043-Q1-K2-G8

Seq. No. 267356

Contig ID 12885_1.R1011 5'-most EST wyr700239744.h1

Method BLASTX
NCBI GI g4538929
BLAST score 170
E value 9.0e-12
Match length 42
% identity 71

NCBI Description (ALO49483) putative nucleic acid binding protein

[Arabidopsis thaliana]

Seq. No. 267357

Contig ID 12888 1.R1011

5'-most EST uC-zmflmo17132d02b1

Method BLASTX NCBI GI g2914700 BLAST score 2134

Match length

% identity



```
0.0e + 00
E value
                   555
Match length
                   77
% identity
                   (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
NCBI Description
                   thaliana]
                   267358
Seq. No.
                   12888 4.R1011
Contig ID
                   uC-zm\overline{f}1b73305b03b2
5'-most EST
                   BLASTX
Method
                   g2914700
NCBI GI
                   176
BLAST score
                   1.0e-12
E value
Match length
                   71
                   55
% identity
                   (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
NCBI Description
                   thaliana]
                   267359
Seq. No.
                   12890 1.R1011
Contig ID
5'-most EST
                   tbg700930374.h1
                   267360
Seq. No.
                   12891 1.R1011
Contig ID
5'-most EST
                   LIB3079-043-Q1-K1-E4
Method
                   BLASTX
NCBI GI
                   g3935141
                   187
BLAST score
                   7.0e-14
E value
                   52
Match length
                   60
% identity
                  (AC005106) T25N20.5 [Arabidopsis thaliana]
NCBI Description
                   267361
Seq. No.
                   12895_1.R1011
Contig ID
5'-most EST
                   LIB189-002-Q1-E1-F7
Method
                   BLASTX
                   q3335374
NCBI GI
                   500
BLAST score
                   3.0e-78
E value
                   249
Match length
                   62
% identity
                  (AC003028) glutaredoxin-like protein [Arabidopsis thaliana]
NCBI Description
                   267362
Seq. No.
                   12896 1.R1011
Contig ID
5'-most EST
                   LIB3079-037-Q1-K1-F8
Seq. No.
                   267363
Contig ID
                   12901 1.R1011
5'-most EST
                   LIB3079-043-Q1-K2-C7
Method
                   BLASTX
NCBI GI
                   g2811066
BLAST score
                   180
                   1.0e-16
E value
```



PUTATIVE PROTEIN-TYROSINE PHOSPHATASE PTEN (MUTATED IN NCBI Description MULTIPLE ADVANCED CANCERS 1) >gi_1916330 (U92437) MMAC1

[Mus musculus]

267364 Seq. No.

12904 1.R1011 Contig ID

LIB3066-023-Q1-K1-A10 5'-most EST

267365 Seq. No.

12906 1.R1011 Contig ID

LIB3079-043-Q1-K2-D7 5'-most EST

267366 Seq. No.

12907 1.R1011 Contig ID

LIB3068-028-Q1-K1-B9 5'-most EST

267367 Seq. No.

12907 2.R1011 Contig ID ntr700072384.hl 5'-most EST

BLASTX Method g2213590 NCBI GI 1160 BLAST score 1.0e-127 E value Match length 540 44 % identity

NCBI Description (AC000348) T7N9.10 [Arabidopsis thaliana]

Seq. No. 267368

12911 1.R1011 Contig ID ypc700803844.hl 5'-most EST

BLASTX Method NCBI GI g4455307 452 BLAST score 2.0e-44 E value 228 Match length 45 % identity

NCBI Description (AL035528) methionyl-tRNA synthetase-like protein

[Arabidopsis thaliana]

267369 Seq. No.

12912 1.R1011 Contig ID 5'-most EST pmx700084006.hl

Method BLASTX g3335378 NCBI GI 199 BLAST score 3.0e-15 E value Match length 98

% identity

NCBI Description (AC003028) Myb-related transcription activator [Arabidopsis

thaliana]

267370 Seq. No.

12912 2.R1011 Contig ID uC-zmflb73116f06b2 5'-most EST

267371 Seq. No.

12914 1.R1011 Contig ID



```
pmx700087964.h1
5'-most EST
                  BLASTX
Method
                  q4432867
NCBI GI
                  545
BLAST score
                  2.0e-55
E value
Match length
                  245
                  43
% identity
                  (AC006300) putative dnaJ-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  267372
Seq. No.
                  12920 1.R1011
Contig ID
                  LIB3137-030-Q1-K1-A8
5'-most EST
                  267373
Seq. No.
                  12923 1.R1011
Contig ID
                  uC-zmflmo17012b02b1
5'-most EST
                  267374
Seq. No.
                  12923 2.R1011
Contig ID
5'-most EST
                  LIB36-019-Q1-E1-F5
                  267375
Seq. No.
                  12923 3.R1011
Contig ID
                  LIB3079-043-Q1-K2-A11
5'-most EST
                  267376
Seq. No.
                  12938 1.R1011
Contig ID
                  LIB3079-043-Q1-K1-C9
5'-most EST
                   267377
Seq. No.
                   12940 1.R1011
Contig ID
                   LIB3180-011-P2-M1-H6
5'-most EST
                   BLASTX
Method
                   g121477
NCBI GI
BLAST score
                   1034
E value
                   1.0e-112
                   422
Match length
 % identity
                   51
NCBI Description GLUTELIN PRECURSOR >gi_82471_pir__S05443 glutelin precursor
                   (clone lambda-RG21) - rice >gi 20227 emb CAA32566 (X14393)
                   preprolglutelin (AA -24 to 476) [Oryza sativa]
                   >gi 226767_prf 1604474A glutelin [Oryza sativa]
                   267378
 Seq. No.
                   12940 4.R1011
 Contig ID
                   LIB3180-049-P2-M1-B3
 5'-most EST
                   267379
 Seq. No.
                   12943 1.R1011
 Contig ID
```

5'-most EST LIB3079-043-Q1-K2-D9

Seq. No. 267380

Contig ID 12947_1.R1011

5'-most EST LIB3079-043-Q1-K2-B12

Method BLASTX NCBI GI g294845

% identity



```
1278
BLAST score
                  1.0e-141
E value
                  324
Match length
                  75
% identity
                  (L13655) membrane protein [Saccharum hybrid cultivar
NCBI Description
                  H65-7052]
                  267381
Seq. No.
                  12947_2.R1011
Contig ID
                  LIB3062-001-Q1-K2-H4
5'-most EST
                  BLASTN
Method
                  g294844
NCBI GI
                  180
BLAST score
                  2.0e-96
E value
                  504
Match length
                   94
% identity
                  Saccharum hybrid cultivar H65-7052 membrane protein mRNA,
NCBI Description
                  complete cds
                   267382
Seq. No.
                   12953_1.R1011
Contig ID
                   LIB3079-042-Q1-K2-F12
5'-most EST
                   BLASTX
Method
                   g4263721
NCBI GI
                   530
BLAST score
                   7.0e-54
E value
                   149
Match length
                   74
% identity
                  (AC006223) putative DNA repair protein RAD50 [Arabidopsis
NCBI Description
                   thaliana]
                   267383
Seq. No.
                   12955 1.R1011
Contig ID
                   LIB3079-042-Q1-K2-G12
5'-most EST
                   267384
Seq. No.
Contig ID
                   12956 1.R1011
                   LIB3088-024-Q1-K1-D5
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1173456
BLAST score
                   328
E value
                   3.0e-30
                   91
Match length
% identity
                   SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN
NCBI Description
                   D3) (SM-D3) >gi_600750 (U15009) Sm D3 [Homo sapiens]
                   267385
Seq. No.
                   12958 1.R1011
Contig ID
                   xsy700209076.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2702270
                   834
BLAST score
                   3.0e-89
E value
                   353
Match length
```

NCBI Description (AC003033) unknown protein [Arabidopsis thaliana]



```
267386
Seq. No.
                  12961 1.R1011
Contig ID
                  LIB3079-043-Q1-K2-A12
5'-most EST
                  BLASTX
Method
                  q4586044
NCBI GI
BLAST score
                  155
E value
                  5.0e-10
                  64
Match length
                  47
% identity
                  (AC007020) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  267387
Seq. No.
                  12962 1.R1011
Contig ID
                  LIB3069-008-Q1-K1-D12
5'-most EST
                  267388
Seq. No.
Contig ID
                   12964 1.R1011
                  LIB3068-027-Q1-K1-E6
5'-most EST
                   BLASTX
Method
                   g1619602
NCBI GI
                   470
BLAST score
                   9.0e-47
E value
                   161
Match length
                   57
% identity
NCBI Description (Y08726) MtN3 [Medicago truncatula]
Seq. No.
                   267389
                   12964 2.R1011
Contig ID
                   uC-zmflb73040g03b1
5'-most EST
                   BLASTX
Method
                   g1619602
NCBI GI
                   260
BLAST score
                   2.0e-22
E value
                   71
Match length
                   66
% identity
NCBI Description (Y08726) MtN3 [Medicago truncatula]
Seq. No.
                   267390
                   12970 1.R1011
Contig ID
                   LIB3079-042-Q1-K2-D12
 5'-most EST
                   BLASTX
Method
                   g4455330
NCBI GI
                   221
BLAST score
                   8.0e-18
E value
                   106
Match length
                   42
 % identity
NCBI Description (AL035525) contains EST gb:T44002 [Arabidopsis thaliana]
                   267391
 Seq. No.
                   12971 1.R1011
 Contig ID
 5'-most EST
                   fdz701166142.h1
                   BLASTX
 Method
                   g4584525
 NCBI GI
                   797
 BLAST score
```

6.0e-85

E value



Match length 211 % identity (AL049607) protein phosphatase 2C-like protein [Arabidopsis NCBI Description thaliana] 267392 Seq. No. 12971 2.R1011 Contig ID uC-zmflb73011a08b1 5'-most EST BLASTX Method g4584525 NCBI GI BLAST score 825 2.0e-88 E value 199 Match length 75 % identity (AL049607) protein phosphatase 2C-like protein [Arabidopsis NCBI Description thaliana] 267393 Seq. No. 12971 3.R1011 Contig ID ypc700803832.h1 5'-most EST BLASTX Method g3482967 NCBI GI 235 BLAST score 2.0e-19 E value 53 Match length 79 % identity (AL031369) Protein phosphatase 2C-like protein [Arabidopsis NCBI Description thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana] 267394 Seq. No. 12982 1.R1011 Contig ID LIB3137-015-Q1-K1-B5 5'-most EST BLASTX Method g4572673 NCBI GI

218 BLAST score 3.0e-17E value Match length 90 50 % identity

(AC006954) putative sarcosine oxidase [Arabidopsis NCBI Description

thaliana]

267395 Seq. No.

12982 3.R1011 Contig ID LIB84-001-Q1-E1-H6 5'-most EST

Method BLASTX NCBI GI q2494736 BLAST score 220 E value 1.0e-17 72 Match length 62 % identity

GLUCOSE INHIBITED DIVISION PROTEIN A NCBI Description

>gi_1001595_dbj_BAA10223_ (D64000) glucose inhibited

division protein A [Synechocystis sp.]

267396 Seq. No.

12982 4.R1011 Contig ID

E value

9.0e-37



```
5'-most EST
                  tfd700574382.h2
Seq. No.
                  267397
Contig ID
                  12982 6.R1011
                  wyr700235124.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2494736
BLAST score
                  472
                  3.0e-47
E value
Match length
                  137
                   69
% identity
                  GLUCOSE INHIBITED DIVISION PROTEIN A
NCBI Description
                  >gi_1001595_dbj_BAA10223_ (D64000) glucose inhibited
                   division protein A [Synechocystis sp.]
                   267398
Seq. No.
                   12983 1.R1011
Contig ID
                  LIB3079-042-Q1-K1-G8
5'-most EST
Method
                  BLASTX
                   q4567251
NCBI GI
                   601
BLAST score
                   3.0e-62
E value
Match length
                   166
                   69
% identity
                   (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
                   267399
Seq. No.
Contig ID
                   12990 1.R1011
                   rvt700551647.h1
5'-most EST
                   BLASTX
Method
                   g3915037
NCBI GI
                   2878
BLAST score
                   0.0e+00
E value
                   646
Match length
                   82
% identity
                   SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
NCBI Description
                   >gi 2570067_emb_CAA04512_ (AJ001071) second sucrose
                   synthase [Pisum sativum]
                   267400
Seq. No.
                   12991 1.R1011
Contig ID
                   pmx700084458.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3132476
BLAST score
                   699
                   1.0e-73
E value
                   206
Match length
                   68
% identity
                   (AC003096) unknown protein [Arabidopsis thaliana]
NCBI Description
                   267401
Seq. No.
                   12997 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73051e10b1
                   BLASTX
Method
NCBI GI
                   g3874447
BLAST score
                   387
```



Match length 260
% identity 35
NCBI Description (Z81039) predicted using Genefinder; cDNA EST EMBL:T01209
comes from this gene; cDNA EST yk278all.3 comes from this
gene; cDNA EST yk278all.5 comes from this gene; cDNA EST
yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com

Seq. No. 267402

Contig ID 13002 1.R1011

5'-most EST LIB3067-031-Q1-K1-B1

Method BLASTX
NCBI GI g2982301
BLAST score 409
E value 1.0e-39
Match length 163
% identity 54

NCBI Description (AF051235) YGL010w-like protein [Picea mariana]

Seq. No. 267403

Contig ID 13007_1.R1011 5'-most EST dyk700103388.h1

Method BLASTX
NCBI GI g3450842
BLAST score 415
E value 2.0e-40
Match length 134
% identity 59

NCBI Description (AF080436) mitogen activated protein kinase kinase [Oryza

sativa]

Seq. No. 267404

Contig ID 13009_1.R1011

5'-most EST LIB3079-042-Q1-K1-D5

Method BLASTX
NCBI GI g4539301
BLAST score 330
E value 2.0e-30
Match length 115
% identity 53

NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis

thaliana]

Seq. No. 267405

Contig ID 13010 1.R1011 5'-most EST uC-zmflb73057g09b1

Method BLASTX
NCBI GI g4490738
BLAST score 471
E value 1.0e-59
Match length 342
% identity 44

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 267406

Contig ID 13010_2.R1011 5'-most EST uC-zmflb73039a02b1

Method BLASTX



NCBI GI g4490738 BLAST score 222 E value 5.0e-29 Match length 129 % identity 52

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 267407

Contig ID 13010_3.R1011 5'-most EST hvj700624222.h1

Seq. No. 267408

Contig ID 13013_1.R1011 5'-most EST qmh700028779.f1

Method BLASTX
NCBI GI g3806016
BLAST score 1966
E value 0.0e+00
Match length 606
% identity 65

NCBI Description (AF053104) peroxisomal targeting signal 1 receptor; PTS1

receptor; Pex5p [Nicotiana tabacum]

Seq. No. 267409

Contig ID 13013_2.R1011 5'-most EST kem700611213.h1

Seq. No. 267410

Contig ID 13013_3.R1011

5'-most EST uC-zmflmo17259g01b1

Method BLASTX
NCBI GI g3603353
BLAST score 236
E value 1.0e-19
Match length 89
% identity 56

NCBI Description (AF074843) peroxisomal targeting signal type 1 receptor

[Arabidopsis thaliana]

Seq. No. 267411

Contig ID 13026_1.R1011 5'-most EST xsy700208852.h1

Method BLASTX
NCBI GI g2072393
BLAST score 2165
E value 0.0e+00
Match length 457
% identity 91

NCBI Description (U29168) similar to human Xeroderma pigmentosum group B DNA

repair protein, Swiss-Prot Accession Number P19447

[Arabidopsis thaliana]

Seq. No. 267412

Contig ID 13027_1.R1011

5'-most EST LIB3079-042-Q1-K1-C4

Method BLASTX NCBI GI g168643



```
508
BLAST score
                    2.0e-51
E value
                   168
Match length
% identity
                    64
                   (L02540) NADPH HC-toxin reductase [Zea mays]
NCBI Description
                    267413
Seq. No.
                    13031 1.R1011
Contig ID
                    uC-zm\overline{f}lmo17066g01b1
5'-most EST
                    BLASTX
Method
                    g3334349
NCBI GI
                    1525
BLAST score
                    0.0e + 00
E value
                    398
Match length
                    83
% identity
                    GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS)
NCBI Description
                    >gi 2564215 emb_CAA05162_ (AJ002062) glycyl-tRNA synthetase
                    [Arabidopsis thaliana]
                    267414
Seq. No.
                    13031 2.R1011
Contig ID
                    kem700611774.h1
5'-most EST
                    BLASTX
Method
                    g3334349
NCBI GI
                    259
BLAST score
                    1.0e-22
E value
                    76
Match length
                    70
% identity
                    GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS)
NCBI Description
                    >gi 2564215 emb_CAA05162_ (AJ002062) glycyl-tRNA synthetase
                    [Arabidopsis thaliana]
                    267415
Seq. No.
                    13037 1.R1011
Contig ID
                    xjt700092212.hl
5'-most EST
                    BLASTX
Method
                    q3024516
NCBI GI
                    765
BLAST score
                    2.0e-81
E value
Match length
                    192
                    78
% identity
NCBI Description RAS-RELATED PROTEIN RAB11C >gi_2160157 (AC000132) Strong
                    similarity to A. thaliana ara-\overline{2} (gb ATHARA2). ESTs
                    gb ATTS2483,gb ATTS2484,gb AA042159 come from this gene. [Arabidopsis thaliana] >gi_2231303 (U74669) ras-related
                     small GTPase [Arabidopsis thaliana]
 Seq. No.
                     267416
                     13040 1.R1011
 Contig ID
                     uC-zmflb73142b07b1
 5'-most EST
                    BLASTX
 Method
                     q3860272
 NCBI GI
```

1878 BLAST score 0.0e + 00E value

435 Match length % identity

NCBI Description (AC005824) putative suppressor protein [Arabidopsis



thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1

protein [Arabidopsis thaliana] 267417 Seq. No. 13041 1.R1011 Contig ID ymt700220976.h1 5'-most EST BLASTX Method g1929056 NCBI GI 1457 BLAST score 1.0e-162 E value 410 Match length 70 % identity (Y12090) putative 3,4-dihydroxy-2-butanone kinase NCBI Description [Lycopersicon esculentum] 267418 Seq. No. 13042 1.R1011 Contig ID LIB3079-041-Q1-K1-G4 5'-most EST 267419 Seq. No. 13044 1.R1011 Contig ID LIB3079-041-Q1-K1-H1 5'-most EST BLASTX Method NCBI GI g3212863 BLAST score 303 2.0e-27 E value Match length 80 75 % identity (AC004005) putative translation initiation factor NCBI Description [Arabidopsis thaliana] 267420 Seq. No. 13048 1.R1011 Contig ID wty700168184.hl 5'-most EST ${\tt BLASTX}$ Method g3668086 NCBI GI 835 BLAST score 2.0e-89 E value 247 Match length 72 % identity

(AC004667) unknown protein [Arabidopsis thaliana] NCBI Description

267421 Seq. No. 13056 1.R1011 Contig ID wyr700237912.h1 5'-most EST 267422

Seq. No. 13057 1.R1011 Contig ID pmx700087442.hl 5'-most EST BLASTX Method

q418596 NCBI GI 222 BLAST score E value 6.0e-18 84 Match length 50 % identity

PUTATIVE 40S RIBOSOMAL PROTEIN YHR148W NCBI Description

>gi 485540_pir__S33911 hypothetical protein YHR148w - yeast



(Saccharomyces cerevisiae) >gi_4014_emb_CAA49237_ (X69480) uORF1 [Saccharomyces cerevisiae] >gi_500654 (U10397) Yhr148wp [Saccharomyces cerevisiae]

Seq. No. 267423

Contig ID 13058_1.R1011

5'-most EST uC-zmroteosinte026c07b1

Seq. No. 267424

Contig ID 13073_1.R1011 5'-most EST wyr700240323.h1

Seq. No. 267425

Contig ID 13076_1.R1011

5'-most EST LIB3079-041-Q1-K1-C8

Seq. No. 267426

Contig ID 13082_1.R1011

5'-most EST LIB189-021-Q1-E1-A9

Seq. No. 267427

Contig ID 13093_1.R1011 5'-most EST uer700583212.h1

Method BLASTX
NCBI GI g4539423
BLAST score 872
E value 6.0e-94
Match length 220
% identity 77

NCBI Description (AL049171) pyrophosphate-dependent phosphofructo-1-kinase

[Arabidopsis thaliana]

Seq. No. 267428

Contig ID 13093 2.R1011

5'-most EST LIB3079-041-Q1-K1-B3

Method BLASTX
NCBI GI g2688822
BLAST score 315
E value 9.0e-34
Match length 131
% identity 62

NCBI Description (U93272) pyrophosphate-dependent phosphofructo-1-kinase

[Prunus armeniaca]

Seq. No. 267429

Contig ID 13093_4.R1011

5'-most EST LIB3137-056-Q1-K1-B11

Method BLASTX
NCBI GI 94539423
BLAST score 192
E value 8.0e-15
Match length 52
% identity 69

NCBI Description (AL049171) pyrophosphate-dependent phosphofructo-1-kinase

[Arabidopsis thaliana]

Seq. No. 267430



13094 1.R1011 Contig ID LIB3079-041-Q1-K1-B4 5'-most EST Seq. No. 267431 13094 2.R1011 Contig ID uC-zmflb73080g05b2 5'-most EST 267432 Seq. No. 13094 3.R1011 Contig ID uC-zmflmo17001g06b1 5'-most EST BLASTX Method g4584255 NCBI GI 549 BLAST score 4.0e-56 E value 130 Match length 72 % identity (Y18471) SINA1p [Vitis vinifera] NCBI Description 267433 Seq. No. 13095 1.R1011 Contig ID uC-zmroteosinte105g05b1 5'-most EST BLASTX Method g541816 NCBI GI 1908 BLAST score 0.0e + 00E value 474 Match length 77 % identity protein kinase - common ice plant >gi 457689 emb CAA82990 NCBI Description (Z30329) protein kinase [Mesembryanthemum crystallinum] 267434 Seq. No. 13095 2.R1011 Contig ID uC-zmflb73266g06a2 5'-most EST BLASTX Method q541816 NCBI GI BLAST score 149 E value 2.0e-09 61 Match length % identity 61 protein kinase - common ice plant >gi_457689_emb_CAA82990_ NCBI Description (Z30329) protein kinase [Mesembryanthemum crystallinum] 267435 Seq. No. Contig ID 13101 1.R1011 uC-zmroteosinte026e11b1 5'-most EST BLASTX Method NCBI GI q3281851

BLAST score 1086 1.0e-119 E value Match length 278 69 % identity

(AL031004) RNA lariat debranching enzyme - like protein NCBI Description

[Arabidopsis thaliana]

267436 Seq. No. 13101 2.R1011 Contig ID

uC-zmflmo17174e02a1 5'-most EST

NCBI Description



```
267437
Seq. No.
                   13107 1.R1011
Contig ID
                   ntr70\overline{0}075629.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g464365
                   750
BLAST score
                   1.0e-79
E value
                   214
Match length
                   68
% identity
                   PEROXIDASE P7 >gi 66306 pir OPNB7 peroxidase (EC 1.11.1.7)
NCBI Description
                   - turnip
                   267438
Seq. No.
Contig ID
                   13109 1.R1011
                   LIB3079-040-Q1-K1-H8
5'-most EST
                   BLASTX
Method
                   g3047109
NCBI GI
                   208
BLAST score
                   4.0e-16
E value
                   71
Match length
                   58
% identity
                   (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
                   267439
Seq. No.
                   13110 1.R1011
Contig ID
5'-most EST
                   LIB3079-040-Q1-K1-H9
Method
                   BLASTX
                   q4490733
NCBI GI
BLAST score
                   499
                   2.0e-50
E value
Match length
                   153
                   61
% identity
                   (AL035709) putative protein [Arabidopsis thaliana]
NCBI Description
                   267440
Seq. No.
Contig ID
                   13115_1.R1011
                   LIB3062-022-Q1-K1-D4
5'-most EST
Method
                   BLASTX
                   q2244975
NCBI GI
BLAST score
                   1472
E value
                   1.0e-164
Match length
                   423
% identity
NCBI Description
                   (Z97340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   267441
Contig ID
                   13122 1.R1011
5'-most EST
                   xyt700342780.hl
                   BLASTX
Method
NCBI GI
                   q4490747
BLAST score
                   582
E value
                   3.0e-60
Match length
                   151
% identity
                   75
```

(AL035708) DnaJ-like protein [Arabidopsis thaliana]



```
Seq. No.
                  267442
                  13123 1.R1011
Contig ID
                  LIB3079-040-Q1-K1-F6
5'-most EST
                  267443
Seq. No.
                  13124 1.R1011
Contig ID
                  uC-zmflmo17109b02b1
5'-most EST
Method
                  BLASTX
                  g283037
NCBI GI
BLAST score
                  1309
                  1.0e-145
E value
Match length
                  278
                  87
% identity
NCBI Description chitinase (EC 3.2.1.14) A - maize
                  267444
Seq. No.
                  13124 2.R1011
Contig ID
                  LIB3068-036-Q1-K1-A7
5'-most EST
                  BLASTX
Method
                  q116333
NCBI GI
                   699
BLAST score
                  7.0e-74
E value
Match length
                   147
                   88
% identity
                  ENDOCHITINASE B PRECURSOR (SEED CHITINASE B) >gi_168443
NCBI Description
                   (M84165) chitinase B [Zea mays]
Seq. No.
                   267445
                   13124 3.R1011
Contig ID
                   LIB3067-001-Q1-K1-B12
5'-most EST
                   BLASTX
Method
                   g116333
NCBI GI
                   206
BLAST score
                   3.0e-16
E value
                   36
Match length
                   100
% identity
NCBI Description ENDOCHITINASE B PRECURSOR (SEED CHITINASE B) >gi_168443
                   (M84165) chitinase B [Zea mays]
                   267446
Seq. No.
                   13124 4.R1011
Contig ID
5'-most EST
                   LIB143-057-Q1-E1-F3
                   BLASTX
Method
                   g283037
NCBI GI
                   633
BLAST score
                   4.0e-66
E value
                   117
Match length
% identity
NCBI Description chitinase (EC 3.2.1.14) A - maize
                   267447
Seq. No.
                   13127 1.R1011
Contig ID
                   uC-zmflmo17160h06b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2760843
BLAST score
                   552
```

37200

5.0e-58

E value



Match length 245 51 % identity

(AC003105) unknown protein [Arabidopsis thaliana] NCBI Description

267448 Seq. No.

13130 1.R1011 Contiq ID uC-zmflb73360g06a1 5'-most EST

267449 Seq. No.

13130 2.R1011 Contig ID

LIB3079-040-Q1-K1-G2 5'-most EST

267450 Seq. No.

13136 1.R1011 Contig ID

LIB3079-040-Q1-K1-D8 5'-most EST

267451 Seq. No.

13137 1.R1011 Contig ID ymt700224572.h1 5'-most EST

BLASTX Method g2352427 NCBI GI 441 BLAST score 2.0e-43 E value 203 Match length 25 % identity

(AF004161) peroxisomal Ca-dependent solute carrier NCBI Description

[Oryctolagus cuniculus]

267452 Seq. No.

13138 1.R1011 Contig ID

 $uC-zm\overline{f}lmo17042h09b1$ 5'-most EST

BLASTX Method g3650033 NCBI GI 895 BLAST score 2.0e-96 E value 310 Match length 61 % identity

(AC005396) unknown protein [Arabidopsis thaliana] NCBI Description

267453 Seq. No.

13138 2.R1011 Contig ID 5'-most EST uC-zmflb73282c07a1

267454 Seq. No.

13140 1.R1011 Contig ID

uC-zmflb73172b02b2 5'-most EST

Method BLASTX NCBI GI g4218187 BLAST score 309 1.0e-27 E value Match length 207 % identity

(AJ010165) leghemoglobin activating factor [Glycine max] NCBI Description

267455 Seq. No.

13141 1.R1011 Contig ID uC-zmf1b73290b08b1 5'-most EST



Method BLASTX q1168537 NCBI GI BLAST score 1947 0.0e + 00E value 503 Match length 73 % identity ASPARTIC PROTEINASE PRECURSOR >gi 82458_pir__JS0732 NCBI Description aspartic proteinase (EC 3.4.23.-) - rice >qi 218143 dbj BAA02242 (D12777) aspartic proteinase [Oryza sativa] 267456 Seq. No. 13141 2.R1011 Contig ID LIB3062-027-Q1-K1-F12 5'-most EST BLASTX Method NCBI GI g2982469 305 BLAST score 2.0e-27 E value 87 Match length 67 % identity (AL022223) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 267457 13150 1.R1011 Contig ID uC-zmflmo17079h02b1 5'-most EST 267458 Seq. No. Contig ID 13150 2.R1011 $uC-zm\overline{f}lmo17068d07b2$ 5'-most EST 267459 Seq. No. 13151 1.R1011 Contig ID LIB3079-040-Q1-K1-C2 5'-most EST 267460 Seq. No. 13152 1.R1011 Contig ID 5'-most EST xdb700339668.h1 267461 Seq. No. 13153 1.R1011 Contig ID LIB3079-040-Q1-K1-C4 5'-most EST BLASTX Method g4580397 NCBI GI BLAST score 334 3.0e-31E value 135 Match length 53 % identity (AC007171) putative RNA helicase [Arabidopsis thaliana] NCBI Description 267462 Seq. No. 13154_1.R1011 Contig ID xsy700209925.hl 5'-most EST

Method BLASTX
NCBI GI g3461820
BLAST score 498
E value 6.0e-50
Match length 175



% identity 56 (AC004138) unknown protein [Arabidopsis thaliana] NCBI Description 267463 Seq. No. 13158 1.R1011 Contig ID $uC-zm\overline{f}lb73055g10b1$ 5'-most EST Method BLASTX g2827516 NCBI GI 449 BLAST score 3.0e-44E value 162 Match length % identity 55 (AL021633) DNA topoisomerase like- protein [Arabidopsis NCBI Description thaliana] 267464 Seq. No. 13158 2.R1011 Contig ID LIB3150-081-P1-N1-B4 5'-most EST BLASTX Method g2827516 NCBI GI 567 BLAST score 4.0e-58 E value 230 Match length 54 % identity (AL021633) DNA topoisomerase like- protein [Arabidopsis NCBI Description thaliana] Seq. No. 267465 13166_1.R1011 Contig ID LIB3079-040-Q1-K1-A7 5'-most EST 267466 Seq. No. 13166 2.R1011 Contig ID hvj700622945.h1 5'-most EST 267467 Seq. No. 13171_1.R1011 Contig ID vux700156742.h1 5'-most EST BLASTX Method a541953 NCBI GI 425 BLAST score 5.0e-42E value 89 Match length 96 % identity ubiquitin extension protein - white lupine NCBI Description >gi_438109_emb_CAA80333_ (Z22612) ubiquitin extension protein [Lupinus albus] Seq. No. 267468 13172 1.R1011 Contig ID uC-zmflmo17171f05b1 5'-most EST BLASTX Method

NCBI GI g4105798
BLAST score 1091
E value 1.0e-119
Match length 253
% identity 69



NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 267469

Contig ID 13172_2.R1011 5'-most EST wty700167295.h1

Method BLASTX
NCBI GI g4105798
BLAST score 695
E value 4.0e-87
Match length 215
% identity 66

NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 267470

Contig ID 13172 4.R1011 5'-most EST wty700167917.h1

Seq. No. 267471

Contig ID 13172 5.R1011

5'-most EST uC-zmflm017214h02b1

Method BLASTX
NCBI GI g4105798
BLAST score 404
E value 1.0e-40
Match length 118
% identity 64

NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 267472

Contig ID 13172_6.R1011 5'-most EST pmx700085586.h1

Method BLASTX
NCBI GI g4105798
BLAST score 223
E value 3.0e-18
Match length 102

% identity 43
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]

Seq. No. 267473

Contig ID 13174_1.R1011

5'-most EST uC-zmflMo17016d03b1

Method BLASTX
NCBI GI g4249403
BLAST score 665
E value 1.0e-69
Match length 249
% identity 57

NCBI Description (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 267474

Contig ID 13174 2.R1011 5'-most EST vux700161594.h1

Seq. No. 267475

Contig ID 13176_1.R1011 5'-most EST clt700042649.f1

BLAST score

1005



```
267476
Seq. No.
                  13177 1.R1011
Contig ID
                  LIB3079-039-Q1-K1-G2
5'-most EST
                  BLASTX
Method
                  q623586
NCBI GI
                  336
BLAST score
                   3.0e-31
E value
                  107
Match length
                   62
% identity
NCBI Description
                  (L29273) putative [Nicotiana tabacum]
                   267477
Seq. No.
                   13178 1.R1011
Contig ID
                  LIB3079-039-Q1-K1-G3
5'-most EST
Method
                  BLASTX
                   q4567201
NCBI GI
BLAST score
                   378
                   4.0e-36
E value
                   112
Match length
                   65
% identity
                   (AC007168) putative aspartate aminotransferase [Arabidopsis
NCBI Description
                   thaliana]
                   267478
Seq. No.
                   13181 1.R1011
Contig ID
                   LIB3079-039-Q1-K1-G8
5'-most EST
                   267479
Seq. No.
                   13182 1.R1011
Contig ID
                   uC-zmflb73128f01a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3451075
                   876
BLAST score
                   3.0e-94
E value
                   250
Match length
                   65
% identity
                  (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                   267480
Seq. No.
                   13182 2.R1011
Contig ID
5'-most EST
                   fwa700099924.h1
Method
                   BLASTX
                   q1931652
NCBI GI
                   913
BLAST score
E value
                   7.0e-99
Match length
                   220
% identity
                   (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog
NCBI Description
                   [Arabidopsis thaliana]
                   267481
Seq. No.
Contig ID
                   13188 1.R1011
5'-most EST
                   uC-zmroteosinte088g08b1
                   BLASTX
Method
NCBI GI
                   g4239692
```



```
1.0e-109
E value
                  239
Match length
                  73
% identity
                  (AJ132745) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  267482
Seq. No.
                  13190 1.R1011
Contig ID
                  pmx700083889.hl
5'-most EST
Method
                  BLASTX
                  q4468796
NCBI GI
BLAST score
                  405
                  1.0e-39
E value
Match length
                  76
                  100
% identity
                  (AJ010439) GST6 protein [Zea mays]
NCBI Description
                  267483
Seq. No.
                  13191 1.R1011
Contig ID
                  uC-zmroteosinte017h11b1
5'-most EST
                   267484
Seq. No.
                  13193 1.R1011
Contig ID
5'-most EST
                   gct701177462.h1
Method
                  BLASTX
                   q4263784
NCBI GI
BLAST score
                   521
                   7.0e-53
E value
Match length
                   176
                   56
% identity
                  (AC006068) putative glycogenin-2 protein [Arabidopsis
NCBI Description
                   thaliana]
                   267485
Seq. No.
Contig ID
                   13194 1.R1011
5'-most EST
                   uC-zmflmo17043f07b1
Method
                   BLASTX
                   q3643085
NCBI GI
BLAST score
                   568
                   3.0e-58
E value
Match length
                   158
                   67
% identity
                  (AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum
NCBI Description
                   crystallinum]
                   267486
Seq. No.
                   13195 1.R1011
Contig ID
                   uC-zmflb73131b09b2
5'-most EST
                   BLASTX
Method
                   g3036840
NCBI GI
BLAST score
                   541
```

6.0e-55 E value 238 Match length

47 % identity

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(AJ222967) cystinosin [Homo sapiens] NCBI Description

>gi_3036851_emb_CAA75882_ (Y15924) cystinosin [Homo

sapiens]



Seq. No. 267487 Contig ID 13195

13195_3.R1011

5'-most EST

LIB148-001-Q1-E1-C1 BLASTX

Method NCBI GI BLAST score E value Match length

g3874889 175 2.0e-12

63

49

% identity NCBI Description

(Z48045) similarity to the transmembranous domains of yeast

ERS1 protein; cDNA EST EMBL:D69878 comes from this gene; cDNA EST EMBL:D66181 comes from this gene; cDNA EST yk413c7.5 comes from this gene [Caenorhabditis elegans]

Seq. No. 267488

Contig ID 13197_1.R1011 5'-most EST LIB84-004-Q1-E1-H3

Method BLASTX
NCBI GI g3878571
BLAST score 193
E value 2.0e-14
Match length 175
% identity 30

NCBI Description (Z46381) Weak similarity with the Ysy6 protein (Yeast) (PIR

accession number JQ0912); cDNA EST EMBL:D32318 comes from this gene; cDNA EST EMBL:D33688 comes from this gene; cDNA

EST EMBL: D34664 comes from this gene; cDNA EST EMB

Seq. No. 267489

Contig ID 13200 1.R1011 5'-most EST wyr700242115.h1

Method BLASTX
NCBI GI g1408222
BLAST score 649
E value 9.0e-68
Match length 160
% identity 82

NCBI Description (U60764) pathogenesis-related protein [Sorghum bicolor]

Seq. No. 267490

Contig ID 13200_3.R1011 5'-most EST wyr700238351.h1

Method BLASTN
NCBI GI g1408221
BLAST score 74

E value 1.0e-33
Match length 90
% identity 96

NCBI Description Sorghum bicolor pathogenesis-related protein (PR-10) mRNA,

complete cds

Seq. No. 267491

Contig ID 13200_4.R1011 5'-most EST wyr700239420.h1

Method BLASTN NCBI GI g1408221

BLAST score 70



5.0e-31 E value 167 Match length 93 % identity NCBI Description Sorghum bicolor pathogenesis-related protein (PR-10) mRNA, complete cds 267492 Seq. No. 13201_1.R1011 Contig ID 5'-most EST dyk700106554.hl Method BLASTX NCBI GI q4490736 BLAST score 563 E value 8.0e-58 Match length 216 38 % identity (AL035708) putative protein [Arabidopsis thaliana] NCBI Description 267493 Seq. No. 13202 1.R1011 Contig ID 5'-most EST $ymt70\overline{0}222143.h1$ Method BLASTX NCBI GI g3298605 BLAST score 188 E value 1.0e-13 Match length 218 26 % identity (AF057365) UDP N-acetylglucosamine transporter [Canis NCBI Description familiaris] 267494 Seq. No. Contig ID 13202 2.R1011 5'-most EST uC-zmflb73006b10a1 267495 Seq. No. 13205 1.R1011 Contig ID 5'-most EST uC-zmflb73116h10b2 Method BLASTX NCBI GI g3097266 BLAST score 632 E value 6.0e-66 Match length 164 % identity 72 (Y17186) translation initiation factor [Pisum sativum] NCBI Description 267496 Seq. No. Contig ID 13205 2.R1011 5'-most EST LIB3151-020-Q1-K1-G3 Method BLASTX q3097266 NCBI GI BLAST score 319 E value 3.0e-71

% identity 77
NCBI Description (Y17186) translation initiation factor [Pisum sativum]

Seq. No. 267497

Match length

Contig ID 13207_1.R1011



```
rvt700552338.h1
5'-most EST
                  BLASTX
Method
                  g3367632
NCBI GI
                  673
BLAST score
                  2.0e-70
E value
                  219
Match length
                  59
% identity
                  (AJ000539) phosphatidylinositol synthase [Arabidopsis
NCBI Description
                  thaliana]
                  267498
Seq. No.
                  13213 1.R1011
Contig ID
5'-most EST
                  LIB3079-039-Q1-K1-C9
                  BLASTX
Method
                  g1663724
NCBI GI
                  688
BLAST score
                  3.0e-72
E value
Match length
                  279
                  50
% identity
                  (U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
NCBI Description
                  267499
Seq. No.
                  13219 1.R1011
Contig ID
                   vux700160467.h1
5'-most EST
                  BLASTX
Method
                   g2281115
NCBI GI
                   232
BLAST score
E value
                   1.0e-18
Match length
                   258
                   27
% identity
                  (AC002330) putative cullin-like 1 protein [Arabidopsis
NCBI Description
                   thaliana]
                   267500
Seq. No.
                   13219 2.R1011
Contig ID
5'-most EST
                   LIB3115-001-Q1-K1-D4
Seq. No.
                   267501
                   13224 1.R1011
Contig ID
                   tzu700206559.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2130141
                   333
BLAST score
                   4.0e-31
E value
                   125
Match length
% identity
                   mudrA protein - maize transposon MuDR >gi_540581 (M76978)
NCBI Description
                   mudrA [Zea mays] >gi 595816 (U14597) mudrA gene product
                   [Zea mays]
                   267502
Seq. No.
Contig ID
                   13228 1.R1011
5'-most EST
                   LIB3079-039-Q1-K1-A3
```

37209

267503

13233 1.R1011

uC-zmflb73061a09b1

Seq. No.

Contig ID 5'-most EST



Method BLASTX
NCBI GI g4581156
BLAST score 723
E value 2.0e-76
Match length 235
% identity 64

NCBI Description (AC006919) putative pyruvate kinase [Arabidopsis thaliana]

Seq. No. 267504

Contig ID 13236_1.R1011

5'-most EST LIB3079-039-Q1-K1-B2

Method BLASTX
NCBI GI g2244898
BLAST score 245
E value 2.0e-20
Match length 93
% identity 53

NCBI Description (Z97338) strong similarity to protein phosphatase 2A

regulatory chain, 74K [Arabidopsis thaliana]

Seq. No. 267505

Contig ID 13238_1.R1011 5'-most EST rvt700550532.h1

Method BLASTX
NCBI GI g3980254
BLAST score 590
E value 8.0e-61
Match length 176
% identity 63

NCBI Description (AJ006053) peroxisomal membrane protein [Arabidopsis

thaliana]

Seq. No. 267506

Contig ID 13240_1.R1011

5'-most EST uC-zmflmo17134b03a1

Method BLASTX
NCBI GI g2191137
BLAST score 197
E value 2.0e-15
Match length 67
% identity 55

NCBI Description (AF007269) similar to the GDSL family of lipolytic enzymes

[Arabidopsis thaliana]

Seq. No. 267507

Contig ID 13241_1.R1011 5'-most EST xsy700212191.h1

Seq. No. 267508

Contig ID 13242 2.R1011

5'-most EST LIB3079-038-Q1-K1-G2

Seq. No. 267509

Contig ID 13246 1.R1011

5'-most EST LIB3059-058-Q1-K1-G9

Method BLASTN NCBI GI g2832242



BLAST score 39 3.0e-12 E value 55 Match length 93 % identity NCBI Description

Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. Contig ID 5'-most EST 267510 13260 1.R1011

LIB3067-025-Q1-K1-F8

Seq. No. Contig ID 5'-most EST 267511 13260 2.R1011 xsy700208715.hl

Seq. No. Contig ID 267512 13264 1.R1011

uC-zmflB73047f11b1 5'-most EST

Method BLASTX g2982303 NCBI GI 1209 BLAST score 1.0e-133 E value Match length 269 83 % identity

MCBI Description

(AF051236) hypothetical protein [Picea mariana]

Seq. No.

267513 13264 2.R1011 Contig ID pmx700085717.h1 5'-most EST

BLASTX Method g2982303 NCBI GI BLAST score 351 4.0e-33 E value 82 Match length

78 % identity

(AF051236) hypothetical protein [Picea mariana] NCBI Description

Seq. No. Contig ID 267514 13267 1.R1011 wyr700241855.h1

5'-most EST

267515

Seq. No. Contig ID

13270 1.R1011

5'-most EST

LIB3180-062-P2-M1-H2

Seq. No.

267516

Contig ID 5'-most EST 13274 1.R1011 ceu700429882.h1

Seq. No.

267517

Contig ID 5'-most EST 13275 1.R1011 qmh700028252.fl

Seq. No.

267518

Contig ID

13279 1.R1011

5'-most EST

LIB3079-038-Q1-K1-D2

Seq. No.



Contig ID 13280 1.R1011

5'-most EST LIB3079-038-Q1-K1-D3

Seq. No. 267520

Contig ID 13281_1.R1011 5'-most EST vux700156618.h1

Seq. No. 267521

Contig ID 13286 1.R1011

5'-most EST LIB3079-038-Q1-K1-E1

Method BLASTX
NCBI GI g4191774
BLAST score 718
E value 9.0e-76
Match length 287
% identity 48

NCBI Description (AC005917) putative beta-1,3-endoglucanase [Arabidopsis

thaliana]

Seq. No. 267522

Contig ID 13289 1.R1011

5'-most EST LIB3079-038-Q1-K1-B1

Seq. No. 267523

Contig ID 13293_1.R1011 5'-most EST uC-zmroB73070b06b1

Seq. No. 267524

Contig ID 13294_1.R1011 5'-most EST uC-zmroB73070h02b1

Method BLASTX
NCBI GI g4587993
BLAST score 494
E value 2.0e-49
Match length 172
% identity 58

NCBI Description (AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No. 267525

Contig ID 13294_2.R1011

5'-most EST LIB3136-014-Q1-K1-G10

Method BLASTX
NCBI GI g4587993
BLAST score 1029
E value 1.0e-129
Match length 420
% identity 59

NCBI Description (AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No. 267526

Contig ID 13298_1.R1011 5'-most EST ceu700430942.h1

Method BLASTX
NCBI GI g1532168
BLAST score 230
E value 8.0e-19
Match length 66



% identity 68
NCBI Description

(U63815) localized according to blastn similarity to EST
sequences; therefore, the coding span corresponds only to
an area of similarity since the initation codon and stop
codon could not be precisely determined [Arabidopsis
thaliana]

Seq. No. 267527

Contig ID 13298_2.R1011

5'-most EST LIB3079-038-Q1-K1-B9

Method BLASTX
NCBI GI g1532168
BLAST score 233
E value 5.0e-19
Match length 66
% identity 65

NCBI Description (U63815) localized according to blastn similarity to EST

sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop codon could not be precisely determined [Arabidopsis

thaliana]

Seq. No. 267528

Contig ID 13298_4.R1011 5'-most EST gct701178093.h1

Method BLASTX
NCBI GI g1532168
BLAST score 152
E value 3.0e-10
Match length 43
% identity 67

NCBI Description (U63815) localized according to blastn similarity to EST

sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop codon could not be precisely determined [Arabidopsis

thaliana]

Seq. No. 267529

Contig ID 13299 1.R1011

5'-most EST uC-zmroteosinte012h06b1

Method BLASTX
NCBI GI g2443329
BLAST score 921
E value 3.0e-99
Match length 293
% identity 64

NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No. 267530

Contig ID 13299 2.R1011 5'-most EST xmt700257592.h1

Method BLASTX
NCBI GI g4567249
BLAST score 1180
E value 1.0e-130
Match length 277
% identity 77

% identity



```
NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]
                  267531
Seq. No.
                  13306 1.R1011
Contig ID
5'-most EST
                  LIB3136-020-Q1-K1-A7
Method
                  BLASTX
                  g2088662
NCBI GI
BLAST score
                  359
E value
                  1.0e-33
Match length
                  147
% identity
                  49
                  (AF002109) unknown protein [Arabidopsis thaliana]
NCBI Description
                  267532
Seq. No.
                  13306 2.R1011
Contig ID
5'-most EST
                  uC-zmflb73027a03a1
                  267533
Seq. No.
                  13311 1.R1011
Contig ID
5'-most EST
                  LIB3079-037-Q1-K1-H5
                  BLASTN
Method
NCBI GI
                  g3821780
BLAST score
                  36
                  2.0e-10
E value
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  267534
Seq. No.
                  13312 1.R1011
Contig ID
5'-most EST
                  LIB3158-018-Q1-K1-F9
                  267535
Seq. No.
                  13314 1.R1011
Contig ID
                  LIB3079-038-Q1-K1-A5
5'-most EST
Seq. No.
                  267536
                  13316 1.R1011
Contig ID
                  uC-zmflmo17011d09b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4204313
BLAST score
                  203
                   1.0e-15
E value
Match length
                   92
                   46
% identity
                  (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   267537
Contig ID
                   13319 1.R1011
5'-most EST
                  LIB3079-038-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                   q4510348
BLAST score
                   298
E value
                   8.0e-27
Match length
                  137
```



```
(AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                  267538
Seq. No.
                  13325 1.R1011
Contig ID
                  LIB3069-037-Q1-K1-E10
5'-most EST
                  267539
Seq. No.
                  13330_1.R1011
Contig ID
5'-most EST
                  LIB3079-037-Q1-K1-G10
                  BLASTX
Method
                  g1653702
NCBI GI
BLAST score
                  584
                  2.0e-60
E value
                  187
Match length
                   61
% identity
                  (D90915) dihydrolipoamide acetyltransferase component (E2)
NCBI Description
                  of pyruvate dehydrogenase complex [Synechocystis sp.]
                  267540
Seq. No.
                  13332 1.R1011
Contig ID
5'-most EST
                  rvt700553179.h1
                  BLASTX
Method
                  g2995366
NCBI GI
                   429
BLAST score
                   1.0e-41
E value
Match length
                   364
% identity
                   34
                  (AL022245) conserved hypothetical protein
NCBI Description
                   [Schizosaccharomyces pombe]
                   267541
Seq. No.
Contig ID
                   13332 2.R1011
                   LIB143-060-Q1-E1-C2
5'-most EST
                   267542
Seq. No.
Contig ID
                   13334 1.R1011
5'-most EST
                   dyk700103346.hl
                   267543
Seq. No.
                   13336 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17339c08b1
                   267544
Seq. No.
                   13343 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73202g10b1
Method
                   BLASTX
NCBI GI
                   g2623297
BLAST score
                   193
E value
                   3.0e-14
Match length
                   62
% identity
                   55
                   (AC002409) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3790583 (AF079180) RING-H2 finger protein RHC1a
```

Seq. No. 267545 Contig ID 13351

13351_1.R1011

[Arabidopsis thaliana]



5'-most EST LIB3079-037-Q1-K1-F12 Method BLASTX NCBI GI q3914424 203 BLAST score 7.0e-16 E value Match length 69 % identity 61 PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8) NCBI Description (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8) >gi 2511592_emb_CAA74027.1_ (Y13693) multicatalytic endopeptidase complex, proteasome component, alpha subunit [Arabidopsis thaliana] 267546 Seq. No. 13353 1.R1011 Contig ID LIB3079-037-Q1-K1-D6 5'-most EST BLASTX Method NCBI GI q3023280 177 BLAST score 7.0e-13 E value 61 Match length 49 % identity AUGMENTER OF LIVER REGENERATION >gi_4096810 (U40494) ALR NCBI Description [Mus musculus] 267547 Seq. No. 13365_1.R1011 Contig ID 5'-most EST uC-zmrob73075a05b1 BLASTX Method g2160190 NCBI GI 465 BLAST score 3.0e-46E value 127 Match length 73 % identity (AC000132) No definition line found [Arabidopsis thaliana] NCBI Description 267548 Seq. No. Contig ID 13366 1.R1011 LIB3079-037-Q1-K1-D5 5'-most EST 267549 Seq. No. Contig ID 13375 1.R1011 ceu700432977.h1 5'-most EST 267550 Seq. No. Contig ID 13377 1.R1011 5'-most EST LIB3079-037-Q1-K1-B4 Seq. No. 267551 13380 1.R1011 Contig ID 5'-most EST LIB3067-032-Q1-K1-A11 Method BLASTX

NCBI GI g1169228 BLAST score 209 E value 1.0e-16 45 Match length 76 % identity



NCBI Description RNA HELICASE-LIKE PROTEIN DB10 >gi_1084413_pir__S42639

helicase-like protein - Wood tobacco

>gi 563986 dbj BAA03763_ (D16247) RNA helicase like protein

DB10 [Nicotiana sylvestris]

Seq. No. 267552

Contig ID 13383 1.R1011

5'-most EST LIB3067-043-Q1-K1-A5

Method BLASTX
NCBI GI g2252843
BLAST score 184
E value 1.0e-13
Match length 60
% identity 62

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 267553

Contig ID 13384 1.R1011

5'-most EST LIB3079-036-Q1-K1-H11

Seq. No. 267554

Contig ID 13385_1.R1011

5'-most EST uC-zmflmo17136d10b1

Method BLASTX
NCBI GI g3834317
BLAST score 948
E value 1.0e-102

E value 1.0e-Match length 241 % identity 72

NCBI Description (AC005679) Similar to CDC16 protein gb_U18291 (CDC16Hs)

from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 267555

Contig ID 13385 2.R1011 5'-most EST uC-zmflb73124f08b1

Method BLASTX

NCBI GI g3834317
BLAST score 322
E value 1.0e-29
Match length 111
% identity 57

NCBI Description (AC005679) Similar to CDC16 protein gb_U18291 (CDC16Hs)

from Homo sapiens. [Arabidopsis thaliana]

Seq. No. 267556

Contig ID 13385_3.R1011

5'-most EST LIB3150-061-Q1-N1-A5

Seq. No. 267557

Contig ID 13385_4.R1011 5'-most EST uC-zmflb73124f06a1

Seq. No. 267558

Contig ID 13393 1.R1011

5'-most EST LIB3079-006-Q1-K1-F3

Seq. No. 267559



Contig ID 13397 1.R1011 LIB3117-008-Q1-K1-E1 5'-most EST BLASTX Method NCBI GI q2129752 BLAST score 315 1.0e-28 E value 124 Match length 51 % identity thioredoxin - Arabidopsis thaliana >gi_992964_emb_CAA84612_ NCBI Description (Z35475) thioredoxin [Arabidopsis thaliana] 267560 Seq. No. 13397 2.R1011 Contig ID 5'-most EST gct701172337.hl Method BLASTX g2982247 NCBI GI BLAST score 148 3.0e-09 E value Match length 39 % identity 67 NCBI Description (AF051206) probable thioredoxin H [Picea mariana] Seq. No. 267561 Contig ID 13398 1.R1011 5'-most EST LIB3150-094-P1-N1-B6 267562 Seq. No. 13400 1.R1011 Contig ID 5'-most EST dyk700102822.h1 267563 Seq. No. 13406 1.R1011 Contig ID LIB3079-036-Q1-K1-D9 5'-most EST Seq. No. 267564 13410 1.R1011 Contig ID 5'-most EST ymt700224123.h1 267565 Seq. No. 13410 2.R1011 Contig ID $uC-zm\overline{f}lb73167e04b2$ 5'-most EST 267566 Seq. No. 13415 1.R1011 Contig ID 5'-most EST LIB143-002-Q1-E1-D6 Method BLASTX q575292 NCBI GI BLAST score

Method BLASTX
NCBI GI g575292
BLAST score 1678
E value 0.0e+00
Match length 368
% identity 88

NCBI Description (X82548) SNF1-related protein kinase [Hordeum vulgare]

Seq. No. 267567

Contig ID 13419 1.R1011

5'-most EST LIB3079-036-Q1-K1-B7

Method BLASTX



NCBI GI g4539423 BLAST score 164 E value 3.0e-11 Match length 58 % identity 57

NCBI Description (AL049171) pyrophosphate-dependent phosphofructo-1-kinase

[Arabidopsis thaliana]

Seq. No. 267568

Contig ID 13427 1.R1011

5'-most EST uC-zmroteosinte001c06b1

Method BLASTX
NCBI GI g1168819
BLAST score 176
E value 4.0e-12
Match length 90
% identity 36

NCBI Description CELL DIVISION CONTROL PROTEIN 91 >gi_626120_pir__S48522

cell division control protein CDC91 - yeast (Saccharomyces

cerevisiae) >gi_469466 (L31649) cdc91 [Saccharomyces cerevisiae] >gi_717072 (U22383) Cdc91p [Saccharomyces

cerevisiae]

Seq. No. 267569

Contig ID 13440 1.R1011

5'-most EST LIB3079-035-Q1-K1-G10

Seq. No. 267570

Contig ID 13441 1.R1011

5'-most EST LIB3079-035-Q1-K1-G4

Seq. No. 267571

Contig ID 13443 1.R1011

5'-most EST LIB3067-019-Q1-K1-H7

Method BLASTX
NCBI GI g3451321
BLAST score 153
E value 4.0e-09
Match length 213
% identity 24

NCBI Description (AL031323) putative transcription or splicing factor

[Schizosaccharomyces pombe]

Seq. No. 267572

Contig ID 13445 1.R1011 5'-most EST uC-zmflb73196h05b1

Method BLASTX
NCBI GI g3608152
BLAST score 406
E value 3.0e-51
Match length 210
% identity 53

NCBI Description (AC005314) hypothetical protein [Arabidopsis thaliana]

Seq. No. 267573

Contig ID 13447_1.R1011 5'-most EST uC-zmflb73124e03b1



Method BLASTX
NCBI GI g4580398
BLAST score 496
E value 2.0e-86
Match length 248
% identity 67

NCBI Description (AC007171) putative protein kinase APK1A [Arabidopsis

thaliana]

Seq. No. 267574

Contig ID 13450_1.R1011 5'-most EST ymt700220337.h1

Method BLASTX
NCBI GI g2961107
BLAST score 218
E value 5.0e-17
Match length 89
% identity 45

NCBI Description (AF042383) TLS-associated protein with SR repeats [Mus

musculus] >gi_2961149 (AF047448) TLS-associated protein

TASR [Homo sapiens]

Seq. No. 267575

Contig ID 13450 2.R1011

5'-most EST LIB3061-031-Q1-K1-H12

Seq. No. 267576

Contig ID 13454 1.R1011

5'-most EST LIB3079-035-Q1-K1-E8

Seq. No. 267577

Contig ID 13455_1.R1011 5'-most EST yyf700348611.h1

Seq. No. 267578

Contig ID 13456_1.R1011

5'-most EST uC-zmroteosinte012e11b1

Method BLASTX
NCBI GI g4455172
BLAST score 703
E value 6.0e-74
Match length 218
% identity 62

NCBI Description (AL035521) putative protein [Arabidopsis thaliana]

Seq. No. 267579

Contig ID 13464 1.R1011

5'-most EST LIB3079-001-Q1-K1-E8

Seq. No. 267580

Contig ID 13465_1.R1011 5'-most EST LIB84-015-Q1-E1-D3

Method BLASTX
NCBI GI g1432056
BLAST score 205
E value 4.0e-16
Match length 49



% identity 76

NCBI Description (U56834) WRKY3 [Petroselinum crispum]

Seq. No. 267581

Contig ID 13466_1.R1011 5'-most EST ntr700074546.h1

Method BLASTX
NCBI GI g2588816
BLAST score 762
E value 2.0e-98
Match length 267
% identity 71

NCBI Description (D88926) cytosolic phosphoglucose isomerase [Dioscorea tokoro] >gi_2588820_dbj_BAA23183_ (D88928) cytosolic

phosphoglucose isomerase [Dioscorea tokoro]

Seq. No. 267582

Contig ID 13466 2.R1011

5'-most EST LIB3079-001-Q1-K1-H7

Method BLASTX
NCBI GI g1346073
BLAST score 476
E value 8.0e-48
Match length 114
% identity 84

NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI)

(PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi_596023 (U17225) glucose-6 phosphate isomerase

[Zea mays]

Seq. No. 267583

Contig ID 13470 1.R1011

5'-most EST uC-zmflmo17273g04b1

Method BLASTX
NCBI GI g125271
BLAST score 1631
E value 0.0e+00
Match length 330
% identity 93

NCBI Description CASEIN KINASE II, ALPHA CHAIN (CK II) (CK2-ALPHA)

>gi_100860_pir__S19726 casein kinase II (EC 2.7.1.-) alpha chain - maize >gi_3318993_pdb_1A60_ Protein Kinase Ck2 (Catalytic Subunit) From Zea Mays >gi_22117_emb_CAA43659_(Y61387) casein kinase II alpha subunit [720 mays]

(X61387) casein kinase II alpha subunit [Zea mays]

Seq. No. 267584

Contig ID 13470_3.R1011 5'-most EST xsy700208611.h1

Method BLASTX
NCBI GI g125271
BLAST score 542
E value 1.0e-55
Match length 113
% identity 92

NCBI Description CASEIN KINASE II, ALPHA CHAIN (CK II) (CK2-ALPHA)

>gi_100860_pir__S19726 casein kinase II (EC 2.7.1.-) alpha
chain - maize >gi_3318993_pdb_1A60 Protein Kinase Ck2



(Catalytic Subunit) From Zea Mays >gi_22117_emb_CAA43659_(X61387) casein kinase II alpha subunit [Zea mays]

Seq. No. 267585

Contig ID 13470_4.R1011 5'-most EST uC-zmflb73317c05b1

Method BLASTX
NCBI GI g125271
BLAST score 480
E value 5.0e-48
Match length 100
% identity 93

NCBI Description CASEIN KINASE II, ALPHA CHAIN (CK II) (CK2-ALPHA)

>gi_100860_pir__S19726 casein kinase II (EC 2.7.1.-) alpha chain - maize >gi_3318993_pdb_1A60_ Protein Kinase Ck2 (Catalytic Subunit) From Zea Mays >gi_22117_emb_CAA43659_

(X61387) casein kinase II alpha subunit [Zea mays]

Seq. No. 267586

Contig ID 13471 1.R1011

5'-most EST LIB3079-002-Q1-K1-H7

Method BLASTX
NCBI GI g2130119
BLAST score 1168
E value 1.0e-145
Match length 298
% identity 91

NCBI Description cyclin Ia - maize

Seq. No. 267587

Contig ID 13471_3.R1011 5'-most EST uC-zmflb73276a06a1

Method BLASTN
NCBI GI g516553
BLAST score 38
E value 5.0e-12
Match length 111
% identity 92

NCBI Description Zea mays B73 cyclin IaZm mRNA, partial cds

Seq. No. 267588

Contig ID 13472 1.R1011

5'-most EST LIB3079-003-Q1-K1-A2

Seq. No. 267589

Contig ID 13473 1.R1011

5'-most EST LIB3069-036-Q1-K1-D11

Seq. No. 267590

Contig ID 13476_1.R1011 5'-most EST wyr700239767.h1

Method BLASTX
NCBI GI g1931647
BLAST score 1730
E value 0.0e+00
Match length 445
% identity 74



```
(U95973) endomembrane protein EMP70 precusor isolog
NCBI Description
                  [Arabidopsis thaliana]
                  267591
Seq. No.
                  13476 2.R1011
Contig ID
                  uC-zmflmo17173g11b1
5'-most EST
Method
                  BLASTX
                  g1931647
NCBI GI
                  391
BLAST score
                  1.0e-37
E value
                  86
Match length
% identity
                  84
                  (U95973) endomembrane protein EMP70 precusor isolog
NCBI Description
                   [Arabidopsis thaliana]
                  267592
Seq. No.
                  13476 5.R1011
Contig ID
                  xyt700346263.h1
5'-most EST
                  BLASTX
Method
                  g1931647
NCBI GI
                  152
BLAST score
                   5.0e-10
E value
                  50
Match length
                   62
% identity
                  (U95973) endomembrane protein EMP70 precusor isolog
NCBI Description
                   [Arabidopsis thaliana]
                   267593
Seq. No.
                   13476 9.R1011
Contig ID
                  uC-zmflmo17258h01b1
5'-most EST
                   BLASTX
Method
                   g1931647
NCBI GI
                   143
BLAST score
                   7.0e-09
E value
                   28
Match length
                   93
% identity
                  (U95973) endomembrane protein EMP70 precusor isolog
NCBI Description
                   [Arabidopsis thaliana]
                   267594
Seq. No.
                   13482 1.R1011
Contig ID
5'-most EST
                   wyr700239060.h1
                   267595
Seq. No.
                   13492 1.R1011
Contig ID
                   cat700017937.rl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2494140
BLAST score
                   209
                   1.0e-16
E value
Match length
                   86
% identity
                   (AC003002) R29515_1 [Homo sapiens] >gi_3068727 (AF058918)
NCBI Description
                   unknown [Homo sapiens]
```

37223

267596

13492 2.R1011

Seq. No. Contig ID



```
LIB3070-006-Q1-N1-A7
5'-most EST
Method
                  BLASTX
                  g2494140
NCBI GI
BLAST score
                  265
                  5.0e-23
E value
                  105
Match length
                  52
% identity
                  (AC003002) R29515_1 [Homo sapiens] >gi_3068727 (AF058918)
NCBI Description
                  unknown [Homo sapiens]
                  267597
Seq. No.
Contig ID
                  13500 1.R1011
                  LIB3079-006-Q1-K1-B1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2760844
BLAST score
                  358
E value
                  2.0e-49
                  169
Match length
                  61
% identity
                  (AC003105) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  267598
Seq. No.
                  13508 1.R1011
Contig ID
5'-most EST
                  LIB3079-006-Q1-K1-F5
                  267599
Seq. No.
Contig ID
                  13513 1.R1011
                  LIB3079-006-Q1-K1-G2
5'-most EST
                   267600
Seq. No.
                  13520 1.R1011
Contig ID
                  LIB3079-007-Q1-K1-C7
5'-most EST
Method
                   BLASTX
                   q3724366
NCBI GI
                   167
BLAST score
E value
                   2.0e-11
Match length
                   62
% identity
NCBI Description (AB018379) unknown ORF [Thermus thermophilus]
Seq. No.
                   267601
Contig ID
                   13521 1.R1011
5'-most EST
                   uC-zmflmo17396g01a1
Seq. No.
                   267602
Contig ID
                   13533 1.R1011
5'-most EST
                   uC-zmflmo17155h10b1
Method
                   BLASTX
NCBI GI
                   g1346073
BLAST score
                   1562
                   1.0e-174
E value
                   309
Match length
                   96
% identity
NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI)
```

37224

[Zea mays]

(PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi 596023 (U17225) glucose-6 phosphate isomerase

BLAST score

Match length

E value

227 1.0e-18

79



```
267603
Seq. No.
                   13539 1.R1011
Contig ID
5'-most EST
                   uC-zmrob73006d02b1
                   BLASTX
Method
NCBI GI
                   g121950
BLAST score
                   317
                   4.0e-29
E value
Match length
                   71
                   89
% identity
NCBI Description
                   HISTONE H1 >gi 22321 emb CAA40362 (X57077) H1 histone [Zea
                   mays]
                   267604
Seq. No.
Contig ID
                   13550 1.R1011
                   uC-zmflb73017h11b1
5'-most EST
Method
                   BLASTX
                   g3176726
NCBI GI
                   534
BLAST score
E value
                   8.0e-87
Match length
                   224
                   73
% identity
NCBI Description
                   (AC002392) putative serine proteinase [Arabidopsis
                   thaliana]
                   267605
Seq. No.
                   13553 1.R1011
Contig ID
                   uC-zmflb73307c04b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q458692
BLAST score
                   209
E value
                   4.0e-16
Match length
                   92
                   43
% identity
NCBI Description
                   (U06631) homologous to mouse gene PC326:GenBank Accession
                   Number M95564 [Homo sapiens]
                   267606
Seq. No.
                   13556 1.R1011
Contig ID
5'-most EST
                   uC-zm\overline{f}lb73137f09b1
                   267607
Seq. No.
                   13557 1.R1011
Contig ID
                   cyk700048684.f1
5'-most EST
Seq. No.
                   267608
                   13561 1.R1011
Contig ID
                   wty70\overline{0}166236.h1
5'-most EST
                   267609
Seq. No.
                   13566 2.R1011
Contig ID
5'-most EST
                   LIB3068-038-Q1-K1-D12
                   BLASTX
Method
NCBI GI
                   g531829
```



% identity 56 (U12390) beta-galactosidase alpha peptide [cloning vector NCBI Description pSport1] Seq. No. 267610 13569 1.R1011 Contig ID 5'-most EST LIB3079-012-Q1-K1-G10 267611 Seq. No. 13570 1.R1011 Contig ID uC-zmflb73198c11b1 5'-most EST 267612 Seq. No. 13570 2.R1011 Contig ID uC-zmrob73045c01a1 5'-most EST 267613 Seq. No. 13571 1.R1011 Contig ID LIB3150-071-P1-N1-H3 5'-most EST BLASTX Method NCBI GI g2275213 BLAST score 356 2.0e-33 E value Match length 173 48 % identity (AC002337) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 267614 13575 1.R1011 Contig ID LIB3079-013-Q1-K1-A12 5'-most EST Seq. No. 267615 13580 1.R1011 Contig ID 5'-most EST uC-zmflmo17223q04b1 Seq. No. 267616 Contig ID 13583 1.R1011 5'-most EST LIB3061-058-Q1-K1-G8 Method BLASTX NCBI GI g2191134 BLAST score 364 E value 2.0e-34 Match length 95 % identity 65 (AF007269) contains weak similarity to Galectin-3 binding NCBI Description protein [Arabidopsis thaliana] Seq. No. 267617 13583 2.R1011 Contig ID LIB3079-013-Q1-K1-H8 5'-most EST Method BLASTX

g4559381 NCBI GI BLAST score 430 2.0e-42 E value Match length 156 % identity

(AC006526) hypothetical protein [Arabidopsis thaliana] NCBI Description



267618 Seq. No. 13584 1.R1011 Contig ID 5'-most EST dyk700102957.h1 BLASTX Method q4104929 NCBI GI 513 BLAST score 3.0e-51E value Match length 650 37 % identity NCBI Description (AF042195) auxin response factor 7 [Arabidopsis thaliana] 267619 Seq. No. 13591_1.R1011 Contig ID 5'-most EST uC-zmroteosinte087g12b2 267620 Seq. No. 13593 1.R1011 Contig ID nwy700444935.h1 5'-most EST Seq. No. 267621 Contig ID 13609_1.R1011 5'-most EST LIB3062-046-Q1-K1-H12 Method BLASTX g4544409 NCBI GI BLAST score 633 E value 1.0e-122 370 Match length 60 % identity (AC006955) putative transcription factor [Arabidopsis NCBI Description thaliana] >gi 4585920 gb AAD25580.1 AC007211 2 (AC007211) putative scarecrow homolog [Arabidopsis thaliana] Seq. No. 267622 13609 2.R1011 Contig ID tfd700570440.h1 5'-most EST Seq. No. 267623 13612 1.R1011 Contig ID LIB3059-048-Q1-K1-F2 5'-most EST Method BLASTX NCBI GI g2224899 BLAST score 382 3.0e - 36E value 269 Match length % identity 37 (U67133) DNA-binding protein PcMYB1 [Petroselinum crispum] NCBI Description 267624 Seq. No. 13612 2.R1011 Contig ID $fwa70\overline{0}098017.h1$ 5'-most EST Method BLASTX

Method BLASTX
NCBI GI g4503523
BLAST score 1030
E value 1.0e-112
Match length 379
% identity 53



NCBI Description UNKNOWN >gi_2351378 (U54558) translation initiation factor eIF3 p66 subunit [Homo sapiens] >gi_4200328_emb_CAA18440_ (AL022313) EIF3-P66 [Homo sapiens]

Seq. No. 267625

Contig ID 13612_3.R1011 5'-most EST uC-zmflb73216h05b2

Seq. No. 267626

Contig ID 13613 1.R1011

5'-most EST LIB3079-017-Q1-K1-A5

Seq. No. 267627

Contig ID 13613_2.R1011 5'-most EST rv1700456986.h1

Method BLASTX
NCBI GI g3264848
BLAST score 176
E value 5.0e-13
Match length 77

% identity 44

NCBI Description (AC005197) UOG1_HUMAN [Homo sapiens]

Seq. No. 267628

Contig ID 13626_1.R1011 5'-most EST uC-zmflb73302a07a1

Seq. No. 267629

Contig ID 13628_1.R1011 5'-most EST uC-zmflb73247h08a2

Seq. No. 267630

Contig ID 13629_1.R1011

5'-most EST LIB3079-019-Q1-K1-C6

Seq. No. 267631

Contig ID 13640_1.R1011

5'-most EST uC-zmroteosinte091g08b2

Seq. No. 267632

Contig ID 13649_1.R1011 5'-most EST uC-zmflb73296f04b2

Method BLASTX
NCBI GI g2642158
BLAST score 439
E value 1.0e-45

Match length 143 % identity 63

NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No. 267633

Contig ID 13649 2.R1011

5'-most EST LIB3158-016-Q1-K1-E7

Seq. No. 267634

Contig ID 13650 1.R1011

5'-most EST LIB3079-021-Q1-K1-A2



```
Method
                  BLASTX
                  g1834379
NCBI GI
                  178
BLAST score
                  9.0e-13
E value
                  98
Match length
                   41
% identity
                  (Y10551) ComAB [Bacillus licheniformis]
NCBI Description
                   267635
Seq. No.
                   13663 1.R1011
Contig ID
                  wen700334779.h1
5'-most EST
Method
                  BLASTX
                   q4454457
NCBI GI
                   457
BLAST score
                   2.0e-45
E value
Match length
                   116
                   75
% identity
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   267636
Seq. No.
                   13664 1.R1011
Contig ID
                   LIB3079-022-Q1-K1-B7
5'-most EST
Method
                   BLASTX
                   g4587615
NCBI GI
                   719
BLAST score
                   4.0e-76
E value
Match length
                   207
% identity
                   65
                  (AC006951) putative acyl-CoA synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   267637
Seq. No.
                   13668_1.R1011
Contig ID
                   clt700046058.f1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2252847
BLAST score
                   563
                   4.0e-58
E value
                   136
Match length
                   79
% identity
                  (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
                   267638
Seq. No.
                   13671 1.R1011
Contig ID
5'-most EST
                   LIB3079-022-Q1-K1-G2
Seq. No.
                   267639
Contig ID
                   13680 1.R1011
5'-most EST
                   LIB3137-011-Q1-K1-C8
                   BLASTX
Method
NCBI GI
                   g1001955
BLAST score
                   632
                   6.0e-66
E value
Match length
                   184
                   72
% identity
```

37229

NCBI Description (U19099) unknown protein [Lycopersicon chilense]



Seq. No. 267640

Contig ID 13681_1.R1011

5'-most EST LIB3079-023-Q1-K1-G1

Seq. No. 267641

Contig ID 13683_1.R1011

5'-most EST uC-zmflmo17100g09b1

Seq. No. 267642

Contig ID 13689_1.R1011

5'-most EST uC-zmflmo17060b06b1

Method BLASTX
NCBI GI g3738302
BLAST score 617
E value 6.0e-64
Match length 233
% identity 58

NCBI Description (AC005309) tubby-like protein [Arabidopsis thaliana]

>gi_4249398 (AC006072) putative tubby protein [Arabidopsis

thaliana]

Seq. No. 267643

Contig ID 13695_1.R1011

5'-most EST LIB3079-025-Q1-K1-C9

Method BLASTX
NCBI GI g3063467
BLAST score 411
E value 6.0e-40
Match length 126
% identity 64

NCBI Description (AC003981) F22013.29 [Arabidopsis thaliana]

Seq. No. 267644

Contig ID 13698_1.R1011

5'-most EST LIB3079-025-Q1-K1-E12

Method BLASTX
NCBI GI g3080433
BLAST score 348
E value 1.0e-41
Match length 138
% identity 66

NCBI Description (AL022605) putative gamma-glutamyltransferase [Arabidopsis

thaliana]

Seq. No. 267645

Contig ID 13700 1.R1011

5'-most EST LIB3079-026-Q1-K1-A12

Seq. No. 267646

Contig ID 13701 1.R1011

5'-most EST LIB3079-026-Q1-K1-A2

Seq. No. 267647

Contig ID 13702_1.R1011 5'-most EST uC-zmflmo17309b04b1

Seq. No. 267648



```
13704_1.R1011
Contig ID
                  LIB3079-026-Q1-K1-A9
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3912919
                  371
BLAST score
                  2.0e-35
E value
                  137
Match length
                  51
% identity
                  (AF001308) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  267649
Seq. No.
Contig ID
                  13705 1.R1011
5'-most EST
                  LIB3079-026-Q1-K1-B1
                  267650
Seq. No.
Contig ID
                  13707 1.R1011
5'-most EST
                  yne700379351.hl
                  BLASTX
Method
NCBI GI
                  g3063453
BLAST score
                  177
E value
                  1.0e-12
Match length
                   51
                   63
% identity
NCBI Description (AC003981) F22013.15 [Arabidopsis thaliana]
                   267651
Seq. No.
                   13708_1.R1011
Contig ID
                   uC-zmflmo17287g10b1
5'-most EST
Method
                   BLASTX
                   g4028155
NCBI GI
BLAST score
                   259
                   2.0e-23
E value
Match length
                   196
% identity
NCBI Description (AF083221) YDR140w homolog [Fugu rubripes]
Seq. No.
                   267652
                   13708 2.R1011
Contig ID
5'-most EST
                   uC-zmflmo17050e03b2
Seq. No.
                   267653
                   13708 4.R1011
Contig ID
5'-most EST
                   tzu700202304.h1
                   267654
Seq. No.
Contig ID
                   13709 1.R1011
5'-most EST
                   LIB3067-033-Q1-K1-E11
Method
                   BLASTN
                   q2062705
NCBI GI
```

NCBI GI g2062705
BLAST score 35
E value 9.0e-10
Match length 35

% identity 100

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 267655

Contig ID 13709 2.R1011



5'-most EST LIB148-044-Q1-E1-E1

267656 Seq. No.

13709 4.R1011 Contig ID

5'-most EST uC-zmromo17030a03a1

267657 Seq. No.

13714 1.R1011 Contig ID

 $uC-zm\overline{f}lb73077d10b2$ 5'-most EST

BLASTX Method NCBI GI g4584346 BLAST score 823 6.0e-88 E value Match length 301 53 % identity

(AC007127) unknown protein [Arabidopsis thaliana] NCBI Description

267658 Seq. No.

13716 1.R1011 Contig ID

5'-most EST uC-zmroteosinte101a06b2

Seq. No. 267659

13717 1.R1011 Contig ID

LIB3059-045-Q1-K1-A12 5'-most EST

BLASTN Method NCBI GI g463151 BLAST score 396 0.0e + 00E value Match length 492 61 % identity

NCBI Description Zea mays high sulfur zein gene, complete cds

267660 Seq. No.

13721_1.R1011 Contig ID tzu700204124.h1 5'-most EST

Seq. No. 267661

13723 1.R1011 Contig ID

5'-most EST LIB3079-026-Q1-K1-F4

Method BLASTX NCBI GI q4506491 BLAST score 511 E value 1.0e-51 Match length 226 46 % identity

NCBI Description replication factor C (activator 1) 4 (37kD)

>gi_1703052_sp_P35249_AC12_HUMAN ACTIVATOR 1 37 KD SUBUNIT (REPLICATION FACTOR C 37 KD SUBUNIT) (A1 37 KD SUBUNIT)

(RF-C 37 KD SUBUNIT) (RFC37) >gi_1498256 (M87339) replication factor C, 37-kDa subunit [Homo sapiens]

Seq. No. 267662

13729 1.R1011 Contig ID uwc700153253.h1 5'-most EST

BLASTX Method NCBI GI q3608137 382 BLAST score



```
4.0e-36
E value
                  351
Match length
                  28
% identity
                  (AC005314) unknown protein [Arabidopsis thaliana]
NCBI Description
                  267663
Seq. No.
                  13731 1.R1011
Contig ID
                  LIB3062-005-Q1-K1-E2
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3170174
                  212
BLAST score
                  2.0e-16
E value
                  107
Match length
                  36
% identity
                  (AF039687) antigen NY-CO-1 [Homo sapiens]
NCBI Description
                  267664
Seq. No.
                  13733 2.R1011
Contig ID
                  uC-zmflb73294c12a1
5'-most EST
                  267665
Seq. No.
                   13745 1.R1011
Contig ID
                   cyk700051846.f1
5'-most EST
                   267666
Seq. No.
                   13748 1.R1011
Contig ID
5'-most EST
                   uC-zmroteosinte033d08b1
Method
                   BLASTX
                   g1220453
NCBI GI
BLAST score
                   1227
                   1.0e-135
E value
Match length
                   301
                   72
% identity
NCBI Description (M79328) alpha-amylase [Solanum tuberosum]
                   267667
Seq. No.
Contig ID
                   13759 1.R1011
                   LIB3150-066-P2-K1-E3
5'-most EST
Method
                   BLASTX
                   g2981439
NCBI GI
                   270
BLAST score
E value
                   1.0e-23
                   74
Match length
                   70
% identity
NCBI Description (AF051853) t-SNARE SED5 [Arabidopsis thaliana]
Seq. No.
                   267668
Contig ID
                   13775 1.R1011
5'-most EST
                   uC-zmflmo17047a11a1
                   267669
Seq. No.
Contig ID
                   13779 1.R1011
```

Contig ID 13779_1.R1011
5'-most EST LIB3079-032-Q1-K1-C1
Method BLASTX
NCBI GI g2739382
BLAST score 185
E value 1.0e-13



Match length 150 % identity 28

NCBI Description (AC002505) myosin heavy chain-like protein [Arabidopsis

thaliana]

Seq. No. 267670

Contig ID 13791_1.R1011 5'-most EST uC-zmflb73130h11a1

Seq. No. 267671

Contig ID 13793_1.R1011

5'-most EST LIB3062-052-Q1-K1-C4

Seq. No. 267672

Contig ID 13795_1.R1011

5'-most EST uC-zmflmo17288a11b1

Method BLASTX
NCBI GI g3776573
BLAST score 898
E value 8.0e-97
Match length 264
% identity 62

NCBI Description (AC005388) Similar to nodulins and lipase homolog F14J9.5

gi_3482914 from Arabidopsis thaliana BAC gb_AC003970. Alternate first exon from 72258 to 72509. [Arabidopsis

thaliana]

Seq. No. 267673

Contig ID 13798 1.R1011

5'-most EST LIB3079-033-Q1-K1-C11

Method BLASTX
NCBI GI g2224915
BLAST score 559
E value 3.0e-57
Match length 156
% identity 69

NCBI Description (U95968) beta-expansin [Oryza sativa]

Seq. No. 267674

Contig ID 13798_2.R1011 5'-most EST ceu700422326.h1

Method BLASTX
NCBI GI g2224915
BLAST score 743
E value 2.0e-90
Match length 225
% identity 68

NCBI Description (U95968) beta-expansin [Oryza sativa]

Seq. No. 267675

Contig ID 13801_1.R1011

5'-most EST LIB14 $\overline{8}$ -044-Q1-E1-E2

Method BLASTX
NCBI GI g3821793
BLAST score 1652
E value 0.0e+00
Match length 333

% identity (Y11526) casein kinase II alpha subunit [Zea mays] NCBI Description 267676 Seq. No. 13801 2.R1011 Contig ID uC-zmroB73014g08b1 5'-most EST Method BLASTN NCBI GI g3821792 BLAST score 297 E value 1.0e-166 377 Match length % identity 96 NCBI Description Z.mays mRNA for casein kinase II alpha subunit Seq. No. 267677 13801 3.R1011 Contig ID LIB3066-045-Q1-K1-D9 5'-most EST Method BLASTX NCBI GI g3821793 BLAST score 314 7.0e-29E value Match length 68 % identity 88 (Y11526) casein kinase II alpha subunit [Zea mays] NCBI Description Seq. No. 267678 13802 1.R1011 Contig ID 5'-most EST LIB3079-033-Q1-K1-E12 Seq. No. 267679 13803 1.R1011 Contig ID LIB3067-051-Q1-K1-G3 5'-most EST Method BLASTX g4567247 NCBI GI

BLAST score 300 3.0e-27 E value 144

Match length 45 % identity

NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]

267680 Seq. No.

Contig ID 13817 1.R1011

5'-most EST LIB3059-019-Q1-K1-F2

267681 Seq. No.

13817 3.R1011 Contig ID ntr700072523.h1 5'-most EST

Seq. No. 267682

Contig ID 13824 1.R1011

LIB3079-035-Q1-K1-C10 5'-most EST

Seq. No. 267683

Contig ID 13830 1.R1011

5'-most EST uC-zmflmo17199b04b1

Method BLASTX NCBI GI q4507223



BLAST score 942 E value 1.0e-101 Match length 404 % identity 56

NCBI Description

signal recognition particle receptor ('docking protein') >gi 134892 sp P08240 SRPR HUMAN SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT (SR-ALPHA) (DOCKING PROTEIN ALPHA)

(DP-ALPHA) >gi_88607_pir__A29440 signal recognition

particle receptor - human >gi_30866_emb_CAA29608_ (X06272)

docking protein [Homo sapiens]

Seq. No. 267684

Contig ID 13830_4.R1011 5'-most EST xmt700265935.h1

Seq. No. 267685

Contig ID 13840 1.R1011

5'-most EST LIB3059-036-Q1-K1-F8

Seq. No. 267686

Contig ID 13841_2.R1011

5'-most EST LIB3079-036-Q1-K1-C10

Seq. No. 267687

Contig ID 13851 1.R1011

5'-most EST LIB3079-036-Q1-K1-H3

Seq. No. 267688

Contig ID 13853_1.R1011 5'-most EST uC-zmrob73050f02b1

Method BLASTX
NCBI GI g3879150
BLAST score 533
E value 5.0e-54
Match length 195
% identity 58

NCBI Description (Z70686) Similarity to Yeast hypothetical protein YKEO

(SW:YKE0_YEAST); cDNA EST yk254g6.3 comes from this gene; cDNA EST yk254g6.5 comes from this gene [Caenorhabditis

elegans]

Seq. No. 267689

Contig ID 13853_2.R1011 5'-most EST fdz701161571.h1

Method BLASTX
NCBI GI g3879150
BLAST score 245
E value 7.0e-21
Match length 71
% identity 70

NCBI Description (Z70686) Similarity to Yeast hypothetical protein YKEO

(SW:YKE0_YEAST); cDNA EST yk254g6.3 comes from this gene; cDNA EST yk254g6.5 comes from this gene [Caenorhabditis

elegans]

Seq. No. 267690

Contig ID 13853_3.R1011



```
5'-most EST
                  LIB3279-054-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g3738157
BLAST score
                  170
                  7.0e-12
E value
Match length
                  63
                  56
% identity
                  (AL031852) conserved hypothetical protein
NCBI Description
                   [Schizosaccharomyces pombe]
                  267691
Seq. No.
                  13854 1.R1011
Contig ID
5'-most EST
                  nbm700471650.h1
Method
                  BLASTX
NCBI GI
                  g2288887
BLAST score
                  1523
E value
                  1.0e-170
Match length
                  415
% identity
                  71
                  (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis
NCBI Description
                  thaliana] >gi 3250736 emb CAA76803 (Y17593) mevalonate
                  diphosphate decarboxylase [Arabidopsis thaliana]
                  >qi 3786002 (AC005499) mevalonate diphosphate decarboxylase
                   [Arabidopsis thaliana]
                  267692
Seq. No.
                  13854 2.R1011
Contig ID
                  uC-zm\overline{f}lmo17337f10a1
5'-most EST
                  267693
Seq. No.
Contig ID
                  13854 3.R1011
5'-most EST
                  LIB3180-023-P2-M1-G11
Method
                  BLASTX
NCBI GI
                  g2288887
BLAST score
                  297
E value
                   6.0e-27
Match length
                  70
% identity
NCBI Description
                  (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis
                  thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate
                  diphosphate decarboxylase [Arabidopsis thaliana]
                   >gi 3786002 (AC005499) mevalonate diphosphate decarboxylase
                   [Arabidopsis thaliana]
                   267694
Seq. No.
Contig ID
                  13854 5.R1011
5'-most EST
                  xmt700265603.h1
Method
                  BLASTX
NCBI GI
                  q2288887
BLAST score
                  184
```

E value 9.0e-14 Match length 43

% identity NCBI Description

(Y14325) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi 3250736 emb CAA76803 (Y17593) mevalonate

diphosphate decarboxylase [Arabidopsis thaliana]

>gi 3786002 (AC005499) mevalonate diphosphate decarboxylase



[Arabidopsis thaliana]

Seq. No. 267695
Contig ID 13861_1.R1011
5'-most EST LIB3079-038-Q1-K1-C7

Seq. No. 267696

Contig ID 13871_1.R1011 5'-most EST pmx700083935.h1

Method BLASTX
NCBI GI g2244792
BLAST score 236
E value 1.0e-19
Match length 141
% identity 38

NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No. 267697

Contig ID 13889 1.R1011

5'-most EST uC-zmroteosinte107g12b2

Method BLASTX
NCBI GI g2632252
BLAST score 261
E value 3.0e-22
Match length 104
% identity 50

NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]

Seq. No. 267698

Contig ID 13893_1.R1011 5'-most EST hvj700620438.h1

Method BLASTX
NCBI GI g1762309
BLAST score 774
E value 2.0e-82
Match length 161
% identity 93

NCBI Description (U53345) AP-1 Golgi-related complex component; clathrin

coated vesicles; clathrin assembly protein [Camptotheca

acuminatal

Seq. No. 267699

Contig ID 13893_2.R1011

5'-most EST LIB3062-010-Q1-K1-E12

Method BLASTX
NCBI GI g2262169
BLAST score 150
E value 2.0e-09
Match length 31
% identity 90

NCBI Description (AC002329) clathrin adaptor protein small chain subunit

(AP19 protein) [Arabidopsis thaliana]

Seq. No. 267700

Contig ID 13897 1.R1011

5'-most EST LIB3066-019-Q1-K1-G9

Method BLASTX



q2190557 NCBI GI 345 BLAST score 2.0e-32 E value Match length 142 51 % identity (AC001229) F5I14.11 [Arabidopsis thaliana] NCBI Description 267701 Seq. No. Contig ID 13898 1.R1011 LIB3079-043-Q1-K1-A7 5'-most EST 267702 Seq. No. 13899 1.R1011 Contig ID 5'-most EST LIB3079-043-Q1-K1-A9 267703 Seq. No. 13901 1.R1011 Contig ID uC-zmflmo17320d03b1 5'-most EST Method BLASTX NCBI GI q4539423 287 BLAST score 6.0e-45E value 165 Match length 54 % identity (AL049171) pyrophosphate-dependent phosphofructo-1-kinase NCBI Description [Arabidopsis thaliana] 267704 Seq. No. 13905 1.R1011 Contig ID 5'-most EST uC-zmromo17006c02a1 267705 Seq. No. 13913 1.R1011 Contig ID 5'-most EST LIB3079-043-Q1-K2-H2 Method BLASTX NCBI GI q1903359 200 BLAST score 4.0e-15 E value 48 Match length % identity NCBI Description (AC000104) F19P19.21 [Arabidopsis thaliana] 267706 Seq. No. 13917 1.R1011 Contig ID uC-zmflb73099d07b1 5'-most EST Method BLASTX g1769887 NCBI GI BLAST score 464 4.0e-46

BLAST score 464
E value 4.0e-46
Match length 170
% identity 52

NCBI Description (X95736) amino acid permease 6 [Arabidopsis thaliana]

Seq. No. 267707

Contig ID 13917_2.R1011 5'-most EST uC-zmflmo17175a08b1

Method BLASTX



```
q3293031
NCBI GI
BLAST score
                  232
E value
                  1.0e-19
Match length
                  100
% identity
                  55
                 (AJ007574) amino acid carrier [Ricinus communis]
NCBI Description
Seq. No.
                  267708
Contig ID
                  13931 1.R1011
                  uC-zmflb73226h03b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3421413
BLAST score
                  631
E value
                  9.0e-66
Match length
                  130
                  91
% identity
                  (AF081922) protein phosphatase 2A 55 kDa B regulatory
NCBI Description
                  subunit [Oryza sativa] >gi_3421415 (AF081923) protein
                  phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]
                  267709
Seq. No.
Contig ID
                  13933 1.R1011
                  ymt700221134.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2191144
BLAST score
                  183
E value
                   3.0e-13
Match length
                  91
% identity
                   41
                  (AF007269) A IG002N01.24 gene product [Arabidopsis
NCBI Description
                  thaliana]
                  267710
Seq. No.
                  13937 1.R1011
Contig ID
                  rv1700455548.h1
5'-most EST
                  BLASTX
Method
                  q2529685
NCBI GI
BLAST score
                  600
E value
                   3.0e-62
                  165
Match length
                   76
% identity
                 (AC002535) putative dimethyladenosine transferase
NCBI Description
                   [Arabidopsis thaliana]
                   267711
Seq. No.
                  13939 1.R1011
Contig ID
                  tzu700201646.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4585976
BLAST score
                   931
                   1.0e-101
E value
Match length
                  261
% identity
NCBI Description (AC005287) Unknown protein [Arabidopsis thaliana]
```

37240

267712

13943 1.R1011

Seq. No. Contig ID



```
5'-most EST
                  LIB3079-045-Q1-K1-E8
                  267713
Seq. No.
Contig ID
                  13943 2.R1011
                  uC-zmflb73135g03b2
5'-most EST
Method
                  BLASTN
                  g3821780
NCBI GI
                  36
BLAST score
E value
                   2.0e-10
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  267714
Seq. No.
                  13943 3.R1011
Contig ID
                  LIB189-014-Q1-E1-E11
5'-most EST
                   267715
Seq. No.
Contig ID
                  13965 1.R1011
5'-most EST
                  LIB3136-006-Q1-K1-B8
Method
                  BLASTN
                   g1935910
NCBI GI
BLAST score
                   88
                   2.0e-41
E value
Match length
                   104
% identity
                   96
NCBI Description Zea mays lethal leaf-spot 1 (lls1) gene, partial cds
                   267716
Seq. No.
                   13966 1.R1011
Contig ID
5'-most EST
                   pmx700089683.h1
Seq. No.
                   267717
Contig ID
                   13970 1.R1011
5'-most EST
                   hbs701185825.h2
Seq. No.
                   267718
                   13974 1.R1011
Contig ID
                   uC-zmflmo17050f06b2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2182029
BLAST score
                   1770
                   0.0e+00
E value
Match length
                   356
                   91
% identity
NCBI Description (Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa]
                   267719
Seq. No.
                   13974 2.R1011
Contig ID
                   uC-zmflmo17173b04b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1480078
BLAST score
                   342
                   5.0e-32
E value
Match length
                   78
% identity
```

NCBI Description (X99696) shaggy-like protein kinase iota [Arabidopsis



thaliana] >gi_2444277 (AF019927) GSK3/shaggy-like protein kinase [Arabidopsis thaliana]

Seq. No. 267720

Contig ID 13974 3.R1011

5'-most EST LIB3062-027-Q1-K1-H6

Method BLASTX
NCBI GI g2129738
BLAST score 199
E value 8.0e-24
Match length 77

% identity 77

NCBI Description shaggy-like kinase dzeta - Arabidopsis thaliana

>gi_1225913_emb_CAA64408_ (X94938) shaggy-like kinase dzeta
[Arabidopsis thaliana] >gi_1669653_emb_CAA70483_ (Y09300)

serine/threonine kinase [Arabidopsis thaliana]

Seq. No. 267721

Contig ID 13974_5.R1011 5'-most EST dyk700102381.h1

Method BLASTX
NCBI GI g2182029
BLAST score 168
E value 1.0e-11
Match length 37
% identity 76

NCBI Description (Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa]

Seq. No. 267722

Contig ID 13975 1.R1011

5'-most EST LIB3079-047-Q1-K1-G7

Seq. No. 267723

Contig ID 13975_2.R1011

5'-most EST LIB3137-003-Q1-K1-G8

Seq. No. 267724

Contig ID 13977 1.R1011

5'-most EST LIB3079-048-Q1-K1-A7

Seq. No. 267725

Contig ID 13978_1.R1011 5'-most EST xmt700268089.h1

Method BLASTX
NCBI GI g3776571
BLAST score 340
E value 2.0e-31
Match length 161
% identity 50

NCBI Description (AC005388) T22H22.18 [Arabidopsis thaliana]

Seq. No. 267726

Contig ID 13978 2.R1011

5'-most EST LIB3079-048-Q1-K1-B3

Seq. No. 267727

Contig ID 13986 1.R1011



uC-zmflMo17062b08b1 5'-most EST BLASTX Method NCBI GI q2288999 BLAST score 1296 1.0e-162 E value 378 Match length 72 % identity NCBI Description (AC002335) electron transfer flavoprotein ubiquinone oxidoreductase isolog [Arabidopsis thaliana] Seq. No. 267728 13988 1.R1011 Contig ID LIB3180-019-P2-M1-H10 5'-most EST Method BLASTX NCBI GI q2828280 BLAST score 1032 1.0e-112 E value Match length 207 % identity 92 (AL021687) putative protein [Arabidopsis thaliana] NCBI Description >gi 2832633 emb CAA16762 (AL021711) putative protein [Arabidopsis thaliana] 267729 Seq. No. Contig ID 13988 2.R1011 5'-most EST uC-zmflb73108q06a1 Method BLASTX NCBI GI q2828280 BLAST score 150 E value 1.0e-12 Match length 46 93 % identity NCBI Description (AL021687) putative protein [Arabidopsis thaliana] >gi 2832633 emb CAA16762 (AL021711) putative protein [Arabidopsis thaliana] 267730 Seq. No. Contig ID 13988 3.R1011 5'-most EST LIB3151-049-P1-K1-C11 Method BLASTX NCBI GI g2828280 BLAST score 457 E value 1.0e-45 Match length 91 % identity NCBI Description (AL021687) putative protein [Arabidopsis thaliana] >gi 2832633 emb CAA16762 (AL021711) putative protein [Arabidopsis thaliana] Seq. No. 267731

Contig ID 13994 1.R1011 5'-most EST ceu700429960.h1 BLASTN Method

NCBI GI q1815627 BLAST score 70 9.0e-31 E value Match length 217



% identity Oryza sativa metallothionein-like type 2 (OsMT-2) mRNA, NCBI Description complete cds 267732 Seq. No. 13994 2.R1011 Contig ID rvt700548552.h1 5'-most EST BLASTN Method NCBI GI q1752830 51 BLAST score 7.0e-20 E value Match length 71 93 % identity Oryza sativa DNA for metallothionein-like protein, complete NCBI Description 267733 Seq. No. 13994 4.R1011 Contig ID uC-zmflmo17417a07a1 5'-most EST 267734 Seq. No. 13994_5.R1011 Contig ID 5'-most EST hbs701182862.h1 BLASTX Method g2497903 NCBI GI BLAST score 167 E value 5.0e-12 44 Match length 82 % identity METALLOTHIONEIN-LIKE PROTEIN TYPE 2 NCBI Description >gi_1752831_dbj_BAA14038_ (D89931) metallothionein-like protein [Oryza sativa] >gi_1815628 (U43530) metallothionein-like type 2 [Oryza sativa] 267735 Seq. No. Contig ID 13998 1.R1011 5'-most EST LIB3079-050-Q1-K1-E10 BLASTX Method NCBI GI q4467152 BLAST score 232 E value 5.0e-1988 Match length % identity 48 (AL035540) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 267736 14009 1.R1011 Contig ID uC-zmflmo17365h02a1 5'-most EST 267737 Seq. No.

14019 1.R1011 Contig ID wty700164193.h1 5'-most EST

 ${\tt BLASTX}$ Method g3645985 NCBI GI BLAST score 482 E value 3.0e-48 84 Match length



```
% identity
                   (AL031581) 1-evidence=predicted by content;
NCBI Description
                  1-method=genefinder;084; 1-method_score=23.36;
                  1-evidence_end; 2-evidence=predicted by match;
                  2-match_accession=AA141041;
                  2-match description=CK01110.3prime CK Drosophila
                  melanogaster
Seq. No.
                  267738
Contig ID
                  14019 2.R1011
                  LIB3088-004-Q1-K1-C12
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3645985
BLAST score
                  478
                  7.0e-48
E value
Match length
                  84
% identity
                  (AL031581) 1-evidence=predicted by content;
NCBI Description
                   1-method=genefinder;084; 1-method_score=23.36;
                   1-evidence end; 2-evidence=predicted by match;
                   2-match accession=AA141041;
                   2-match description=CK01110.3prime CK Drosophila
                  melanogaster
Seq. No.
                   267739
                   14019 3.R1011
Contig ID
                  LIB3156-012-Q1-K1-D10
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3645985
BLAST score
                   272
E value
                   2.0e-23
Match length
                   47
% identity
                  (AL031581) 1-evidence=predicted by content;
NCBI Description
                   1-method=genefinder;084; 1-method_score=23.36;
                   1-evidence end; 2-evidence=predicted by match;
                   2-match accession=AA141041;
                   2-match description=CK01110.3prime CK Drosophila
                   melanogaster
                   267740
Seq. No.
                   14019 4.R1011
Contig ID
                   xmt70\overline{0}265443.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                   g3645985
BLAST score
                   410
                   7.0e-40
E value
                   72
Match length
                   96
% identity
                  (AL031581) 1-evidence=predicted by content;
NCBI Description
                   1-method=genefinder;084; 1-method_score=23.36;
                   1-evidence end; 2-evidence=predicted by match;
                   2-match accession=AA141041;
                   2-match description=CK01110.3prime CK Drosophila
```

Seq. No. 267741

melanogaster



Contig ID 14033 1.R1011

5'-most EST LIB3079-053-Q1-K1-E11

Seq. No. 267742

Contig ID 14036_1.R1011

5'-most EST LIB3079-053-Q1-K1-F6

Method BLASTX
NCBI GI g3201554
BLAST score 420
E value 2.0e-41
Match length 117
% identity 68

NCBI Description (AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No. 267743

Contig ID 14040 1.R1011

5'-most EST LIB3079-054-Q1-K1-D6

Method BLASTN
NCBI GI g2642212
BLAST score 83
E value 3.0e-38
Match length 111
% identity 94

NCBI Description Zea mays nitrate-induced NOI protein gene, complete cds

Seq. No. 267744

Contig ID 14040 2.R1011

5'-most EST uC-zmflmo17116b06b1

Seq. No. 267745

Contig ID 14041 1.R1011

5'-most EST LIB3152-053-P1-K1-H2

Method BLASTX
NCBI GI g1705807
BLAST score 497
E value 1.0e-49
Match length 270
% identity 39

NCBI Description ENDOCHITINASE A2 PRECURSOR >gi 1362059_pir S56694

chitinase (EC 3.2.1.14) class I - garden pea >gi_598347

(L37876) chitinase class I [Pisum sativum]

Seq. No. 267746

Contig ID 14044_2.R1011

5'-most EST LIB3079-054-Q1-K1-G5

Seq. No. 267747

Contig ID 14047 1.R1011

5'-most EST LIB3079-055-Q1-K1-B1

Seq. No. 267748

Contig ID 14059_1.R1011

5'-most EST LIB3079-056-Q1-K1-B9

Method BLASTX
NCBI GI g2213600
BLAST score 501
E value 1.0e-50



Match length 164 % identity 62

NCBI Description (AC000348) T7N9.20 [Arabidopsis thaliana]

Seq. No. 267749

Contig ID 14064 1.R1011

5'-most EST LIB3079-056-Q1-K1-C9

Method BLASTX
NCBI GI g1848214
BLAST score 169
E value 8.0e-12
Match length 50
% identity 62

NCBI Description (Y11210) uracil phosphoribosyltransferase [Nicotiana

tabacum]

Seq. No. 267750

Contig ID 14070 1.R1011

5'-most EST uC-zmroteosinte009g03b1

Method BLASTX
NCBI GI g2911055
BLAST score 312
E value 1.0e-28
Match length 135
% identity 48

NCBI Description (AL021961) putative protein [Arabidopsis thaliana]

Seq. No. 267751

Contig ID 14075_1.R1011 5'-most EST uC-zmflb73216h08b2

Method BLASTX
NCBI GI g2864625
BLAST score 1155
E value 1.0e-127
Match length 329

% identity 71

NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 267752

Contig ID 14085 1.R1011

5'-most EST LIB3152-008-P1-K1-H4

Method BLASTX
NCBI GI g3213227
BLAST score 285
E value 6.0e-25
Match length 197
% identity 34

NCBI Description (AF035209) putative v-SNARE Vtila [Mus musculus]

>gi_3421062 (AF035823) 29-kDa Golgi SNARE [Mus musculus]

Seq. No. 267753

Contig ID 14090 1.R1011

5'-most EST LIB3062-035-Q1-K1-G7

Seq. No. 267754

Contig ID 14096_1.R1011 5'-most EST uC-zmflb73256h11b1



Method BLASTX NCBI GI g4098647 BLAST score 1280 0.0e+00E value Match length 439 % identity 76 (U80668) homogentisate 1,2-dioxygenase [Arabidopsis NCBI Description thaliana] 267755 Seq. No. 14096 2.R1011 Contig ID 5'-most EST LIB3068-049-Q1-K1-D6 Method BLASTX NCBI GI q4098647 BLAST score 262 E value 9.0e-23 Match length 113 80 % identity NCBI Description (U80668) homogentisate 1,2-dioxygenase [Arabidopsis thaliana] 267756 Seq. No. Contig ID 14114 1.R1011 5'-most EST cat700020237.r1 Method BLASTX NCBI GI q2642158 BLAST score 196 E value 5.0e-15 70 Match length % identity NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana] 267757 Seq. No. 14117 1.R1011 Contig ID LIB36-001-Q1-E1-E5 5'-most EST 267758 Seq. No. 14120 1.R1011 Contig ID 5'-most EST LIB3088-050-Q1-K1-G8 267759 Seq. No. 14126 1.R1011 uC-zmflb73192c01b1 5'-most EST Method ${\tt BLASTX}$ NCBI GI g4584525 BLAST score 382 4.0e-70 E value Match length 181

Contig ID

73 % identity

NCBI Description (AL049607) protein phosphatase 2C-like protein [Arabidopsis

thaliana]

267760 Seq. No.

Contig ID 14126 2.R1011

LIB3180-019-P2-M1-F12 5'-most EST

267761 Seq. No.



```
14132 1.R1011
Contig ID
5'-most EST
                  LIB3088-050-Q1-K1-E12
                  267762
Seq. No.
                  14137 1.R1011
Contig ID
5'-most EST
                  LIB3069-031-Q1-K1-G7
Method
                  BLASTX
NCBI GI
                  g2129648
BLAST score
                  474
E value
                  3.0e-47
Match length
                  211
% identity
                  48
                  MYB-related protein 33,3K - Arabidopsis thaliana
NCBI Description
                  >gi_1263095_emb_CAA90809_ (Z54136) MYB-related protein
                  [Arabidopsis thaliana]
                  267763
Seq. No.
                  14137 2.R1011
Contig ID
5'-most EST
                  uC-zmflmo17180d03b1
                  BLASTX
Method
                  g2129648
NCBI GI
BLAST score
                  543
                  2.0e-55
E value
Match length
                  156
% identity
                  69
                  MYB-related protein 33,3K - Arabidopsis thaliana
NCBI Description
                  >gi_1263095_emb_CAA90809_ (Z54136) MYB-related protein
                  [Arabidopsis thaliana]
Seq. No.
                  267764
                  14137 3.R1011
Contig ID
                  uC-zmflmo17054g04b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2129648
BLAST score
                  457
E value
                  1.0e-45
Match length
                  104
                  79
% identity
NCBI Description
                  MYB-related protein 33,3K - Arabidopsis thaliana
                   >gi 1263095_emb_CAA90809_ (Z54136) MYB-related protein
                   [Arabidopsis thaliana]
                  267765
Seq. No.
                  14137 5.R1011
Contig ID
                  uC-zmflmo17271b02b1
5'-most EST
                  267766
Seq. No.
                  14138 1.R1011
Contig ID
5'-most EST
                  LIB189-021-Q1-E1-E11
Method
                  BLASTX
                  g542176
NCBI GI
BLAST score
                   351
```

BLAST score 351 E value 8.0e-33 Match length 97 % identity 75

NCBI Description probable finger protein WZF1 - wheat

>gi 485814 dbj BAA03901 (D16415) WZF1 [Triticum aestivum]



>gi 485816 dbj BAA03902_ (D16416) WZF1 [Triticum aestivum]

Seq. No. 267767

Contig ID 14138_2.R1011

5'-most EST LIB3088-050-Q1-K1-E9

Method BLASTX
NCBI GI g542176
BLAST score 229
E value 1.0e-18
Match length 73
% identity 67

NCBI Description probable finger protein WZF1 - wheat

>gi_485814_dbj_BAA03901_ (D16415) WZF1 [Triticum aestivum] >gi_485816_dbj_BAA03902_ (D16416) WZF1 [Triticum aestivum]

Seq. No. 267768

Contig ID 14138_3.R1011 5'-most EST wyr700238361.h1

Method BLASTN
NCBI GI g441220
BLAST score 34
E value 2.0e-09
Match length 34
% identity 100

NCBI Description Wheat gene for WZF1, complete cds

Seq. No. 267769

Contig ID 14138 4.R1011 5'-most EST wyr700240118.h1

Seq. No. 267770

Contig ID 14145_1.R1011 5'-most EST ceu700433002.h1

Seq. No. 267771

Contig ID 14145_2.R1011

5'-most EST LIB3088-050-Q1-K1-F8

Seq. No. 267772

Contig ID 14146_1.R1011

5'-most EST uC-zmflmo17176g11b1

Seq. No. 267773

Contig ID 14150 1.R1011

5'-most EST LIB3137-036-Q1-K1-G12

Seq. No. 267774

Contig ID 14152_1.R1011

5'-most EST uC-zmflmo17185g10b1

Seq. No. 267775

Contig ID 14155 1.R1011

5'-most EST LIB3088-005-Q1-K1-E2

Method BLASTX
NCBI GI g4185511
BLAST score 570
E value 1.0e-58



Match length 139 % identity 77

NCBI Description (AF102822) actin depolymerizing factor 4 [Arabidopsis

thaliana]

Seq. No. 267776

Contig ID 14157_1.R1011

5'-most EST uC-zmroteosinte100a05b2

Method BLASTX
NCBI GI g1769901
BLAST score 864
E value 8.0e-93
Match length 252

% identity 65

NCBI Description (X95737) proline transporter 1 [Arabidopsis thaliana]

>gi_2088642 (AF002109) proline transporter 1 [Arabidopsis

thaliana]

Seq. No. 267777

Contig ID 14157_3.R1011

5'-most EST uC-zmflb73166e06b2

Method BLASTX
NCBI GI g1769901
BLAST score 993
E value 1.0e-108

Match length 277 % identity 70

NCBI Description (X95737) proline transporter 1 [Arabidopsis thaliana]

>qi 2088642 (AF002109) proline transporter 1 [Arabidopsis

thaliana]

Seq. No. 267778

Contig ID 14157_6.R1011 5'-most EST fwa700097626.h1

Seq. No. 267779

Contig ID 14168 1.R1011 5'-most EST nbm700467163.h1

Seq. No. 267780

Contig ID 14168 2.R1011

5'-most EST uC-zmflmo17240b02a1

Seq. No. 267781

Contig ID 14168_3.R1011

5'-most EST LIB3158-003-Q1-K1-C5

Seq. No. 267782

Contig ID 14171_1.R1011

5'-most EST uC-zmflmo17001g04b1

Seq. No. 267783

Contig ID 14171_2.R1011 5'-most EST uC-zmrob73033g04a1

Seq. No. 267784

Contig ID 14171 4.R1011



5'-most EST LIB3136-020-Q1-K1-C4

267785 Seq. No.

Contig ID 14175 1.R1011 uC-zmrob73056q11a1 5'-most EST

267786 Seq. No.

14175 2.R1011 Contig ID

5'-most EST $uC-zm\overline{f}lmo17264c12a2$

267787 Seq. No.

Contig ID 14180 1.R1011

LIB3088-049-Q1-K1-G3 5'-most EST

Method BLASTX NCBI GI q1703053 BLAST score 352 2.0e-33 E value

88 Match length 72 % identity

NCBI Description ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD

SUBUNIT) (A1 40 KD SUBUNIT) (RF-C 40 KD SUBUNIT) (RFC40) >gi_2134397_pir__I50704 replication factor C/activator 1 subunit - chicken >gi_527669 (U12438) replication factor

C/activator 1 subunit [Gallus gallus]

Seq. No. 267788

14182 1.R1011 Contig ID

LIB3158-005-Q1-K1-D11 5'-most EST

BLASTX Method NCBI GI q3738283 BLAST score 306 7.0e-28 E value Match length 58

% identity

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

267789 Seq. No.

14186 1.R1011 Contig ID

5'-most EST LIB3088-049-Q1-K1-H6

Seq. No. 267790

14187 1.R1011 Contig ID uer700582856.h1 5'-most EST

Method BLASTX NCBI GI g2129578 BLAST score 1144 1.0e-126 E value Match length 244

87 % identity

NCBI Description dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >qi 928932 emb CAA89205 (Z49239) homolog of

dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi 1585435 prf 2124427B diamide resistance gene

[Arabidopsis thaliana]

267791 Seq. No.

Contig ID 14194_2.R1011



```
5'-most EST
                   uC-zmflmo17356c05a1
                   267792
Seq. No.
Contig ID
                   14197 1.R1011
                   uC-zm\overline{f}lmo17048c11b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1208496
BLAST score
                   191
E value
                   5.0e-14
Match length
                   55
% identity
                   62
NCBI Description
                  (D38124) EREBP-3 [Nicotiana tabacum]
                   267793
Seq. No.
Contig ID
                   14197 2.R1011
5'-most EST
                   uC-zmflb73157d07b2
Method
                   BLASTX
NCBI GI
                   g1208496
BLAST score
                   189
E value
                   3.0e-14
Match length
                   55
                   62
% identity
NCBI Description
                  (D38124) EREBP-3 [Nicotiana tabacum]
                   267794
Seq. No.
Contig ID
                   14197 3.R1011
5'-most EST
                   uC-zmflmo17404a03a1
Seq. No.
                   267795
Contig ID
                   14198 1.R1011
5'-most EST
                   pmx700087627.hl
Method
                   BLASTX
NCBI GI
                   q4432823
BLAST score
                   400
E value
                   1.0e-38
Match length
                   209
% identity
                   46
NCBI Description
                  (AC006593) hypothetical protein [Arabidopsis thaliana]
                   267796
Seq. No.
Contig ID
                   14200 1.R1011
5'-most EST
                   wty700168414.h1
Method
                   BLASTX
NCBI GI
                   g123183
BLAST score
                   427
E value
                   7.0e-53
Match length
                   132
                   79
% identity
NCBI Description HOMEOTIC PROTEIN KNOTTED-1 >gi 100888 pir S14283 homeotic
                   protein Kn-1 - maize >gi 22351 emb CAA43605 (X61308) Kn1
                   [Zea mays] >gi 227607 prf 170\overline{7}304\overline{A} Knotted-1 gene [Zea
                   mays]
```

Seq. No. 267797

Contig ID 14203_1.R1011 5'-most EST uC-zmroB73014c08b1

Method BLASTX



NCBI GI g2980795 BLAST score 775 E value 2.0e-82 Match length 170 % identity 86

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 267798

Contig ID 14203_3.R1011

5'-most EST LIB1 $4\overline{3}$ -002-Q1-E1-G2

Method BLASTX
NCBI GI g2980795
BLAST score 465
E value 2.0e-46
Match length 110
% identity 81

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 267799

Contig ID 14205_1.R1011

5'-most EST LIB3068-044-Q1-K1-D8

Seq. No. 267800

Contig ID 14210_1.R1011

5'-most EST LIB3068-013-Q1-K1-C7

Method BLASTX
NCBI GI g2462749
BLAST score 547
E value 1.0e-55
Match length 305
% identity 40

NCBI Description (AC002292) Putative Serine/Threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 267801

Contig ID 14211_1.R1011 5'-most EST nbm700475491.h1

Method BLASTX
NCBI GI g2789660
BLAST score 2140
E value 0.0e+00
Match length 615
% identity 67

NCBI Description (AF040102) p105 [Arabidopsis thaliana]

Seq. No. 267802

Contig ID 14211 2.R1011

5'-most EST LIB3088-049-Q1-K1-A6

Seq. No. 267803

Contig ID 14211_3.R1011 5'-most EST tfd700571058.h1

Seq. No. 267804

Contig ID 14214_1.R1011 5'-most EST clt700043328.f1



267805 Seq. No.

14219 1.R1011 Contig ID fC-zmle700432332a4 5'-most EST

BLASTX Method g3047084 NCBI GI BLAST score 1271 1.0e-140 E value Match length 313 75 % identity

(AF058914) similar to aminoacyl-tRNA synthetases NCBI Description

[Arabidopsis thaliana]

267806 Seq. No.

14219 3.R1011 Contig ID $uC-zm\overline{f}lb73200d01a1$ 5'-most EST

BLASTX Method q3435196 NCBI GI 145 BLAST score 3.0e-09E value 34 Match length 74 % identity

(AF067773) glutamyl-tRNA synthetase [Arabidopsis thaliana] NCBI Description

267807 Seq. No.

14221 1.R1011 Contig ID $nwy70\overline{0}447956.h1$ 5'-most EST

BLASTX Method g585165 NCBI GI 1649 BLAST score 0.0e + 00E value 363 Match length 83 % identity

GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM NCBI Description

(G6PD) >gi_2129985_pir__S60287 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - potato

>gi_471345_emb_CAA52442_ (X74421) glucose-6-phosphate
1-dehydrogenase [Solanum tuberosum]

267808 Seq. No.

14222 1.R1011 Contig ID cjh700197286.h1 5'-most EST

267809 Seq. No.

14223 1.R1011 Contig ID

LIB148-004-Q1-E1-C4 5'-most EST

Method BLASTX NCBI GI q3236238 BLAST score 1101 E value 1.0e-120 Match length 449 53 % identity

(AC004684) putative ARF1 GTPase activating protein NCBI Description

[Arabidopsis thaliana] >gi_4519792 dbj BAA75744.1

(AB017876) Asp1 [Arabidopsis thaliana]

Seq. No. 267810

Contig ID 14227 1.R1011



5'-most EST LIB3088-047-Q1-K1-G5

267811 Seq. No.

14232 1.R1011 Contig ID

5'-most EST uC-zmflmo17293e08b1

BLASTX Method g2511594 NCBI GI BLAST score 975 E value 1.0e-106 Match length 223 % identity 81

NCBI Description (Y13694) multicatalytic endopeptidase complex, proteasome

precursor, beta subunit [Arabidopsis thaliana]

>gi_2827525_emb_CAA16533_ (AL021633) multicatalytic.

endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] $>gi_3421099$ (AF043529) 20S

proteasome subunit PBA1 [Arabidopsis thaliana]

Seq. No. 267812

14232 2.R1011 Contig ID ntr700077458.h1 5'-most EST

Method BLASTX q2511594 NCBI GI 497 BLAST score E value 4.0e-50 Match length 108 % identity 86

(Y13694) multicatalytic endopeptidase complex, proteasome NCBI Description

precursor, beta subunit [Arabidopsis thaliana]

>gi_2827525_emb_CAA16533_ (AL021633) multicatalytic

endopeptidase complex, proteasome precursor, beta subunit

[Arabidopsis thaliana] >gi 3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]

267813 Seq. No.

Contig ID 14232_3.R1011

5'-most EST uC-zmrob73055b02a1

Method BLASTX NCBI GI a2511594 BLAST score 347 E value 1.0e-32 Match length 88 % identity

NCBI Description (Y13694) multicatalytic endopeptidase complex, proteasome

precursor, beta subunit [Arabidopsis thaliana]

>gi_2827525_emb_CAA16533_ (AL021633) multicatalytic

endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S

proteasome subunit PBA1 [Arabidopsis thaliana]

267814 Seq. No.

Contig ID 14232 4.R1011

5'-most EST LIB3150-095-P2-K1-F10

267815 Seq. No.

14233 1.R1011 Contig ID

5'-most EST LIB3136-020-Q1-K1-C12



Method BLASTX
NCBI GI g1171577
BLAST score 366
E value 3.0e-34
Match length 368
% identity 32

NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 267816

Contig ID 14233 2.R1011

5'-most EST uC-zmflmo17060e06b1

Seq. No. 267817

Contig ID 14235 1.R1011

5'-most EST LIB189-011-Q1-E1-B10

Method BLASTX
NCBI GI g2632105
BLAST score 1061
E value 0.0e+00
Match length 427
% identity 74

NCBI Description (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]

>gi_4539426_emb_CAB38959.1_ (AL049171) arginyl-tRNA

synthetase [Arabidopsis thaliana]

Seq. No. 267818

Contig ID 14235 2.R1011

5'-most EST LIB3088-021-Q1-K1-F7

Method BLASTX
NCBI GI g2632105
BLAST score 384
E value 4.0e-37
Match length 95
% identity 74

NCBI Description (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]

>gi_4539426_emb_CAB38959.1_ (AL049171) arginyl-tRNA

synthetase [Arabidopsis thaliana]

Seq. No. 267819

Contig ID 14235 4.R1011

5'-most EST LIB3157-016-Q1-K1-B5

Method BLASTX
NCBI GI g2632106
BLAST score 499
E value 1.0e-50
Match length 136

% identity 72

NCBI Description (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 267820

Contig ID 14238_1.R1011

5'-most EST LIB3088-047-Q1-K1-F7

Method BLASTX
NCBI GI g4432840
BLAST score 191
E value 2.0e-14
Match length 101

BLAST score

Match length

% identity

E value

563

177

62

1.0e-57



% identity (AC006283) unknown protein [Arabidopsis thaliana] NCBI Description 267821 Seq. No. 14240 1.R1011 Contig ID uC-zmflb73178a04a1 5'-most EST BLASTX Method NCBI GI g4406769 BLAST score 166 E value 2.0e-11 Match length 51 % identity 69 (AC006836) putative translin [Arabidopsis thaliana] NCBI Description Seq. No. 267822 Contig ID 14243 1.R1011 5'-most EST uC-zmflmo17219f12b1 Method BLASTX NCBI GI g2492952 BLAST score 1589 E value 1.0e-177 Match length 390 % identity 75 NCBI Description CHORISMATE SYNTHASE 1 PRECURSOR (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1) >gi_542026_pir__S40410 chorismate synthase (EC 4.6.1.4) 1 precursor - tomato >gi_410482_emb_CAA79859_ (Z21796)
chorismate synthase 1 [Lycopersicon esculentum] 267823 Seq. No. Contig ID 14244 1.R1011 5'-most EST uC-zmflm017207g12b1 Method BLASTX NCBI GI g4454048 BLAST score 255 E value 1.0e-21 Match length 82 % identity 56 NCBI Description (AL035394) putative protein [Arabidopsis thaliana] Seq. No. 267824 Contig ID 14246 1.R1011 5'-most EST LIB3088-047-Q1-K1-D6 Seq. No. 267825 Contig ID 14246 2.R1011 5'-most EST fdz701164265.h1 Seq. No. 267826 14253 1.R1011 Contig ID 5'-most EST LIB3068-004-Q1-K1-C11 Method BLASTX NCBI GI g3355474

NCBI GI

E value

BLAST score



```
NCBI Description
                  (AC004218) unknown protein [Arabidopsis thaliana]
                  267827
Seq. No.
Contig ID
                  14257 1.R1011
5'-most EST
                  xyt700345964.h1
Method
                  BLASTX
NCBI GI
                  g3414809
BLAST score
                  434
E value
                  2.0e-42
Match length
                  277
                  4
% identity
NCBI Description
                  (AF061529) rjs [Mus musculus]
                  267828
Seq. No.
Contig ID
                  14260 1.R1011
                  LIB3088-047-Q1-K1-C1
5'-most EST
Method
                  BLASTN
NCBI GI
                  g3341977
BLAST score
                  264
E value
                  1.0e-147
                  298
Match length
                  98
% identity
NCBI Description Zea mays cytokinin oxidase (ckx1) gene, complete cds
                  267829
Seq. No.
Contig ID
                  14261 1.R1011
5'-most EST
                  uC-zmflmo17332c01a1
                  267830
Seq. No.
                  14263 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17179f02b1
                  BLASTX
Method
NCBI GI
                  q4586253
BLAST score
                  588
E value
                   1.0e-60
Match length
                  123
% identity
                   90
NCBI Description
                  (AL049640) auxilin-like protein [Arabidopsis thaliana]
Seq. No.
                  267831
Contig ID
                  14263 2.R1011
5'-most EST
                  uC-zmroteosinte049h11b1
Method
                  BLASTX
NCBI GI
                  g4586253
BLAST score
                  366
E value
                  1.0e-36
Match length
                  190
                  51
% identity
NCBI Description
                  (AL049640) auxilin-like protein [Arabidopsis thaliana]
Seq. No.
                  267832
                  14264 1.R1011
Contig ID
                  xmt700265558.h1
5'-most EST
                  BLASTX
Method
```

37259

g3478700

1.0e-104



Match length 300 % identity 65

NCBI Description (AF034387) AFT protein [Arabidopsis thaliana]

Seq. No. 267833

Contig ID 14264 2.R1011 5'-most EST fdz701165148.h1

Seq. No. 267834

Contig ID 14264_3.R1011 5'-most EST nbm700471830.h1

Method BLASTN
NCBI GI g531030
BLAST score 58
E value 1.0e-23
Match length 86
% identity 92

NCBI Description Pennisetum ciliare apomixis-associated mRNA

>gi_531483_emb_Z36546_PCAPOSPA3 P.ciliare (Higgins)

apospory associated mRNA, 876bp

>gi_549985_gb_U13149_PCU13149 Pennisetum ciliare possible apospory-associated mRNA clone pSUB 3-1a, partial cds

Seq. No. 267835

Contig ID 14264 4.R1011

5'-most EST LIB3088-037-Q1-K1-G2

Seq. No. 267836

Contig ID 14265 1.R1011

5'-most EST LIB3060-013-Q1-K1-C1

Method BLASTX
NCBI GI g4263709
BLAST score 195
E value 2.0e-14
Match length 57

Match length 57 % identity 61

NCBI Description (AC006223) unknown protein [Arabidopsis thaliana]

Seq. No. 267837

Contig ID 14265 2.R1011

5'-most EST LIB3088-047-Q1-K1-D10

Seq. No. 267838

Contig ID 14266 1.R1011

5'-most EST LIB3137-006-Q1-K1-G12

Seq. No. 267839

Contig ID 14273 1.R1011

5'-most EST LIB3152-005-P1-K1-F12

Method BLASTX
NCBI GI g4587571
BLAST score 724
E value 2.0e-76
Match length 226

% identity 61

NCBI Description (AC006550) Belongs to the PF_01027 Uncharacterized protein family UPF0005 with 7 transmembrane domains. [Arabidopsis



thaliana]

267840 Seq. No. Contig ID 14279 1.R1011 nbm700468662.h1 5'-most EST Method BLASTX g3367521 NCBI GI BLAST score 210 E value 3.0e-16 Match length 217 27 % identity NCBI Description (AC004392) Similar to gb_U08285 membrane-associated salt-inducible protein from Nicotiana tabacum. ESTs gb_T44131 and gb_T04378 come from this gene. [Arabidopsis thaliana] 267841 Seq. No. 14284 1.R1011 Contig ID 5'-most EST cyk700050040.f1 BLASTX Method NCBI GI g1076621 BLAST score 268 E value 5.0e-23 Match length 96 55 % identity NCBI Description cytochrome b5 - common tobacco >gi 296386 emb CAA50575 (X71441) cytochrome b5 [Nicotiana tabacum] 267842 Seq. No. 14289 1.R1011 Contig ID 5'-most EST LIB143-027-Q1-E1-C7 Seq. No. 267843 Contig ID 14291_1.R1011 5'-most EST $uC-zm\overline{f}lmo17262b10b1$ Method BLASTX NCBI GI g4559384 BLAST score 182 E value 7.0e-1379 Match length % identity 46 NCBI Description (AC006526) unknown protein [Arabidopsis thaliana] Seq. No. 267844 14291 2.R1011 Contig ID 5'-most EST uC-zmroteosinte010f12b1

Seq. No. 267845

Contig ID 14291_3.R1011

5'-most EST LIB3060-045-Q1-K1-E2

Seq. No. 267846

Contig ID 14291_5.R1011

5'-most EST uC-zmroteosinte066a04b1

Seq. No. 267847

Contig ID 14291 8.R1011



```
5'-most EST
                   cat700021505.r1
                   267848
Seq. No.
                   14292 1.R1011
Contig ID
5'-most EST
                  mwy700441743.h1
Method
                   BLASTX
NCBI GI
                   g2398533
BLAST score
                   405
E value
                   3.0e-39
Match length
                   100
                   76
% identity
NCBI Description (Y13725) Transcription factor [Arabidopsis thaliana]
Seq. No.
                   267849
                   14293 1.R1011
Contig ID
5'-most EST
                   cat700016853.rl
                   267850
Seq. No.
                   14307 2.R1011
Contig ID
5'-most EST
                  LIB148-053-Q1-E1-G7
Method
                   BLASTX
NCBI GI
                  g3075389
BLAST score
                   269
E value
                   4.0e-23
Match length
                   119
% identity
                   54
NCBI Description (AC004484) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   267851
Contig ID
                   14311 1.R1011
5'-most EST
                   LIB3088-046-Q1-K1-E9
Method
                   BLASTX
NCBI GI
                   g399853
BLAST score
                   335
E value
                   2.0e-31
Match length
                   80
% identity
                   86
NCBI Description HISTONE H2B.1 >gi_283041_pir__S28048 histone H2B - maize
                  >gi_22323_emb_CAA40564_ (X57312) H2B histone [Zea mays]
Seq. No.
                   267852
Contig ID
                   14312 1.R1011
5'-most EST
                  LIB3088-046-Q1-K1-F10
Seq. No.
                   267853
Contig ID
                   14315 1.R1011
5'-most EST
                  LIB3067-016-Q1-K1-B4
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2760832
BLAST score 625
E value 7.0e-65
Match length 225
% identity 61

NCBI Description (AC003105) similar to barley ids-4 gene product

[Arabidopsis thaliana]

Seq. No. 267854

Match length

% identity

51

```
Contig ID
                   14318 1.R1011
5'-most EST
                   nbm70\overline{0}470541.h1
Seq. No.
                   267855
                   14318 2.R1011
Contig ID
5'-most EST
                   ntr700077354.h1
Method
                   BLASTX
NCBI GI
                   g3024652
BLAST score
                   193
E value
                   1.0e-14
Match length
                   127
% identity
                   41
NCBI Description SORCIN >gi 1655733 (U39069) sorcin [Schistosoma japonicum]
Seq. No.
                   267856
Contig ID
                   14318 3.R1011
5'-most EST
                   LIB3060-044-Q1-K1-B9
Seq. No.
                   267857
Contig ID
                   14320 1.R1011
5'-most EST
                   LIB3136-021-Q1-K1-C6
Method
                   BLASTX
NCBI GI
                   g2252863
BLAST score
                   490
E value
                   5.0e-49
Match length
                   180
% identity
                   55
NCBI Description (AF013294) similar to nucleolin protein [Arabidopsis
                   thaliana]
Seq. No.
                   267858
Contig ID
                   14331 1.R1011
5'-most EST
                   hbs701186254.h1
Seq. No.
                   267859
                   14333 1.R1011
Contig ID
5'-most EST
                   xmt70\overline{0}264938.h1
Method
                   BLASTX
                   g2746333
NCBI GI
BLAST score
                   183
E value
                   5.0e-13
Match length
                   69
% identity
                   45
NCBI Description (AF037204) RING zinc finger protein [Homo sapiens]
                   >gi_3387925 (AF070558) RING zinc finger protein RZF [Homo
                   sapiens]
                   267860
Seq. No.
Contig ID
                   14333 2.R1011
5'-most EST
                   rvt700549778.h1
Method
                   BLASTX
NCBI GI
                   g2746333
BLAST score
                  172
E value
                   4.0e-12
```

NCBI Description (AF037204) RING zinc finger protein [Homo sapiens]

>gi_3387925 (AF070558) RING zinc finger protein RZF [Homo sapiens]

Seq. No. 267861

Contig ID 14333_3.R1011 5'-most EST xyt700345248.h1

Method BLASTX
NCBI GI g2746333
BLAST score 166
E value 2.0e-11
Match length 47
% identity 53

NCBI Description (AF037204) RING zinc finger protein [Homo sapiens]

>gi_3387925 (AF070558) RING zinc finger protein RZF [Homo

sapiens]

Seq. No. 267862

Contig ID 14334 1.R1011

5'-most EST LIB30\(\overline{6}\)0-025-Q1-K1-G9

Method BLASTX
NCBI GI g1946368
BLAST score 363
E value 3.0e-34
Match length 220
% identity 40

NCBI Description (U93215) unknown protein [Arabidopsis thaliana]

Seq. No. 267863

Contig ID 14335 1.R1011

5'-most EST LIB3067-009-Q1-K1-F7

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 267864

Contig ID 14339 1.R1011

5'-most EST LIB3061-012-Q1-K1-D10

Method BLASTX
NCBI GI g2959370
BLAST score 231
E value 7.0e-19
Match length 104
% identity 38

NCBI Description (AL022117) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 267865

Contig ID 14340_1.R1011 5'-most EST yyf700352354.h1

Method BLASTX
NCBI GI g3367522
BLAST score 643
E value 4.0e-67
Match length 203



% identity 62

NCBI Description (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 267866

Contig ID 14340_2.R1011 5'-most EST uC-zmrob73059c08a1

Method BLASTX
NCBI GI g3367522
BLAST score 206
E value 4.0e-16
Match length 60
% identity 67

NCBI Description (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 267867

Contig ID 14342 1.R1011

5'-most EST LIB3136-050-Q1-K1-B5

Method BLASTX
NCBI GI g2135053
BLAST score 190
E value 7.0e-14
Match length 148
% identity 29

NCBI Description E1B 19K/Bcl-2-interacting protein Nip2 - human >gi 558844

(U15173) BCL2/adenovirus E1B 19kD-interacting protein 2

[Homo sapiens]

Seq. No. 267868

Contig ID 14343_1.R1011 5'-most EST gct701177361.h1

Seq. No. 267869

Contig ID 14350_1.R1011

5'-most EST uC-zmrob73052e05a1

Seq. No. 267870

Contig ID 14352_1.R1011 5'-most EST xsy700211623.h1

Method BLASTX
NCBI GI g3822036
BLAST score 431
E value 5.0e-42
Match length 188
% identity 50

NCBI Description (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]

Seq. No. 267871

Contig ID 14352 2.R1011

5'-most EST LIB30 $\overline{8}$ 8-045-Q1-K1-H2

55

Method BLASTX
NCBI GI g3822036
BLAST score 240
E value 3.0e-20
Match length 101

% identity



```
NCBI Description (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
                   267872
Seq. No.
Contig ID
                   14355 1.R1011
5'-most EST
                  LIB3180-055-P2-M1-C3
Method
                  BLASTX
NCBI GI
                  q2133698
BLAST score
                  269
E value
                   2.0e-23
Match length
                  99
% identity
                   51
                  oligosaccharyltransferase 48K chain - fruit fly (Drosophila
NCBI Description
                  melanogaster) (fragment) >gi_963028_emb_CAA57079_ (X81207)
                  oligosaccharyltransferase 48kDa subunit [Drosophila
                  melanogaster]
Seq. No.
                   267873
Contig ID
                   14355 2.R1011
5'-most EST
                  uC-zmflb73055a09b1
Method
                  BLASTX
NCBI GI
                  g2133698
BLAST score
                  272
E value
                  1.0e-23
Match length
                  87
% identity
                  59
NCBI Description oligosaccharyltransferase 48K chain - fruit fly (Drosophila
                  melanogaster) (fragment) >gi_963028_emb_CAA57079_ (X81207)
                  oligosaccharyltransferase 48kDa subunit [Drosophila
                  melanogaster]
Seq. No.
                   267874
                   14355 3.R1011
Contig ID
5'-most EST
                  pmx700082519.h1
Method
                  BLASTX
NCBI GI
                  g2662375
BLAST score
                  914
E value
                   1.0e-98
Match length
                  379
% identity
                   47
NCBI Description
                  (D89060) oligosaccharyltransferase [Homo sapiens]
Seq. No.
                  267875
                  14355 5.R1011
Contig ID
5'-most EST
                  uwc700152365.h1
Method
                  BLASTX
NCBI GI
                  g2662377
BLAST score
                  262
E value
                  1.0e-22
                  94
Match length
% identity
                   48
```

NCBI Description (D89063) oligosaccharyltransferase [Mus musculus]

Seq. No. 267876

Contig ID 14355_9.R1011 5'-most EST cjh700196438.h1

Seq. No. 267877



Contig ID 14361 1.R1011

5'-most EST LIB3151-019-Q1-K1-A11

Method BLASTX
NCBI GI g549564
BLAST score 209
E value 8.0e-31
Match length 158
% identity 44

NCBI Description HYPOTHETICAL 16.9 KD PROTEIN IN SURE-CYSC INTERGENIC REGION (ORFO) >gi_2121169_pir__I55083 hypothetical protein (59

min. region) - Escherichia coli >gi_433711 (L07942) ORFO [Escherichia coli] >gi_882639 (U29579) alternate gene name

ygbB; ORFO of L07942; ORF_f159 [Escherichia coli] >gi 1789103 (AE000358) orf, hypothetical protein

[Escherichia coli]

Seq. No. 267878

Contig ID 14369 1.R1011

5'-most EST LIB3088-039-Q1-K1-H2

Method BLASTX
NCBI GI g116054
BLAST score 499
E value 3.0e-50
Match length 135
% identity 71

NCBI Description CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK)

>gi_280393_pir__A43713 calcium-dependent protein kinase (EC
2.7.1.-) - soybean >gi_169931 (M64987) Glycine max calcium

dependent protein kinase mRNA. [Glycine max]

Seq. No. 267879

Contig ID 14369_3.R1011 5'-most EST nbm700466204.h1

Method BLASTX
NCBI GI g116054
BLAST score 445
E value 1.0e-44
Match length 102
% identity 88

NCBI Description CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK)

>gi_280393_pir__A43713 calcium-dependent protein kinase (EC
2.7.1.-) - soybean >gi_169931 (M64987) Glycine max calcium

dependent protein kinase mRNA. [Glycine max]

Seq. No. 267880

Contig ID 14370_1.R1011 5'-most EST fC-zmle700439614a4

Seq. No. 267881

Contig ID 14377 1.R1011

5'-most EST LIB3159-020-Q1-K1-B2

Method BLASTX
NCBI GI g4572679
BLAST score 268
E value 8.0e-32
Match length 102

% identity 59



NCBI Description (AC006954) RSZp22 splicing factor; contains RNA recognition motif [Arabidopsis thaliana]

Seq. No. 267882

Contig ID 14377 2.R1011

5'-most EST uC-zmflmo17054e03b1

Method BLASTX
NCBI GI g4572679
BLAST score 267
E value 4.0e-23
Match length 60
% identity 77

NCBI Description (AC006954) RSZp22 splicing factor; contains RNA recognition

motif [Arabidopsis thaliana]

Seq. No. 267883

Contig ID 14377_3.R1011 5'-most EST fwa700101269.h1

Method BLASTX
NCBI GI g4572679
BLAST score 405
E value 1.0e-39
Match length 110
% identity 69

NCBI Description (AC006954) RSZp22 splicing factor; contains RNA recognition

motif [Arabidopsis thaliana]

Seq. No. 267884

Contig ID 14377 4.R1011

5'-most EST uC-zmflmo17281b07b1

Method BLASTX
NCBI GI g3281869
BLAST score 284
E value 2.0e-26
Match length 87
% identity 71

NCBI Description (AL031004) RSZp22 splicing factor [Arabidopsis thaliana]

>gi 3435094 (AF033586) 9G8-like SR protein [Arabidopsis

thaliana]

Seq. No. 267885

Contig ID 14377_5.R1011 5'-most EST hbs701184485.h1

Seq. No. 267886

Contig ID 14381 1.R1011

5'-most EST LIB3088-045-Q1-K1-D9

Method BLASTX
NCBI GI g1314712
BLAST score 225
E value 2.0e-18
Match length 48
% identity 88

NCBI Description (U54615) calcium-dependent protein kinase [Arabidopsis

thaliana]

Seq. No. 267887

```
Contig ID
                   14382 1.R1011
5'-most EST
                  LIB3088-045-Q1-K1-E1
Method
                  BLASTX
                  g3413500
NCBI GI
BLAST score
                   410
E value
                   7.0e-40
                  133
Match length
                   62
% identity
                  (AJ005589) protein tyrosine phosphatase [Pisum sativum]
NCBI Description
Seq. No.
                   267888
                  14387_1.R1011
Contig ID
5'-most EST
                  LIB3088-045-Q1-K1-D1
                   267889
Seq. No.
                   14387 2.R1011
Contig ID
5'-most EST
                  LIB3159-020-Q1-K1-H11
                   267890
Seq. No.
Contig ID
                   14390 1.R1011
5'-most EST
                  LIB148-018-Q1-E1-H7
Method
                   BLASTX
                   g4200165
NCBI GI
BLAST score
                   1472
E value
                   1.0e-164
Match length
                   326
% identity
                   82
NCBI Description (Y16262) neutral invertase [Daucus carota]
                   267891
Seq. No.
Contig ID
                   14392 1.R1011
5'-most EST
                   ymt700221354.h1
Method
                   BLASTX
NCBI GI
                   q1711618
BLAST score
                   267
E value
                   4.0e-23
Match length
                   104
                   47
% identity
NCBI Description
                  LOW AFFINITY SULPHATE TRANSPORTER 3 >gi_1085993_pir__S51765
                   low affinity sulphate transporter - Stylosanthes hamata
                   >gi_607188_emb_CAA57831_ (X82454) low affinity sulphate
                   transporter [Stylosanthes hamata]
Seq. No.
                   267892
Contig ID
                   14396_1.R1011
5'-most EST
                   LIB3066-024-Q1-K1-E5
Method
                  BLASTX
NCBI GI
                   g544437
BLAST score
                   588
E value
                   2.0e-60
Match length
                  164
% identity
                   65
NCBI Description
                  GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN)
                  >gi_296358_emb CAA47018 (X66377) CIT-SAP [Citrus sinensis]
```

Seq. No. 267893 Contig ID 14396 2.R1011

```
5'-most EST
                   uC-zmflb73071e08b3
Method
                   BLASTX
NCBI GI
                   q2746232
BLAST score
                   208
E value
                   2.0e-16
Match length
                   64
% identity
                   59
NCBI Description
                  (AF037051) glutathione peroxidase [Gossypium hirsutum]
Seq. No.
                   267894
Contig ID
                   14414_1.R1011
                   LIB3088-045-Q1-K1-B1
5'-most EST
Method
                   BLASTN
NCBI GI
                   q22123
BLAST score
                   73
E value
                   1.0e-32
Match length
                   132
% identity
                   45
NCBI Description Maize alcohol dehydrogenase 1 gene (Adh1-1S)
Seq. No.
                   267895
Contig ID
                   14416_1.R1011
5'-most EST
                   uC-zmflb73030c03b1
Method
                   BLASTX
NCBI GI
                   q4454033
BLAST score
                   800
E value
                   2.0e-85
Match length
                   232
% identity
                   63
NCBI Description
                  (AL035394) putative potassium transport protein
                   [Arabidopsis thaliana]
Seq. No.
                   267896
Contig ID
                   14416 2.R1011
5'-most EST
                   cyk700048259.f1
Method
                   BLASTX
NCBI GI
                   g4454033
BLAST score
                   573
E value
                   1.0e-118
Match length
                   398
% identity
                   54
NCBI Description
                  (AL035394) putative potassium transport protein
                   [Arabidopsis thaliana]
Seq. No.
                   267897
Contig ID
                   14416 3.R1011
5'-most EST
                  xdb700341929.h1
Seq. No.
                  267898
Contig ID
                  14420 1.R1011
                  uC-zmflb73279c03b1
```

5'-most EST uC-zmflb73279c03b Method BLASTX NCBI GI g3075391 BLAST score 479 E value 6.0e-48 Match length 156

64

% identity



NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]

Seq. No. 267899

Contig ID 14422_1.R1011

5'-most EST LIB3088-044-Q1-K1-G8

Method BLASTX
NCBI GI g3063697
BLAST score 194
E value 1.0e-14
Match length 57
% identity 70

NCBI Description (AL022537) putative myb-protein (partial) [Arabidopsis

thaliana]

Seq. No. 267900

Contig ID 14432_1.R1011 5'-most EST nwy700448148.h1

Seq. No. 267901

Contig ID 14437 1.R1011

5'-most EST LIB31 $\overline{3}6$ -026-Q1-K1-A5

Method BLASTX
NCBI GI g2132842
BLAST score 550
E value 7.0e-56
Match length 258
% identity 41

NCBI Description probable membrane protein YOL077c - yeast (Saccharomyces

cerevisiae) >gi_1419909_emb_CAA99087_ (Z74819) ORF YOL077c

[Saccharomyces cerevisiae]

Seq. No. 267902

Contig ID 14437_4.R1011 5'-most EST cyk700047552.f1

Seq. No. 267903

Contig ID 14443 1.R1011

5'-most EST LIB31 $\overline{5}$ 9-008-Q1-K1-H2

Seq. No. 267904

Contig ID 14443_4.R1011 5'-most EST uC-zmflb73222h03a1

Seq. No. 267905

Contig ID 14448_1.R1011 5'-most EST hbs701183887.h1

Seq. No. 267906

Contig ID 14459 1.R1011

5'-most EST LIB143-015-Q1-E1-A11

Method BLASTX
NCBI GI g4263521
BLAST score 426
E value 1.0e-41
Match length 105
% identity 71

NCBI Description (AC004044) putative WD-repeat protein [Arabidopsis



thaliana]

 Seq. No.
 267907

 Contig ID
 14465_1.R1011

 5'-most EST
 dyk700106240.h1

 Method
 BLASTX

NCBI GI g3413717
BLAST score 488
E value 5.0e-49
Match length 116
% identity 76

NCBI Description (AC004747) unknown protein [Arabidopsis thaliana] >gi 3643590 (AC005395) unknown protein [Arabidopsis

thaliana]

Seq. No. 267908

Contig ID 14470 1.R1011

5'-most EST LIB3088-044-Q1-K1-A6

Method BLASTX
NCBI GI g1122931
BLAST score 174
E value 2.0e-12
Match length 103
% identity 35

NCBI Description (U25174) serine-threonine phosphatase [Homo sapiens]

Seq. No. 267909

Contig ID 14475 1.R1011

5'-most EST LIB3088-042-Q1-K1-C9

Seq. No. 267910

Contig ID 14478 1.R1011

5'-most EST LIB3136-056-Q1-K1-D11

Method BLASTX
NCBI GI g1172874
BLAST score 482
E value 4.0e-48
Match length 208
% identity 47

NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR

>gi_479589_pir__S34823 dehydration-induced protein RD22 Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
[Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene
[Arabidopsis thaliana]

Seq. No. 267911

Contig ID 14478 2.R1011

5'-most EST LIB31 $\overline{3}$ 6-037-P1-K1-D11

Method BLASTX
NCBI GI g1172874
BLAST score 289
E value 1.0e-47
Match length 199
% identity 50

NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR

>gi_479589_pir__S34823 dehydration-induced protein RD22 Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22



[Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene [Arabidopsis thaliana]

Seq. No. 267912

Contig ID 14480 1.R1011

5'-most EST LIB3088-043-Q1-K1-G4

Seq. No. 267913

Contig ID 14495 1.R1011

5'-most EST LIB3088-043-Q1-K1-E7

Seq. No. 267914

Contig ID 14498 1.R1011

5'-most EST LIB3067-060-Q1-K1-C4

Seq. No. 267915

Contig ID 14503 1.R1011

5'-most EST LIB3088-043-Q1-K1-F3

Seq. No. 267916

Contig ID 14507 1.R1011

5'-most EST LIB3088-043-Q1-K1-F9

Method BLASTX
NCBI GI g4388730
BLAST score 332

E value 1.0e-30 Match length 103 65

NCBI Description (AC006413) hypothetical protein [Arabidopsis thaliana]

Seq. No. 267917

Contig ID 14508_1.R1011

5'-most EST LIB3088-043-Q1-K1-E3

Method BLASTX
NCBI GI g4006875
BLAST score 334
E value 2.0e-30
Match length 142
% identity 51

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 267918

Contig ID 14508_2.R1011

5'-most EST LIB3137-030-Q1-K1-F10

Method BLASTX
NCBI GI 94006875
BLAST score 179
E value 4.0e-13
Match length 107
% identity 41

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 267919

Contig ID 14514_1.R1011 5'-most EST pmx700091409.h1

Method BLASTX NCBI GI g4455293



```
BLAST score
                   316
E value
                   2.0e-36
Match length
                   182
                   55
% identity
NCBI Description
                  (AL035528) putative protein [Arabidopsis thaliana]
                   267920
Seq. No.
                   14515 1.R1011
Contig ID
5'-most EST
                   ntr700072774.h1
Method
                   BLASTX
NCBI GI
                   q3549679
BLAST score
                   672
E value
                   4.0e-70
Match length
                   282
                   51
% identity
NCBI Description
                 (AL031394) putative protein [Arabidopsis thaliana]
                   267921
Seq. No.
                   14522 1.R1011
Contig ID
5'-most EST
                   xsy700207995.h1
Method
                   BLASTX
NCBI GI
                   g4389444
BLAST score
                   280
                   1.0e-24
E value
Match length
                   104
% identity
                   53
NCBI Description
                  (AE001574) hypothetical 23.1kd-like protein [Drosophila
                  melanogaster]
                   267922
Seq. No.
Contig ID
                   14526 1.R1011
5'-most EST
                   LIB3088-043-Q1-K1-B11
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
E value
                   1.0e-10
Match length
                   48
% identity
                   67
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   267923
Seq. No.
Contig ID
                   14535 1.R1011
5'-most EST
                   pmx700086492.h1
Method
                   BLASTX
NCBI GI
                   q1617200
BLAST score
                   1735
E value
                   0.0e+00
Match length
                   464
```

% identity 71

NCBI Description (Y08607) Shaggy-like kinase 6 [Nicotiana tabacum]

Seq. No. 267924

14535 2.R1011 Contig ID LIB148-034-Q1-E1-B7 5'-most EST

Method BLASTX NCBI GI g1877393

BLAST score 656



E value 1.0e-68 Match length 132 % identity 93

NCBI Description (Y11527) serine/threonine protein kinase [Oryza sativa]

Seq. No. 267925

Contig ID 14541_1.R1011 5'-most EST fwa700100831.h1

Seq. No. 267926

Contig ID 14541_2.R1011 5'-most EST uC-zmflb73152g12b1

Seq. No. 267927

Contig ID 14541_3.R1011 5'-most EST uC-zmflb73152g12a1

Seq. No. 267928

Contig ID 14541_4.R1011 5'-most EST uC-zmflb73236f06a1

Seq. No. 267929

Contig ID 14542 1.R1011

5'-most EST uC-zmflmo17012f10a1

Seq. No. 267930

Contig ID 14545_1.R1011

5'-most EST LIB143-019-Q1-E1-D8

Method BLASTX
NCBI GI g4455188
BLAST score 337
E value 6.0e-31
Match length 359

% identity 35

NCBI Description (AL035521) putative protein [Arabidopsis thaliana]

Seq. No. 267931

Contig ID 14545_2.R1011 5'-most EST uC-zmflmo17240e06a1

Seq. No. 267932

Contig ID 14550 1.R1011

5'-most EST LIB30 $\overline{6}$ 9-057-Q1-K1-D9

Method BLASTX
NCBI GI g939779
BLAST score 757
E value 2.0e-80
Match length 155
% identity 92

NCBI Description (L46397) MADS box protein [Zea mays]

Seq. No. 267933

Contig ID 14556_1.R1011 5'-most EST cjh700197580.h1

Seq. No. 267934

Contig ID 14558 1.R1011



```
5'-most EST
                   LIB3088-042-Q1-K1-G3
Method
                   BLASTX
NCBI GI
                   q4539459
BLAST score
                   213
E value
                   8.0e-17
                   52
Match length
% identity
                   65
                  (AL049500) putative protein [Arabidopsis thaliana]
NCBI Description
                   267935
Seq. No.
Contig ID
                   14561 1.R1011
5'-most EST
                   yyf70\overline{0}351710.h1
Method
                   BLASTX
NCBI GI
                   g4587553
BLAST score
                   332
                   8.0e-31
E value
Match length
                   126
% identity
                   60
NCBI Description
                  (AC006577) F15I1.20 [Arabidopsis thaliana]
Seq. No.
                   267936
Contig ID
                   14562 1.R1011
5'-most EST
                   ymt700221106.h1
Method
                   BLASTX
NCBI GI
                   g2827715
BLAST score
                   326
E value
                   1.0e-31
Match length
                   115
% identity
                   67
NCBI Description
                  (AL021684) receptor protein kinase - like protein
                   [Arabidopsis thaliana]
Seq. No.
                   267937
                   14562 2.R1011
Contig ID
5'-most EST
                   xdb70\overline{0}338314.h1
Seq. No.
                   267938
Contig ID
                   14567 1.R1011
5'-most EST
                   wyr700238839.hl
Method
                   BLASTX
NCBI GI
                   q4107099
BLAST score
                   317
E value
                   9.0e-29
Match length
                   119
% identity
                   50
NCBI Description
                   (AB015141) AHP1 [Arabidopsis thaliana]
                   >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis
                   thaliana]
Seq. No.
                   267939
Contig ID
                   14572 1.R1011
```

5'-most EST LIB3088-042-Q1-K1-E8

Seq. No. 267940

Contig ID 14573 1.R1011

LIB3136-045-Q1-K1-D4 5'-most EST

BLASTX Method

٥.



NCBI GI q4115939 BLAST score 211 E value 8.0e-17 Match length 45 % identity 39

NCBI Description (AF118223) contains similarity to Methanobacterium

thermoautotrophicum transcriptional regulator (GB:AE000850)

[Arabidopsis thaliana]

Seq. No. 267941

Contig ID 14583 1.R1011 5'-most EST ymt700218560.h1

Seq. No. 267942

Contig ID 14583 3.R1011 5'-most EST gct701169033.h1

267943 Seq. No.

Contig ID 14585 1.R1011

5'-most EST LIB3088-042-Q1-K1-C7

Method BLASTX NCBI GI g122022 BLAST score 306 E value 6.0e-28 Match length 88 % identity 73

NCBI Description HISTONE H2B >gi 283025 pir S22323 histone H2B - wheat

>gi 21801 emb CAA42530 (X $\overline{59}$ 873) histone H2B [Triticum

aestivum

Seq. No. 267944

Contig ID 14594 1.R1011 5'-most EST wyr700242120.h1

Method BLASTX NCBI GI q3548802 BLAST score 659 E value 3.0e-69 Match length 174 70 % identity

NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]

>gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein

[Nicotiana tabacum] [Arabidopsis thaliana]

267945 Seq. No.

Contig ID 14596 1.R1011

5'-most EST uC-zmflb73155f11b2

Method BLASTX NCBI GI g4325371 BLAST score 708 E value 2.0e-74Match length 246 % identity 54

NCBI Description (AF128396) contains similarity to Medicago truncatula N7

protein (GB:Y17613) [Arabidopsis thaliana]

Seq. No. 267946

Contig ID 14596_2.R1011



```
5'-most EST
                   cyk700048859.f1
                   267947
Seq. No.
                   14596 3.R1011
Contig ID
5'-most EST
                   LIB3159-016-Q1-K1-A2
                   {\tt BLASTX}
Method
NCBI GI
                   g4325371
BLAST score
                   254
                   7.0e-22
E value
Match length
                   61
% identity
                   72
NCBI Description
                  (AF128396) contains similarity to Medicago truncatula N7
                   protein (GB:Y17613) [Arabidopsis thaliana]
                   267948
Seq. No.
Contig ID
                   14596 4.R1011
5'-most EST
                   uC-zmflmo17060a01b1
                   267949
Seq. No.
Contig ID
                   14596 5.R1011
5'-most EST
                   uC-zmflb73047f05b1
                   BLASTX
Method
NCBI GI
                   g4325371
BLAST score
                   200
E value
                   5.0e-20
Match length
                   76
% identity
                   64
NCBI Description
                   (AF128396) contains similarity to Medicago truncatula N7
                   protein (GB:Y17613) [Arabidopsis thaliana]
Seq. No.
                   267950
Contig ID
                   14603_1.R1011
5'-most EST
                   LIB3088-042-Q1-K1-A10
Method
                   BLASTX
NCBI GI
                   q4262225
BLAST score
                   842
E value
                   4.0e-90
Match length
                   307
% identity
                   50
NCBI Description
                   (AC006200) putative phosphatidic acid phosphatase
                   [Arabidopsis thaliana]
Seq. No.
                   267951
Contig ID
                   14603 2.R1011
5'-most EST
                   LIB189-010-Q1-E1-H8
Method
                   BLASTX
NCBI GI
                   g4262225
BLAST score
                   154
E value
                   2.0e-12
Match length
                   110
                   38
```

% identity NCBI Description

(AC006200) putative phosphatidic acid phosphatase

[Arabidopsis thaliana]

Seq. No. 267952

Contig ID 14603 3.R1011 5'-most EST tfd700570906.h1

Method

BLASTX

```
Seq. No.
                   267953
Contig ID
                   14611 1.R1011
5'-most EST
                   LIB3088-041-Q1-K1-H7
Method
                   BLASTX
NCBI GI
                   q4519936
BLAST score
                   209
E value
                   2.0e-16
Match length
                   165
% identity
                   28
NCBI Description (AB019186) RPR1 [Oryza sativa]
Seq. No.
                   267954
Contig ID
                   14612 1.R1011
5'-most EST
                   cat700016417.rl
Seq. No.
                   267955
Contig ID
                   14623 1.R1011
5'-most EST
                   LIB3088-040-Q1-K1-H12
Seq. No.
                   267956
Contig ID
                   14630 1.R1011
5'-most EST
                   uC-zmflb73239d02b2
Method
                   BLASTX
NCBI GI
                   g2245026
BLAST score
                   403
E value
                   5.0e-39
Match length
                   114
% identity
                   70
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   267957
Contig ID
                   14630 3.R1011
5'-most EST
                   LIB3180-018-P2-M1-D5
Method
                   BLASTX
NCBI GI
                   q2245026
BLAST score
                   147
E value
                   2.0e-20
Match length
                   99
% identity
NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   267958
Contig ID
                   14630 4.R1011
5'-most EST
                   ntr700072692.h1
Method
                   BLASTX
NCBI GI
                   g2245026
BLAST score
                   307
E value
                   7.0e-28
Match length
                   86
% identity
                   70
NCBI Description
                  (Z97341) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   267959
Contig ID
                   14652 1.R1011
5'-most EST
                   uC-zm\overline{f}lb73095a02b1
```



g3327389 NCBI GI BLAST score 1974 0.0e+00E value Match length 491 % identity 79 NCBI Description (AC004483) putative DNA replication licensing factor, mcm5 [Arabidopsis thaliana] Seq. No. 267960 Contig ID 14659 1.R1011 5'-most EST LIB3088-038-Q1-K1-H1 267961 Seq. No. Contig ID 14661 1.R1011 5'-most EST LIB3088-038-Q1-K1-H11 267962 Seq. No. Contig ID 14669 1.R1011

Seq. No. 267963 Contig ID

5'-most EST

14671 1.R1011 5'-most EST LIB3088-038-Q1-K1-E5

fwa700100337.h1

Seq. No. 267964

Contig ID 14679_1.R1011

5'-most EST LIB3066-022-Q1-K1-A11

Method BLASTX NCBI GI g1617274 BLAST score 986 E value 1.0e-107 Match length 244 74 % identity

NCBI Description (Z72152) AMP-binding protein [Brassica napus]

Seq. No. 267965

Contig ID 14686 1.R1011

5'-most EST uC-zmflmo17190b07b1

Method BLASTX NCBI GI q3372233 BLAST score 747 E value 4.0e-79202 Match length % identity 69

NCBI Description (AF019248) RNA polymerase I, II and III 24.3 kDa subunit

[Arabidopsis thaliana]

Seq. No. 267966

Contig ID 14686 2.R1011

5'-most EST uC-zmroteosinte088h10b1

Method BLASTX NCBI GI g3372233 BLAST score 440 E value 1.0e-43 Match length 126 % identity

NCBI Description (AF019248) RNA polymerase I, II and III 24.3 kDa subunit



[Arabidopsis thaliana]

267967 Seq. No. Contig ID 14693 1.R1011 5'-most EST hvj700619059.h1 Method BLASTX g2129826 NCBI GI BLAST score 2226 0.0e+00E value Match length 505 85 % identity NCBI Description dynamin-like protein phragmoplastin 5 - soybean >gi 1218004 (U36430) SDL5A [Glycine max] 267968 Seq. No. Contig ID 14695 1.R1011 LIB3088-038-Q1-K1-C5 5'-most EST Method BLASTX NCBI GI g4510395 BLAST score 553 E value 7.0e-57Match length 142 67 % identity NCBI Description (AC006587) putative beta-galactosidase precursor [Arabidopsis thaliana] Seq. No. 267969 14702 1.R1011 Contig ID 5'-most EST LIB143-060-Q1-E1-C9 Seq. No. 267970 14702 2.R1011 Contig ID LIB3088-038-Q1-K1-E2 5'-most EST Method BLASTX NCBI GI g285313 BLAST score 521 E value 1.0e-52 Match length 319 36 % identity NCBI Description hyuC - Pseudomonas sp Seq. No. 267971 Contig ID 14705 1.R1011 5'-most EST LIB3088-037-Q1-K1-F6 Seq. No. 267972 Contig ID 14713_1.R1011 5'-most EST uC-zmflb73022q03b1 Method BLASTX NCBI GI g4104060 BLAST score 1280 E value 1.0e-141 Match length 331 75 % identity

Seq. No. 267973

NCBI Description

(AF031231) S222 [Triticum aestivum]



Contig ID 14713 2.R1011

5'-most EST LIB3137-027-Q1-K1-D11

Seq. No. 267974

14713 3.R1011 Contig ID 5'-most EST uC-zmflB73022g03b1

Method BLASTX NCBI GI q4104060 BLAST score 480 4.0e-48 E value Match length 216 % identity 49

NCBI Description (AF031231) S222 [Triticum aestivum]

Seq. No. 267975

14716 1.R1011 Contig ID 5'-most EST uC-zmflb73259f08a1

267976 Seq. No.

Contig ID 14717 1.R1011

uC-zmflmo17239f10a1 5'-most EST

Method BLASTX NCBI GI g3204103 BLAST score 155 E value 2.0e-10 Match length 37 81 % identity

NCBI Description (AJ006761) hypothetical protein [Cicer arietinum]

267977 Seq. No.

Contig ID 14722 1.R1011

5'-most EST LIB3069-003-Q1-K1-H6

Seq. No. 267978

Contig ID 14723 1.R1011 5'-most EST cjh700194567.h1

Seq. No. 267979

14728 1.R1011 Contig ID uwc700154889.hl 5'-most EST

267980 Seq. No.

14734 1.R1011 Contig ID 5'-most EST xyt700347225.h1

Seq. No. 267981

Contig ID 14735 1.R1011

5'-most EST LIB3180-018-P2-M1-H8

Method BLASTX NCBI GI g3242705 BLAST score 534 E value 2.0e-54Match length 127

76 % identity

NCBI Description (AC003040) putative nicotinate phosphoribosyltransferase

[Arabidopsis thaliana]



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267982
Seq. No.
                  14741 1.R1011
Contig ID
                  LIB3088-037-Q1-K1-A2
5'-most EST
                  BLASTX
Method
                  q3482917
NCBI GI
                  153
BLAST score
                  3.0e-10
E value
                  45
Match length
                  60
% identity
                   (AC003970) Similar to Glucose-6-phosphate dehydrogenases,
NCBI Description
                  gi 2276344, gi 2829880, gi 2352919 and others. [Arabidopsis
                  thaliana]
                  267983
Seq. No.
                  14742 1.R1011
Contig ID
                  yyf700349582.h1
5'-most EST
                  BLASTX
Method
                  g4193320
NCBI GI
BLAST score
                   616
                   5.0e-64
E value
                  114
Match length
                   100
% identity
                  (AF045473) histone deacetylase [Zea mays]
NCBI Description
                  267984
Seq. No.
                   14747 1.R1011
Contig ID
5'-most EST
                  LIB3136-017-Q1-K1-A7
Method
                   BLASTX
                   g3953470
NCBI GI
                   339
BLAST score
                   2.0e-31
E value
Match length
                   300
                   35
% identity
NCBI Description (AC002328) F20N2.15 [Arabidopsis thaliana]
                   267985
Seq. No.
Contig ID
                   14750_1.R1011
                   uC-zmflb73302g03a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q729103
                   1066
BLAST score
                   1.0e-116
E value
Match length
                   215
% identity
                   CHALCONE--FLAVONONE ISOMERASE >gi_542181_pir__S41570
NCBI Description
                   chalcone isomerase (EC 5.5.1.6) - maize
                   >gi_396149_emb_CAA80441_ (Z22760) chalcone flavonone
                   isomerase [Zea mays]
                   267986
```

Seq. No. 267986 Contig ID 14753 1.R1011

5'-most EST uC-zmflmo17262h04b1

Method BLASTX NCBI GI g1871577

BLAST score 246 E value 2.0e-20 Match length 174 % identity (Y11553) putative 21kD protein precursor [Medicago sativa] NCBI Description Seq. No. 267987 Contig ID 14762 1.R1011 5'-most EST fdz701161621.h1 Method BLASTX g1931647 NCBI GI BLAST score 1082 E value 1.0e-118 Match length 243 81 % identity (U95973) endomembrane protein EMP70 precusor isolog NCBI Description [Arabidopsis thaliana] 267988 Seq. No. Contig ID 14766 1.R1011 5'-most EST LIB3088-036-Q1-K1-B3 Method BLASTN q4007864 51 2.0e-19 67 94 NCBI Description Zea mays HRGP gene, AC1503 line

NCBI GI BLAST score E value Match length % identity

14782 1.R1011

Seq. No. 267989 Contig ID 14768 1.R1011 5'-most EST LIB3279-007-P1-K1-B6

267990 Seq. No.

LIB3088-035-Q1-K1-F11 5'-most EST Method BLASTX g3386615 NCBI GI BLAST score 391

6.0e-38 E value Match length 108 % identity 72

Contig ID

NCBI Description (AC004665) putative phosphomannomutase [Arabidopsis thaliana]

267991

Seq. No. 14786 1.R1011 Contig ID

5'-most EST LIB3279-050-P1-K1-G12

Method BLASTX NCBI GI g399853 BLAST score 263 E value 6.0e-23 Match length 67 81 % identity

NCBI Description HISTONE H2B.1 >gi 283041 pir S28048 histone H2B - maize >gi 22323 emb CAA40564 (X57312) H2B histone [Zea mays]

267992 Seq. No.

14790 1.R1011 Contig ID

5'-most EST LIB3088-035-Q1-K1-E4



Contig ID 14802 1.R1011

5'-most EST LIB3088-035-Q1-K1-C6

Seq. No. 267994

Contig ID 14815 1.R1011

5'-most EST LIB148-061-Q1-E1-F11

Seq. No. 267995

Contig ID 14823_1.R1011 5'-most EST fdz701158340.h1

Seq. No. 267996

Contig ID 14827_1.R1011

5'-most EST LIB3088-034-Q1-K1-A6

Method BLASTX
NCBI GI 94506921
BLAST score 161
E value 1.0e-10
Match length 69

% identity 45

NCBI Description small glutamine-rich tetratricopeptide repeat

(TPR)-containing >gi_2909372_emb_CAA11565_ (AJ223828) small

glutamine-rich tetratricopeptide (SGT) [Homo sapiens]

 $>gi_4235146$ (AC006538) small glutamine-rich

tetratricopeptide (SGT) [Homo sapiens]

>gi_4539082_emb_CAB39725.1_ (AJ133129) small glutamine-rich tetratricopeptide repeat containing protein [Homo sapiens]

Seq. No. 267997

Contig ID 14828_1.R1011

5'-most EST LIB3088-034-Q1-K1-B5

Seq. No. 267998

Contig ID 14833_1.R1011 5'-most EST xdb700339070.h1

Method BLASTX
NCBI GI g2264369
BLAST score 171
E value 6.0e-12
Match length 94
% identity 33

NCBI Description (AC002354) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 267999

Contig ID 14834_1.R1011 5'-most EST xyt700347106.h1

Seq. No. 268000

Contig ID 14834_2.R1011 5'-most EST xmt700258830.h1

Seq. No. 268001

Contig ID 14839 1.R1011 5'-most EST ceu700431186.h1



Contig ID 14841 1.R1011

5'-most EST LIB3062-022-Q1-K1-D2

Method BLASTX
NCBI GI g4415936
BLAST score 242
E value 8.0e-20
Match length 229
% identity 31

NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]

Seq. No. 268003

Contig ID 14841 2.R1011

5'-most EST LIB3060-028-Q1-K1-F8

Seq. No. 268004

Contig ID 14845 1.R1011

5'-most EST uC-zmflmo17160e02b1

Method BLASTX
NCBI GI g4102839
BLAST score 1411
E value 0.0e+00
Match length 435
% identity 73

NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No. 268005

Contig ID 14847_1.R1011 5'-most EST uC-zmflb73122h11a1

Seq. No. 268006

Contig ID 14849_1.R1011 5'-most EST xjt700095162.h1

Method BLASTX
NCBI GI g443509
BLAST score 256
E value 2.0e-21
Match length 200
% identity 34

NCBI Description Triacylglycerol Acylhydrolase (E.C.3.1.1.3) Complex With

Diethylphosophate

Seq. No. 268007

Contig ID 14851 1.R1011

5'-most EST LIB3088-032-Q1-K1-H8

Seq. No. 268008

Contig ID 14860 1.R1011

5'-most EST LIB3062-020-Q1-K1-B9

Method BLASTX
NCBI GI g3618316
BLAST score 145
E value 7.0e-12
Match length 56
% identity 68

NCBI Description (AB001886) zinc finger protein [Oryza sativa]



Contig ID 14861_1.R1011 5'-most EST uC-zmflB73004e06b1

Method BLASTX
NCBI GI g133955
BLAST score 352
E value 3.0e-33
Match length 72
% identity 93

NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S4 (BASIC PROTEIN)

>gi_70877_pir__R3ZM4 ribosomal protein S4 - maize
chloroplast >gi_12412_emb_CAA25754_ (X01608) pot. basic
protein homologous to bacterial ribosome assembly protein
S4 (aa 1-201) [Zea mays] >gi_902224_emb_CAA60288_ (X86563)

ribosomal protein S4 [Zea mays]

Seq. No. 268010

Contig ID 14863_1.R1011 5'-most EST uC-zmflb73274e10a1

Seq. No. 268011

Contig ID 14864 1.R1011

5'-most EST LIB3088-032-Q1-K1-F6

Seq. No. 268012

Contig ID 14868_1.R1011 5'-most EST nwy700443651.h1

Seq. No. 268013

Contig ID 14873_1.R1011 5'-most EST xsy700209275.h1

Method BLASTN
NCBI GI g293905
BLAST score 619
E value 0.0e+00
Match length 699
% identity 98

NCBI Description Zea mays TATA-binding protein mRNA, complete cds

Seq. No. 268014

Contig ID 14881 1.R1011

5'-most EST uC-zmflmo17078h12b1

Method BLASTX
NCBI GI g1488297
BLAST score 534
E value 4.0e-63
Match length 189
% identity 72

NCBI Description (U63530) osRAD23 [Oryza sativa]

Seq. No. 268015

Contig ID 14881_2.R1011

5'-most EST LIB189-023-Q1-E1-H11

Method BLASTX
NCBI GI g1488297
BLAST score 244



E value 1.0e-20 Match length 65 75

NCBI Description (U63530) osRAD23 [Oryza sativa]

Seq. No. 268016

Contig ID 14882 1.R1011

5'-most EST uC-zmroteosinte028b11b1

Seq. No. 268017

Contig ID 14888_1.R1011 5'-most EST pmx700082933.h1

Seq. No. 268018

Contig ID 14889 1.R1011

5'-most EST LIB3088-032-Q1-K1-C11

Seq. No. 268019

Contig ID 14890 1.R1011

5'-most EST LIB3059-012-Q1-K1-D7

Method BLASTX
NCBI GI g4056477
BLAST score 444
E value 8.0e-44
Match length 143
% identity 41

NCBI Description (AC005896) putative RNA binding protein [Arabidopsis

thaliana]

Seq. No. 268020

Contig ID 14902_1.R1011

5'-most EST uC-zmromo17112a12a1

Seq. No. 268021

Contig ID 14906_1.R1011

5'-most EST uC-zmflmo17075e02a1

Seq. No. 268022

Contig ID 14911 1.R1011

5'-most EST LIB3088-031-Q1-K1-G3

Seq. No. 268023

Contig ID 14920_2.R1011 5'-most EST nbm700464752.h1

Seq. No. 268024

Contig ID 14921_1.R1011 5'-most EST tzu700201794.h1

Method BLASTX
NCBI GI g3334441
BLAST score 215
E value 5.0e-17
Match length 111
% identity 42

NCBI Description HYPOTHETICAL 47.9 KD PROTEIN T517.9 IN CHROMOSOME II

>gi_2642161 (AC003000) hypothetical protein [Arabidopsis

thaliana]



```
Seq. No.
                  268025
Contig ID
                  14922 1.R1011
5'-most EST
                  LIB3088-031-Q1-K1-B5
                  BLASTX
Method
                  q3551954
NCBI GI
BLAST score
                   666
                   1.0e-69
E value
Match length
                   261
% identity
                   46
                   (AF082030) senescence-associated protein 5 [Hemerocallis
NCBI Description
                  hybrid cultivar]
                  268026
Seq. No.
                  14930 1.R1011
Contig ID
5'-most EST
                  uC-zmroteosinte023e07b2
Seq. No.
                   268027
                   14934 1.R1011
Contig ID
5'-most EST
                  LIB3069-054-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                   g3874344
BLAST score
                   343
                   1.0e-31
E value
                   232
Match length
% identity
                   39
                  (Z81035) predicted using Genefinder; Similarity to Human
NCBI Description
                   HA0609 protein (TR:Q15050); cDNA EST EMBL:D70929 comes from
                   this gene; cDNA EST EMBL:D73473 comes from this gene; cDNA
                   EST EMBL: C08351 comes from this gene; cDNA EST EMBL
                   268028
Seq. No.
Contig ID
                   14939 1.R1011
5'-most EST
                  LIB3088-030-Q1-K1-A3
                   268029
Seq. No.
Contig ID
                   14951 1.R1011
5'-most EST
                  LIB3136-056-Q1-K1-F7
Method
                   BLASTX
NCBI GI
                   q2854153
BLAST score
                   410
E value
                   1.0e-39
                   177
Match length
% identity
                  (AF045640) No definition line found [Caenorhabditis
NCBI Description
                   elegans]
Seq. No.
                   268030
Contig ID
                   14952_1.R1011
5'-most EST
                   uC-zmroteosinte119q09b2
```

Method BLASTX
NCBI GI g4506223
BLAST score 635
E value 8.0e-66
Match length 361
% identity 37

NCBI Description proteasome (prosome, macropain) 26S subunit, non-ATPase, 13



>gi_3618343_dbj_BAA33214_ (AB009398) 26S proteasome subunit p40.5 [Homo sapiens]

Seq. No. 268031

Contig ID 14952_2.R1011 5'-most EST wyr700240288.h1

Method BLASTX
NCBI GI g4506223
BLAST score 164
E value 5.0e-11
Match length 80
% identity 44

NCBI Description proteasome (prosome, macropain) 26S subunit, non-ATPase, 13

>gi 3618343 dbj BAA33214 (AB009398) 26S proteasome subunit

p40.5 [Homo sapiens]

Seq. No. 268032

Contig ID 14952_3.R1011 5'-most EST xsy700213183.h1

Seq. No. 268033

Contig ID 14952_4.R1011

5'-most EST uC-zmflmo17424e11a1

Seq. No. 268034

Contig ID 14952_5.R1011 5'-most EST qmh700026576.f1

Seq. No. 268035

Contig ID 14952_9.R1011 5'-most EST wty700172949.h1

Seq. No. 268036

Contig ID 14952_11.R1011 5'-most EST nbm700477789.h1

Seq. No. 268037

Contig ID 14963_1.R1011 5'-most EST uC-zmrob73075c08b1

Seq. No. 268038

Contig ID 14963_2.R1011

5'-most EST LIB189-032-Q1-E1-D6

Seq. No. 268039

Contig ID 14963_3.R1011 5'-most EST xsy700214458.h1

Seq. No. 268040

Contig ID 14963_4.R1011 5'-most EST ymt700219135.h1

Seq. No. 268041

Contig ID 14963_5.R1011 5'-most EST uC-zmflmo17245b11a1

Seq. No. 268042



```
14963 6.R1011
Contig ID
                   LIB3115-007-Q1-K1-B5
5'-most EST
                   268043
Seq. No.
                   14977 1.R1011
Contig ID
                   uC-zm\overline{f}1b73274e11a1
5'-most EST
                   268044
Seq. No.
Contig ID
                   14985 1.R1011
5'-most EST
                   LIB3181-006-P1-K2-D4
                   BLASTX
Method
                   g1944000
NCBI GI
BLAST score
                   1505
                   1.0e-168
E value
                   306
Match length
% identity
                   93
                  (AB002109) protein kinase [Oryza sativa]
NCBI Description
Seq. No.
                   268045
                   14994 1.R1011
Contig ID
5'-most EST
                   xmt70\overline{0}257403.h2
                   BLASTX
Method
                   g3738306
NCBI GI
                   474
BLAST score
E value
                   3.0e-88
                   356
Match length
% identity
                   49
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
                   268046
Seq. No.
                   14995_1.R1011
Contig ID
                   LIB3156-021-Q1-K1-F8
5'-most EST
Method
                   BLASTX
                   q4544390
NCBI GI
                   247
BLAST score
E value
                   1.0e-20
Match length
                   80
% identity
NCBI Description (AC007047) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   268047
Contig ID
                   15008 1.R1011
                   pmx700082558.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4099508
BLAST score
                   1320
E value
                   1.0e-146
Match length
                   263
```

% identity 100

NCBI Description (U87949) proliferating cell nuclear antigen [Zea mays]

Seq. No. 268048

15008 2.R1011 Contiq ID

5'-most EST LIB3088-026-Q1-K1-G1

Method BLASTX g2499442 NCBI GI BLAST score 226



E value 2.0e-18 Match length 47 % identity 98

NCBI Description PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA)

>gi_1076822_pir__S52115 proliferating cell nuclear antigen
(PCNA) homolog - maize >gi_732990_emb_CAA55669_ (X79065)

proliferative cell nuclear antigen [Zea mays]

>qi 1093954 prf 2105195A proliferating cell nuclear

antiqen [Zea mays]

Seq. No. 268049

Contig ID 15008_3.R1011 5'-most EST rv1700453879.h1

Method BLASTX
NCBI GI g2499442
BLAST score 672
E value 9.0e-71
Match length 132
% identity 100

NCBI Description PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA)

>gi_1076822_pir__S52115 proliferating cell nuclear antigen
(PCNA) homolog - maize >gi_732990_emb_CAA55669_ (X79065)

proliferative cell nuclear antigen [Zea mays]

>gi 1093954 prf 2105195A proliferating cell nuclear

antigen [Zea mays]

Seq. No. 268050

Contig ID 15028_1.R1011 5'-most EST vqh700053192.r1

Method BLASTX
NCBI GI g2109293
BLAST score 1390
E value 1.0e-154
Match length 336
% identity 77

NCBI Description (U97568) serine/threonine protein kinase [Arabidopsis

thaliana]

Seq. No. 268051

Contig ID 15029_1.R1011

5'-most EST LIB3088-024-Q1-K1-H4

Seq. No. 268052

Contig ID 15029_2.R1011 5'-most EST xdb700340915.h1

Method BLASTX
NCBI GI g2654559
BLAST score 189
E value 2.0e-14
Match length 88
% identity 43

NCBI Description (AF006621) embryonic lung protein [Homo sapiens]

Seq. No. 268053

Contig ID 15030_1.R1011

5'-most EST LIB3062-010-Q1-K1-H11



```
268054
Seq. No.
Contig ID
                   15030 2.R1011
                   LIB3159-013-Q1-K1-C9
5'-most EST
Seq. No.
                   268055
                   15030 3.R1011
Contig ID
5'-most EST
                   xmt700257961.h1
                   268056
Seq. No.
                   15031 1.R1011
Contig ID
                   LIB3088-024-Q1-K1-E2
5'-most EST
                   BLASTX
Method
                   g4538978
NCBI GI
                   531
BLAST score
                   1.0e-53
E value
Match length
                   167
                   58
% identity
                  (AL049487) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   268057
Seq. No.
                   15031 2.R1011
Contig ID
                   uC-zm\overline{f}lmo17281c08b1
5'-most EST
Method
                   BLASTX
                   g4538978
NCBI GI
BLAST score
                   300
                   3.0e-27
E value
Match length
                   96
                   57
% identity
                  (AL049487) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   268058
Seq. No.
                   15031 5.R1011
Contig ID
                   uwh70\overline{0}207176.h1
5'-most EST
Method
                   BLASTX
                   q4538978
NCBI GI
BLAST score
                   184
E value
                   2.0e-13
Match length
                   61
% identity
NCBI Description
                  (AL049487) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   268059
Contig ID
                   15032 1.R1011
5'-most EST
                   LIB3088-024-Q1-K1-E4
Seq. No.
                   268060
Contig ID
                   15044 1.R1011
5'-most EST
                   LIB3088-024-Q1-K1-C2
Method
                   BLASTX
NCBI GI
                   g2462822
```

234 BLAST score E value 3.0e-19 79 Match length % identity

(AF000657) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 268061



Contig ID 15045_1.R1011

5'-most EST LIB3088-024-Q1-K1-D6

Seq. No. 268062

Contig ID 15048_1.R1011

5'-most EST LIB3088-023-Q1-K1-F9

Seq. No. 268063

Contig ID 15048_2.R1011 5'-most EST uC-zmflb73121d06a1

Seq. No. 268064

Contig ID 15048_3.R1011 5'-most EST uer700580592.h1

Seq. No. 268065

Contig ID 15049 1.R1011

5'-most EST LIB3088-023-Q1-K1-H1

Seq. No. 268066

Contig ID 15052 1.R1011 5'-most EST nbm700470718.h1

Seq. No. 268067

Contig ID 15053_1.R1011 5'-most EST qmh700027263.f1

Seq. No. 268068

Contig ID 15058_1.R1011 5'-most EST zla700379777.h1

Method BLASTX
NCBI GI g3309583
BLAST score 465
E value 8.0e-47
Match length 104
% identity 83

NCBI Description (AF073830) fructose-6-phosphate

2-kinase/fructose-2,6-bisphosphatase [Solanum tuberosum]

Seq. No. 268069

Contig ID 15062_1.R1011

5'-most EST LIB3088-023-Q1-K1-B8

Seq. No. 268070

Contig ID 15069 1.R1011

5'-most EST LIB3088-022-Q1-K1-H10

Seq. No. 268071

Contig ID 15069_2.R1011 5'-most EST gwl700615211.h1

Seq. No. 268072

Contig ID 15071_1.R1011 5'-most EST hbs701183957.h1

Method BLASTX NCBI GI g4467139 BLAST score 364



E value 2.0e-34 Match length 114 % identity 65

NCBI Description (AL035540) putative protein phosphatase-2c [Arabidopsis

thaliana]

Seq. No. 268073

Contig ID 15073_1.R1011 5'-most EST fdz701162975.h1

Method BLASTX
NCBI GI g1168609
BLAST score 1834
E value 0.0e+00
Match length 519
% identity 66

NCBI Description AUXIN-RESISTANCE PROTEIN AXR1 >gi 479664 pir S35071

auxin-resistance protein AXR1 - Arabidopsis thaliana >gi_304104 (L13922) ubiquitin-activating enzyme E1 [Arabidopsis thaliana] >gi_2388579 (AC000098) Match to Arabidopsis AXR1 (gb_ATHAXR1122). [Arabidopsis thaliana] >gi_448755_prf__1917337A ubiquitin-activating enzyme E1

[Arabidopsis thaliana]

Seq. No. 268074

Contig ID 15073_4.R1011 5'-most EST hvj700622608.h1

Method BLASTX
NCBI GI g3831455
BLAST score 347
E value 9.0e-33
Match length 83
% identity 77

NCBI Description (AC005700) putative ubiquitin activating enzyme

[Arabidopsis thaliana]

Seq. No. 268075

Contig ID 15075 1.R1011

5'-most EST LIB3088-022-Q1-K1-F3

Method BLASTX
NCBI GI g2935527
BLAST score 237
E value 1.0e-19
Match length 128
% identity 41

NCBI Description (AF049068) pollen allergen [Pinus radiata]

Seq. No. 268076

Contig ID 15077_1.R1011 5'-most EST pmx700087203.h1

Seq. No. 268077

Contig ID 15078 1.R1011

5'-most EST LIB3088-022-Q1-K1-C2

Seq. No. 268078

Contig ID 15084 1.R1011 5'-most EST tzu700204569.h1

BLAST score

Match length

% identity

E value

418

246 38

1.0e-40



```
268079
Seq. No.
                  15094 1.R1011
Contig ID
                  dyk700106954.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q100226
BLAST score
                  807
                  4.0e-86
E value
Match length
                  346
% identity
                  47
                  hypothetical protein - tomato >gi 19275 emb CAA78112
NCBI Description
                   (Z12127) protein of unknown function [Lycopersicon
                  esculentum] >gi 445619 prf 1909366A Leu zipper protein
                   [Lycopersicon esculentum]
Seq. No.
                  268080
                  15094 2.R1011
Contig ID
                  uC-zmflmo17404b11a1
5'-most EST
                  268081
Seq. No.
                  15094 3.R1011
Contig ID
                  uC-zmflmo17398h05a1
5'-most EST
Seq. No.
                  268082
                  15095 1.R1011
Contig ID
5'-most EST
                  LIB3117-008-Q1-K1-D5
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  36
                  1.0e-10
E value
Match length
                  36
                  100
% identity
                 Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
                  268083
Seq. No.
                  15095 2.R1011
Contig ID
5'-most EST
                  uC-zmflmo17118h09b1
                   268084
Seq. No.
                   15099 1.R1011
Contig ID
                  wyr700242408.hl
5'-most EST
Seq. No.
                   268085
                   15101 1.R1011
Contig ID
5'-most EST
                  LIB3088-020-Q1-K1-F12
                   268086
Seq. No.
Contig ID
                   15112_1.R1011
5'-most EST
                  LIB3088-019-Q1-K1-D5
Method
                   BLASTX
NCBI GI
                   g1644402
```

NCBI Description (U73524) putative ATP/GTP-binding protein [Homo sapiens]



```
Seq. No.
                  268087
                  15126 1.R1011
Contig ID
                  uC-zm\overline{f}lmo17219h09b1
5'-most EST
                  268088
Seq. No.
                  15127 1.R1011
Contig ID
                  LIB189-033-Q1-E1-C9
5'-most EST
                  BLASTX
Method
                  g3927825
NCBI GI
BLAST score
                   1531
                   1.0e-171
E value
Match length
                   320
% identity
                   89
                   (AC005727) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana]
                   268089
Seq. No.
                   15127 2.R1011
Contig ID
                   pmx700090888.h1
5'-most EST
                   BLASTX
Method
                   q3522929
NCBI GI
BLAST score
                   395
                   1.0e-107
E value
Match length
                   310
                   69
% identity
                   (AC002535) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana] >gi_3738279 (AC005309) putative
                   dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
                   268090
Seq. No.
                   15127 3.R1011
Contig ID
                   uC-zmflmo17038b10a1
5'-most EST
                   268091
Seq. No.
                   15127 4.R1011
Contig ID
                   LIB3062-034-Q1-K1-B10
5'-most EST
                   BLASTX
Method
                   g2351580
NCBI GI
                   296
BLAST score
                   1.0e-26
E value
                   163
Match length
% identity
                   (U82433) thymidine diphospho-glucose 4-6-dehydratase
NCBI Description
                   homolog [Prunus armeniaca]
                   268092
Seq. No.
                   15127_5.R1011
Contig ID
5'-most EST
                   uC-zmflb73255b11b1
                   BLASTX
Method
                   g3927825
NCBI GI
                   474
BLAST score
                   7.0e-60
E value
```

160 Match length % identity

(AC005727) putative dTDP-glucose 4-6-dehydratase NCBI Description

[Arabidopsis thaliana]



```
Seq. No.
                   268093
Contig ID
                   15127 6.R1011
5'-most EST
                   nwy70\overline{0}446925.h1
Seq. No.
                   268094
Contig ID
                   15129 1.R1011
5'-most EST
                   LIB3137-001-Q1-K1-D4
Method
                   BLASTX
NCBI GI
                   q2497538
BLAST score
                   1761
                   0.0e + 00
E value
Match length
                   395
% identity
                   88
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 466350 (L08632)
NCBI Description
                   pyruvate kinase [Glycine max]
Seq. No.
                   268095
Contig ID
                   15129 2.R1011
5'-most EST
                   uC-zmflb73328f08a1
Seq. No.
                   268096
Contig ID
                   15133 1.R1011
5'-most EST
                   hbs701184666.h1
Method
                   BLASTX
NCBI GI
                   g1091678
BLAST score
                   379
                   1.0e-36
E value
Match length
                   120
% identity
                   64
NCBI Description activator-like transposable element [Pennisetum glaucum]
                   268097
Seq. No.
                   15134 1.R1011
Contig ID
5'-most EST
                   ntr700076672.h1
                   268098
Seq. No.
                   15137 1.R1011
Contig ID
5'-most EST
                   cat700020378.rl
Method
                   BLASTX
NCBI GI
                   g2827715
BLAST score
                   312
                   1.0e-57
E value
Match length
                   142
% identity
                   78
                  (AL021684) receptor protein kinase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   268099
Seq. No.
Contig ID
                   15139 1.R1011
5'-most EST
                   uC-zmflb73418f02a1
                   268100
```

Contig ID 15141 1.R1011 pmx700088747.h1 5'-most EST

Method BLASTX NCBI GI g1914685 BLAST score 463



```
E value
                   8.0e-46
                  140
Match length
% identity
                  65
                  (Y12014) RAD23 protein, isoform II [Daucus carota]
NCBI Description
                  268101
Seq. No.
Contig ID
                  15142 1.R1011
5'-most EST
                  LIB3061-035-Q1-K1-E8
Method
                  BLASTX
NCBI GI
                  q4566530
BLAST score
                  491
E value
                   4.0e-49
Match length
                  259
                  38
% identity
NCBI Description
                  (AF109733) SWI/SNF-related, matrix-associated,
                  actin-dependent regulator of chromatin D1 [Homo sapiens]
                  268102
Seq. No.
Contig ID
                   15142 2.R1011
5'-most EST
                  LIB3150-075-P2-N2-F10
                   268103
Seq. No.
Contig ID
                   15143 1.R1011
5'-most EST
                  LIB3088-014-Q1-K1-F9
                   268104
Seq. No.
Contig ID
                   15144 1.R1011
5'-most EST
                  pmx700084820.h1
Method
                   BLASTX
NCBI GI
                  q3738319
BLAST score
                  572
E value
                   4.0e-59
Match length
                  158
% identity
                   66
                  (AC005170) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   268105
Seq. No.
                   15148 1.R1011
Contig ID
5'-most EST
                   ypc700804422.h1
Method
                   BLASTX
NCBI GI
                   g3935183
BLAST score
                   326
                   7.0e-30
E value
Match length
                  165
                   43
% identity
NCBI Description (AC004557) F17L21.26 [Arabidopsis thaliana]
                   268106
Seq. No.
                   15150 1.R1011
Contig ID
5'-most EST
                   cyk700050385.f1
                   BLASTX
Method
```

Method BLASTX
NCBI GI g3402758
BLAST score 253
E value 2.0e-21
Match length 133
% identity 43

NCBI Description (AL031187) serine/threonine kinase - like protein



[Arabidopsis thaliana]

 Seq. No.
 268107

 Contig ID
 15155_1.R1011

 5'-most EST
 hbs701180752.h1

Method BLASTX
NCBI GI g2832685
BLAST score 639
E value 1.0e-66
Match length 231
% identity 60

NCBI Description (AL021712) putative protein [Arabidopsis thaliana]

Seq. No. 268108

Contig ID 15157_1.R1011 5'-most EST uC-zmrob73019d12b1

Seq. No. 268109

Contig ID 15157_6.R1011 5'-most EST xmt700264465.h1

Seq. No. 268110

Contig ID 15157_9.R1011 5'-most EST nbm700467761.h1

Seq. No. 268111

Contig ID 15157_10.R1011 5'-most EST LIB36-002-Q1-E1-D8

Method BLASTN
NCBI GI g3821780
BLAST score 37
E value 2.0e-11
Match length 49

% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 268112

Contig ID 15163_1.R1011 5'-most EST vux700156892.h1

Method BLASTX
NCBI GI g2459440
BLAST score 253
E value 2.0e-21
Match length 143
% identity 35

NCBI Description (AC002332) putative receptor kinase [Arabidopsis thaliana]

Seq. No. 268113

Contig ID 15163_2.R1011 5'-most EST nbm700465480.h1

Seq. No. 268114

Contig ID 15166_1.R1011 5'-most EST LIB84-030-Q1-E1-D11

Seq. No. 268115

Contig ID 15168 1.R1011



5'-most EST uC-zmflmo17221d01b1

Method BLASTX
NCBI GI g3763927
BLAST score 560
E value 5.0e-61
Match length 234
% identity 57

NCBI Description (AC004450) putative carboxyphosphoenolpyruvate mutase

[Arabidopsis thaliana]

Seq. No. 268116

Contig ID 15168_2.R1011 5'-most EST uC-zmflb73301a02a1

Seq. No. 268117

Contig ID 15168_3.R1011

5'-most EST LIB3059-034-Q1-K1-F7

Method BLASTX
NCBI GI g224508
BLAST score 524
E value 2.0e-53
Match length 109
% identity 98

NCBI Description zein A20 [Zea mays]

Seq. No. 268118

Contig ID 15171 1.R1011

5'-most EST LIB3088-013-Q1-K1-E1

Seq. No. 268119

Contig ID 15172_1.R1011 5'-most EST tfd700574593.h1

Method BLASTX
NCBI GI g3402750
BLAST score 271
E value 7.0e-24
Match length 136
% identity 38

NCBI Description (AL031187) putative protein [Arabidopsis thaliana]

Seq. No. 268120

Contig ID 15174 1.R1011

5'-most EST LIB3088-013-Q1-K1-F1

Method BLASTX
NCBI GI g4006827
BLAST score 445
E value 3.0e-44
Match length 121
% identity 66

NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 268121

Contig ID 15175 1.R1011

5'-most EST LIB3088-013-Q1-K1-F4

Seq. No. 268122

Contig ID 15177_1.R1011



```
5'-most EST
                  LIB3062-006-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  g2281103
BLAST score
                  268
E value
                   4.0e-23
                   94
Match length
                   49
% identity
                   (AC002333) Glucan endo-1,3-beta glucosidase isolog
NCBI Description
                   [Arabidopsis thaliana]
                   268123
Seq. No.
                   15177 2.R1011
Contig ID
5'-most EST
                   cyk700051632.f1
                   BLASTX
Method
                   g2281103
NCBI GI
BLAST score
                   260
E value
                   2.0e-22
Match length
                   76
% identity
                   57
                   (AC002333) Glucan endo-1,3-beta glucosidase isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   268124
                   15177 3.R1011
Contig ID
                   LIB3068-014-Q1-K1-D1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2281103
BLAST score
                   208
E value
                   2.0e-16
                   68
Match length
                   53
% identity
                  (AC002333) Glucan endo-1,3-beta glucosidase isolog
NCBI Description
                   [Arabidopsis thaliana]
                   268125
Seq. No.
                   15184 1.R1011
Contig ID
                   LIB3088-012-Q1-K1-G4
5'-most EST
                   268126
Seq. No.
                   15188 1.R1011
Contig ID
                   fC-zmle700446705b1
5'-most EST
                   268127
Seq. No.
                   15189 1.R1011
Contig ID
                   uC-zmflm017205f08b1
5'-most EST
                   BLASTX
Method
                   g4581203
NCBI GI
                   1133
BLAST score
                   1.0e-124
E value
Match length
                   283
                   74
% identity
                  (Y17912) cyclic nucleotide and calmodulin-regulated ion
NCBI Description
                   channel [Arabidopsis thaliana]
```

37302

268128

15190 1.R1011

afb700381041.h1

Seq. No.

Contig ID 5'-most EST



Contig ID 15195_1.R1011

5'-most EST LIB3088-012-Q1-K1-E2

Method BLASTX
NCBI GI g2119046
BLAST score 424
E value 2.0e-41
Match length 141
% identity 65

NCBI Description small nuclear ribonucleoprotein U1A - Arabidopsis thaliana

>gi_1050430_emb_CAA90283_ (Z49991) UlsnRNP-specific protein

[Arabidopsis thaliana] >gi_2529669 (AC002535)

UlsnRNP-specific protein, $\overline{\text{U}}$ 1A [Arabidopsis thaliana]

Seq. No. 268130

Contig ID 15197_1.R1011 5'-most EST qmh700028551.f1

Method BLASTX
NCBI GI g1168940
BLAST score 930
E value 1.0e-100
Match length 277

Match length 277 % identity 66

NCBI Description CHORISMATE MUTASE PRECURSOR (CM-1) >gi_629509_pir__S38958

chorismate mutase precursor - Arabidopsis thaliana >gi_429153_emb_CAA81286_ (Z26519) chorismate mutase

precursor [Arabidopsis thaliana]

Seq. No. 268131

Contig ID 15197_2.R1011 5'-most EST ypc700799129.h1

Method BLASTX
NCBI GI g1168940
BLAST score 252
E value 1.0e-21
Match length 88
% identity 59

NCBI Description CHORISMATE MUTASE PRECURSOR (CM-1) >gi 629509 pir__S38958

chorismate mutase precursor - Arabidopsis thaliana
>gi_429153_emb_CAA81286_ (Z26519) chorismate mutase

precursor [Arabidopsis thaliana]

Seq. No. 268132

Contig ID 15197_4.R1011

5'-most EST uC-zmflmo17331b01a1

Method BLASTX
NCBI GI g4512122
BLAST score 148
E value 2.0e-09
Match length 48
% identity 62

NCBI Description (AF131219) chorismate mutase 3 [Arabidopsis thaliana]

Seq. No. 268133

Contig ID 15197_5.R1011 5'-most EST clt700045669.f1



Method BLASTX
NCBI GI g1168940
BLAST score 182
E value 2.0e-13
Match length 57
% identity 65

NCBI Description CHORISMATE MUTASE PRECURSOR (CM-1) >gi_629509_pir__S38958

chorismate mutase precursor - Arabidopsis thaliana >gi_429153_emb_CAA81286_ (Z26519) chorismate mutase

precursor [Arabidopsis thaliana]

Seq. No. 268134

Contig ID 15198_1.R1011 5'-most EST wyr700242603.h1

Method BLASTX
NCBI GI g1362151
BLAST score 1096
E value 1.0e-120
Match length 216
% identity 94

NCBI Description mitogen-activated protein kinase 1 homolog (clone Aspk9) -

oat >gi 871984 emb CAA56314 (X79993) MAP KINASE [Avena

sativa]

Seq. No. 268135

Contig ID 15203_1.R1011

5'-most EST LIB3088-012-Q1-K1-B6

Method BLASTX
NCBI GI g2642153
BLAST score 320
E value 3.0e-29
Match length 118
% identity 52

NCBI Description (AC003000) unknown protein [Arabidopsis thaliana]

>gi 2795810 (AC003674) unknown protein [Arabidopsis

thaliana]

Seq. No. 268136

Contig ID 15204_1.R1011 5'-most EST tzu700206824.h1

Method BLASTX
NCBI GI g4512676
BLAST score 263
E value 2.0e-22
Match length 125
% identity 42

NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]

Seq. No. 268137

Contig ID 15208 1.R1011

5'-most EST uC-zmflmo17307e06b1

Method BLASTX
NCBI GI g3953471
BLAST score 433
E value 2.0e-67
Match length 271
% identity 56



```
(AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
                  268138
Seq. No.
                  15208 2.R1011
Contig ID
                  uC-zmroteosinte034e11b1
5'-most EST
                  BLASTX
Method
                  a600872
NCBI GI
BLAST score
                  1397
                  1.0e-155
E value
                  324
Match length
                  94
% identity
                  (U17897) starch branching enzyme I [Zea mays] >gi_3309178
NCBI Description
                   (AF072724) starch branching enzyme I [Zea mays]
                  268139
Seq. No.
                  15208 3.R1011
Contig ID
                  fwa700097830.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q600872
                   1337
BLAST score
                   1.0e-148
E value
                   250
Match length
                   98
% identity
                  (U17897) starch branching enzyme I [Zea mays] >gi_3309178
NCBI Description
                   (AF072724) starch branching enzyme I [Zea mays]
                   268140
Seq. No.
                   15212 1.R1011
Contig ID
5'-most EST
                   pmx700083403.h1
Seq. No.
                   268141
                   15213 1.R1011
Contig ID
                   vqh700053206.r1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1172556
BLAST score
                   673
                   2.0e-70
E value
Match length
                   275
                   49
% identity
                  36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
NCBI Description
                   (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                   (POM 36) >gi_629729_pir_S46925 porin II, 36K - potato
                   >gi_1076681_pir__B55364_porin (clone pPOM 36.2) - potato
                   mitochondrion >gi_515360_emb_CAA56600_ (X80387) 36kDA porin
                   II [Solanum tuberosum]
                   268142
Seq. No.
```

Contig ID 15213_4.R1011

5'-most EST uC-zmflmo17131c04a1

Method BLASTX
NCBI GI g1172555
BLAST score 168
E value 8.0e-12
Match length 48
% identity 67

NCBI Description 34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN

(VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)



(POM 34) >gi_629720_pir__S46936 34K porin - potato >gi_1076682_pir__A55364 porin (clone pPOM-34) - potato mitochondrion >gi_516166_emb_CAA56599_ (X80386) 34 kDA porin [Solanum tuberosum]

Seq. No. 268143 15217 1.R1011 Contig ID LIB3088-012-Q1-K1-A7 5'-most EST 268144 Seq. No. 15218 1.R1011 Contig ID LIB3088-011-Q1-K1-H2 5'-most EST BLASTX Method q4585871 NCBI GI 281 BLAST score 7.0e-25 E value Match length 76 % identity (AC005850) Unknown protein [Arabidopsis thaliana] NCBI Description 268145 Seq. No. 15220 1.R1011 Contig ID LIB3088-011-Q1-K1-E7 5'-most EST 268146 Seq. No. 15223 1.R1011 Contig ID cjh700194219.h1 5'-most EST BLASTX Method NCBI GI g2829910 BLAST score 251 5.0e-21 E value Match length 77 61 % identity (AC002291) Unknown protein, contains regulator of NCBI Description chromosome condensation motifs [Arabidopsis thaliana] 268147 Seq. No. 15225 1.R1011 Contig ID LIB3067-056-Q1-K1-E8 5'-most EST 268148 Seq. No. 15231 1.R1011 Contig ID wyr700239567.h1 5'-most EST BLASTX Method g2213610 NCBI GI 362 BLAST score 4.0e-34 E value Match length 142 50 % identity NCBI Description (AC000103) F21J9.4 [Arabidopsis thaliana] 268149 Seq. No. 15231 2.R1011 Contig ID LIB3088-009-Q1-K1-H4 5'-most EST

BLASTX

210

g2213610

Method

NCBI GI

BLAST score



```
2.0e-16
E value
Match length
                  88
                  48
% identity
                  (AC000103) F21J9.4 [Arabidopsis thaliana]
NCBI Description
                  268150
Seq. No.
                  15231 4.R1011
Contig ID
5'-most EST
                  LIB84-026-Q1-E1-D11
                  BLASTX
Method
                  g3095075
NCBI GI
                  191
BLAST score
                   2.0e-14
E value
                   62
Match length
                   61
% identity
                  (AF031471) pollen allergen [Juniperus oxycedrus]
NCBI Description
Seq. No.
                   268151
                   15231 5.R1011
Contig ID
5'-most EST
                   LIB3062-045-Q1-K1-D11
                   268152
Seq. No.
                   15231 6.R1011
Contig ID
                   LIB3068-057-Q1-K1-H12
5'-most EST
                   268153
Seq. No.
                   15236 1.R1011
Contig ID
                   LIB3150-032-Q1-N1-G6
5'-most EST
                   BLASTX
Method
                   q3776566
NCBI GI
BLAST score
                   437
                   3.0e-43
E value
                   127
Match length
                   74
% identity
                  (AC005388) Strong similarity to histone H2A gb_AJ006768
NCBI Description
                   from Cicer arietinum. [Arabidopsis thaliana]
                   268154
Seq. No.
                   15237 1.R1011
Contig ID
5'-most EST
                   LIB3088-011-Q1-K1-C4
                   268155
Seq. No.
                   15239 1.R1011
Contig ID
                   uC-zm\overline{f}1b73232f03b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2062167
BLAST score
                   269
                   2.0e-23
E value
                   69
Match length
                   75
% identity
                   (AC001645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No. 268156

Contig ID 15243_1.R1011 5'-most EST uC-zmflb73015g08b1

Method BLASTX NCBI GI g4586250



```
BLAST score
                  457
                  2.0e-45
E value
Match length
                  193
% identity
                  49
                  (AL049640) adenine DNA glycosylase like protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  268157
Contig ID
                  15246 1.R1011
5'-most EST
                  gct701177004.h1
Method
                  BLASTX
NCBI GI
                  g2342724
BLAST score
                  365
E value
                  3.0e - 34
Match length
                  164
                  51
% identity
NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]
Seq. No.
                  268158
Contig ID
                  15247 1.R1011
5'-most EST
                  LIB3151-022-Q1-K1-F7
Seq. No.
                  268159
Contig ID
                  15249 1.R1011
5'-most EST
                  fdz701160510.h1
Method
                  BLASTX
NCBI GI
                  g1653516
BLAST score
                  218
E value
                   3.0e-17
Match length
                  79
% identity
                  52
NCBI Description (D90914) hypothetical protein [Synechocystis sp.]
Seq. No.
                  268160
                  15251 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73345d11a2
Method
                  BLASTX
NCBI GI
                  g585960
BLAST score
                  161
                  1.0e-10
E value
Match length
                  40
                  80
% identity
NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT
                   >gi 433665 emb CAA81412 (Z26753) Sec61 beta-subunit
                  homolog [Arabidopsis thaliana]
Seq. No.
                   268161
Contig ID
                  15251_2.R1011
5'-most EST
                  LIB3088-010-Q1-K1-H5
Method
                  BLASTX
                  g585960
NCBI GI
BLAST score
                  156
```

Method BLASTX
NCBI GI g585960
BLAST score 156
E value 4.0e-10
Match length 40
% identity 78

NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT

>gi_433665_emb_CAA81412_ (Z26753) Sec61 beta-subunit



homolog [Arabidopsis thaliana]

```
Seq. No.
                    268162
                    15251 4.R1011
Contig ID
                    cyk700048359.fl
5'-most EST
Seq. No.
                    268163
                    15254 1.R1011
Contig ID
                    uC-zm\overline{f}lb73130e01b2
5'-most EST
                    BLASTX
Method
                    q1352460
NCBI GI
BLAST score
                    460
                    2.0e-45
E value
                    96
Match length
                    94
% identity
                    IN2-1 PROTEIN >gi 100896 pir S17743 In2-1 protein - maize
NCBI Description
                    >gi_22347_emb_CAA\overline{4}1447_{\overline{(X58573)}} In2-1 [Zea mays]
                    268164
Seq. No.
                    15254 2.R1011
Contig ID
                    xsy700209610.hl
5'-most EST
                    BLASTX
Method
NCBI GI
                    g4218011
BLAST score
                    1355
                    1.0e-150
E value
Match length
                    364
                    70
% identity
                    (AC006135) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                    >gi 4309721_gb_AAD15491_ (AC006439) putative
                    serine/threonine protein kinase [Arabidopsis thaliana]
                     268165
Seq. No.
                     15254 3.R1011
Contig ID
                    uC-zm\overline{f}1b73185d12a1
5'-most EST
                    BLASTX
Method
                    g4218011
NCBI GI
                     292
BLAST score
                     3.0e-26
E value
Match length
                     65
                     85
% identity
                    (AC006135) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                    >gi_4309721_gb_AAD15491_ (AC006439) putative
serine/threonine protein kinase [Arabidopsis thaliana]
                     268166
Seq. No.
                     15254 4.R1011
Contig ID
                     tzu700206346.h1
5'-most EST
                     BLASTX
Method
                     q1352460
NCBI GI
BLAST score
                     983
                     1.0e-107
E value
Match length
                     194
                     98
% identity
                    IN2-1 PROTEIN >gi_100896_pir__S17743 In2-1 protein - maize
NCBI Description
                     >gi_22347_emb_CAA\overline{4}1447_{\overline{1}}(X58\overline{57}3) In2-1 [Zea mays]
```

268167 Seq. No.



Contig ID 15254_5.R1011 5'-most EST uC-zmflb73185d12b1

Method BLASTN
NCBI GI g22346
BLAST score 46
E value 2.0e-16
Match length 46
% identity 100

NCBI Description Maize In2-1 mRNA

Seq. No. 268168

Contig ID 15254 6.R1011 5'-most EST pmx700091219.h1

Seq. No. 268169

Contig ID 15254_7.R1011 5'-most EST uC-zmflb73130e01a1

Method BLASTN
NCBI GI g22346
BLAST score 200
E value 1.0e-108
Match length 264
% identity 94

NCBI Description Maize In2-1 mRNA

Seq. No. 268170

Contig ID 15258_1.R1011 5'-most EST zuv700356693.h1

Method BLASTX
NCBI GI g2706455
BLAST score 318
E value 1.0e-39
Match length 197
% identity 44

NCBI Description (AL021046) probable involvement in transcription initiation

[Schizosaccharomyces pombe]

Seq. No. 268171

Contig ID 15260_1.R1011 5'-most EST xsy700211006.h1

Seq. No. 268172

Contig ID 15260 2.R1011

5'-most EST LIB3088-011-Q1-K1-B2

Seq. No. 268173

Contig ID 15271 1.R1011 5'-most EST ntr700073256.h1

Seq. No. 268174

Contig ID 15278 1.R1011

5'-most EST LIB3088-009-Q1-K1-H3

Seq. No. 268175

Contig ID 15279 1.R1011

5'-most EST LIB3088-010-Q1-K1-A1



Seq. No. 268176

Contig ID 15285_1.R1011

5'-most EST uC-zmflmo17235a06b1

Method BLASTX
NCBI GI g3421109
BLAST score 938
E value 1.0e-101
Match length 204
% identity 87

NCBI Description (AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis

thaliana]

Seq. No. 268177

Contig ID 15285_2.R1011 5'-most EST hvj700622027.h1

Method BLASTX
NCBI GI g2982322
BLAST score 637
E value 1.0e-66
Match length 134
% identity 90

NCBI Description (AF051246) probable proteasome subunit [Picea mariana]

Seq. No. 268178

Contig ID 15292_1.R1011 5'-most EST uC-zmrob73049c11a1

Seq. No. 268179

Contig ID 15293_1.R1011 5'-most EST uwc700155960.h1

Method BLASTX
NCBI GI g2852449
BLAST score 1419
E value 1.0e-157
Match length 376
% identity 73

NCBI Description (D88207) protein kinase [Arabidopsis thaliana] >gi_2947061 (AC002521) putative protein kinase [Arabidopsis thaliana]

Seq. No. 268180

Contig ID 15293_2.R1011 5'-most EST wty700169861.h1

Method BLASTX
NCBI GI g2852449
BLAST score 412
E value 2.0e-48
Match length 110
% identity 88

NCBI Description (D88207) protein kinase [Arabidopsis thaliana] >gi_2947061 (AC002521) putative protein kinase [Arabidopsis thaliana]

Seq. No. 268181

Contig ID 15293_4.R1011

5'-most EST LIB3088-009-Q1-K1-G7

Method BLASTX NCBI GI g2852449 BLAST score 460



E value 2.0e-49
Match length 132
% identity 75

NCBI Description (D88207) protein kinase [Arabidopsis thaliana] >gi_2947061 (AC002521) putative protein kinase [Arabidopsis thaliana]

Seq. No. 268182

Contig ID 15293_5.R1011

5'-most EST uC-zmflmo17219c10b1

Seq. No. 268183

Contig ID 15295_1.R1011

5'-most EST LIB3088-009-Q1-K1-G3

Seq. No. 268184

Contig ID 15302_1.R1011 5'-most EST xjt700094011.h1

Method BLASTX
NCBI GI g3047124
BLAST score 325
E value 7.0e-30
Match length 130
% identity 47

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

Seq. No. 268185

Contig ID 15305 1.R1011

5'-most EST LIB3115-001-Q1-K1-H12

Seq. No. 268186

Contig ID 15309_1.R1011 5'-most EST xjt700096267.h1

Method BLASTX
NCBI GI g3292830
BLAST score 761
E value 2.0e-80
Match length 574
% identity 39

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 268187

Contig ID 15309_4.R1011

5'-most EST uC-zmflmo17108b04b1

Method BLASTX
NCBI GI g4539465
BLAST score 341
E value 8.0e-32
Match length 190
% identity 45

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 268188

Contig ID 15310_1.R1011 5'-most EST clt700044985.f1

Method BLASTX NCBI GI g4510389 BLAST score 776



E value 1.0e-82 Match length 203 % identity 76

NCBI Description (AC007017) putative solute carrier protein [Arabidopsis

thaliana]

Seq. No. 268189

Contig ID 15312 1.R1011

5'-most EST LIB3115-005-Q1-K1-A11

Method BLASTN
NCBI GI g1159878
BLAST score 73
E value 1.0e-32

Match length 121 % identity 90

NCBI Description A.fatua mRNA for DNA-binding protein (clone ABF2)

Seq. No. 268190

Contig ID 15312 2.R1011 5'-most EST hbs701184617.h1

Seq. No. 268191

Contig ID 15317_1.R1011 5'-most EST wyr700238777.h1

Seq. No. 268192

Contig ID 15317_2.R1011 5'-most EST rvt700550673.h1

Method BLASTX
NCBI GI g2224911
BLAST score 806
E value 5.0e-86
Match length 191
% identity 81

NCBI Description (U93048) somatic embryogenesis receptor-like kinase [Daucus

carota]

Seq. No. 268193

Contig ID 15317_4.R1011

5'-most EST LIB3088-008-Q1-K1-F4

Seq. No. 268194

Contig ID 15317_5.R1011 5'-most EST uC-zmflb73135g02b2

Method BLASTX
NCBI GI 94490310
BLAST score 1307
E value 1.0e-144
Match length 273
% identity 91

NCBI Description (AL035678) somatic embryogenesis receptor-like kinase-like

protein [Arabidopsis thaliana]



Seq. No. 268196

Contig ID 15320 2.R1011

5'-most EST LIB3088-008-Q1-K1-G4

Seq. No. 268197

Contig ID 15331 1.R1011 5'-most EST nbm700477588.h1

Method BLASTX
NCBI GI g135861
BLAST score 156
E value 5.0e-10
Match length 186
% identity 29

NCBI Description INTERFERON-RELATED PROTEIN PC4 (TPA INDUCED SEQUENCE 7)

(TIS7 PROTEIN) >gi_321269_pir__A44989 interferon-related protein TIS7 - mouse >gi_54806 emb CAA35258 (X17400) TIS7

protein (AA 1-449) [Mus sp.]

Seq. No. 268198

Contig ID 15331_3.R1011 5'-most EST rvt700550671.h1

Seq. No. 268199

Contig ID 15334 1.R1011

5'-most EST uC-zmflmo17249c12a1

Seq. No. 268200

Contig ID 15337_1.R1011 5'-most EST qmh700029653.f1

Method BLASTX
NCBI GI g1345881
BLAST score 617
E value 4.0e-64
Match length 130
% identity 88

NCBI Description CYTOCHROME B5 >gi 1076743 pir S46307 cytochrome b5 - rice

>gi_414705_emb_CAA53366_ (X75670) cytochrome b5 [Oryza

sativa]

Seq. No. 268201

Contig ID 15343 1.R1011

5'-most EST LIB3088-008-Q1-K1-C3

Method BLASTX
NCBI GI g3738325
BLAST score 367
E value 6.0e-35
Match length 111
% identity 69

NCBI Description (AC005170) putative CaMB-channel protein [Arabidopsis

thaliana]

Seq. No. 268202

Contig ID 15344_1.R1011 5'-most EST ypc700799467.h1

Method BLASTX NCBI GI g2654868 BLAST score 1119



E value 1.0e-123 Match length 338 % identity 62

NCBI Description (AF015301) RbohAp108 [Arabidopsis thaliana]

Seq. No. 268203

Contig ID 15346_1.R1011 5'-most EST uC-zmroB73013g08b1

Seq. No. 268204

Contig ID 15347_1.R1011 5'-most EST xjt700096235.h1

Method BLASTX
NCBI GI g1915960
BLAST score 653
E value 4.0e-68
Match length 190
% identity 64

NCBI Description (Y07636) peptidylprolyl isomerase [Triticum aestivum]

Seq. No. 268205

Contig ID 15353 1.R1011

5'-most EST LIB3088-008-Q1-K1-A5

Seq. No. 268206

Contig ID 15358_1.R1011 5'-most EST ceu700421668.h1

Seq. No. 268207

Contig ID 15360_3.R1011 5'-most EST xyt700344345.h1

Method BLASTX
NCBI GI g3004565
BLAST score 201
E value 1.0e-15
Match length 63
% identity 60

NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 268208

Contig ID 15364 1.R1011

5'-most EST LIB3180-051-P2-M1-B10

Method BLASTX
NCBI GI g3687243
BLAST score 251
E value 2.0e-21
Match length 61
% identity 80

NCBI Description (AC005169) putative ribosomal protein [Arabidopsis

thaliana]

Seq. No. 268209

Contig ID 15364 2.R1011 5'-most EST cat700020616.r1

Seq. No. 268210

Contig ID 15366 1.R1011

```
5'-most EST
                   uC-zmroB73028h03b1
Seq. No.
                   268211
Contiq ID
                   15375 1.R1011
5'-most EST
                   cyk700051709.f1
Seq. No.
                   268212
Contig ID
                  15379 1.R1011
5'-most EST
                  rvt700552482.h1
Method
                  BLASTX
NCBI GI
                  g1084427
BLAST score
                  299
E value
                   1.0e-26
Match length
                   65
% identity
                  71
                  gip1 protein - garden petunia >gi_825524 emb_CAA60677_
NCBI Description
                   (X87225) gip1 [Petunia x hybrida]
Seq. No.
                   268213
Contiq ID
                   15380 1.R1011
5'-most EST
                  uC-zmromo17096e08a1
Seq. No.
                  268214
Contig ID
                  15382 1.R1011
5'-most EST
                  LIB148-002-Q1-E1-F11
Method
                  BLASTX
NCBI GI
                  q3894168
BLAST score
                  175
E value
                   4.0e-12
Match length
                  92
% identity
                   43
NCBI Description
                  (AC005312) similar to phloem-specific lectin [Arabidopsis
                  thaliana]
Seq. No.
                  268215
Contig ID
                  15385 1.R1011
5'-most EST
                  LIB3088-007-Q1-K1-G10
Seq. No.
                  268216
Contig ID
                  15386 1.R1011
5'-most EST
                  LIB3088-007-Q1-K1-G11
Seq. No.
                  268217
Contig ID
                  15387 1.R1011
5'-most EST
                  LIB3088-007-Q1-K1-G12
```

 Seq. No.
 268218

 Contig ID
 15391_1.R1011

 5'-most EST
 vux700156940.h1

 Method
 BLASTX

 NCBI GI
 g1665817

 BLAST score
 353

BLAST score 353 E value 4.0e-33 Match length 160 % identity 44

NCBI Description (D87466) Similar to S.cerevisiae hypothetical protein L3111

(S59316) [Homo sapiens]



```
268219
Seq. No.
Contig ID
                  15392 1.R1011
                  uC-zmflMo17010g07b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3075391
                  299
BLAST score
                  2.0e-26
E value
Match length
                  268
                   40
% identity
                  (AC004484) unknown protein [Arabidopsis thaliana]
NCBI Description
                  268220
Seq. No.
                  15392 2.R1011
Contig ID
                  uC-zmroteosinte037b10b1
5'-most EST
                  268221
Seq. No.
                  15397 1.R1011
Contig ID
                  wyr700243404.h1
5'-most EST
                   268222
Seq. No.
                   15397 2.R1011
Contig ID
5'-most EST
                  LIB3180-049-P2-M1-D1
                   268223
Seq. No.
                   15402 1.R1011
Contig ID
                   LIB3088-007-Q1-K1-C11
5'-most EST
Method
                   BLASTX
                   g1916290
NCBI GI
                   244
BLAST score
                   1.0e-20
E value
                   97
Match length
                   47
% identity
NCBI Description (U89876) ALY [Mus musculus]
                   268224
Seq. No.
                   15404 1.R1011
Contig ID
5'-most EST
                   LIB3137-035-Q1-K1-H7
                   268225
Seq. No.
                   15405 2.R1011
Contig ID
5'-most EST
                   uC-zmflmo17022h07b1
                   268226
Seq. No.
                   15416 1.R1011
Contig ID
5'-most EST
                   hvj700622616.h1
Method
                   BLASTX
NCBI GI
                   q1708464
```

Method BLASTX
NCBI GI g1708464
BLAST score 762
E value 1.0e-141
Match length 468
% identity 57

NCBI Description PUTATIVE DIHYDROXY-ACID DEHYDRATASE PRECURSOR (DAD)

(2,3-DIHYDROXY ACID HYDROLYASE) >gi_1213255_emb_CAA93689_

(Z69795) unknown [Schizosaccharomyces pombe]

Seq. No. 268227



Contig ID 15416_2.R1011 5'-most EST uC-zmflmo17056f08a1

Seq. No. 268228

Contig ID 15418_1.R1011 5'-most EST afb700381803.h1

Method BLASTX
NCBI GI g1084454
BLAST score 412
E value 1.0e-40
Match length 85
% identity 88

NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp1 - rice >gi_600765 (L29471) cyclophilin 1 [Oryza sativa]

Seq. No. 268229

Contig ID 15420 1.R1011

5'-most EST LIB3088-007-Q1-K1-B4

Method BLASTX
NCBI GI g2160182
BLAST score 158
E value 3.0e-10
Match length 53
% identity 53

NCBI Description (AC000132) ESTs gb_ATTS1236,gb_T43334,gb_N97019,gb_AA395203

come from this gene. [Arabidopsis thaliana]

Seq. No. 268230

Contig ID 15426 1.R1011

5'-most EST LIB3069-030-Q1-K1-B7

Method BLASTX
NCBI GI g3687245
BLAST score 159
E value 2.0e-10
Match length 32
% identity 81

NCBI Description (AC005169) putative ribosomal protein [Arabidopsis

thaliana]

Seq. No. 268231

Contig ID 15427 1.R1011

5'-most EST uC-zmroteosinte023d07b2

Method BLASTX
NCBI GI 94585988
BLAST score 1605
E value 1.0e-179
Match length 394
% identity 75

NCBI Description (AC005287) Similar to phosphoprotein phosphatase 2A

regulatory subunit [Arabidopsis thaliana]

Seq. No. 268232

Contig ID 15434_1.R1011

5'-most EST LIB3069-002-Q1-K1-A8

Method BLASTX
NCBI GI g3687223
BLAST score 351



E value 5.0e-33
Match length 169
% identity 51
NCBI Description (AC0051

NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No. 268233

Contig ID 15435_1.R1011 5'-most EST uC-zmflb73300h06b1

Method BLASTX
NCBI GI g2459412
BLAST score 642
E value 1.0e-66
Match length 381
% identity 39

NCBI Description (AC002332) putative G9a protein [Arabidopsis thaliana]

Seq. No. 268234

Contig ID 15438 1.R1011

5'-most EST LIB3150-057-Q1-N1-G2

Method BLASTX
NCBI GI 94262146
BLAST score 158
E value 2.0e-10
Match length 46
% identity 63

NCBI Description (AC005275) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 268235

Contig ID 15438_2.R1011 5'-most EST fdz701163805.h1

Method BLASTX
NCBI GI 94262146
BLAST score 149
E value 2.0e-09
Match length 46
% identity 59

NCBI Description (AC005275) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 268236

Contig ID 15438_3.R1011 5'-most EST uC-zmflb73172e03b2

Method BLASTX
NCBI GI 94262146
BLAST score 160
E value 7.0e-11
Match length 52
% identity 60

NCBI Description (AC005275) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 268237

Contig ID 15443 1.R1011

5'-most EST LIB30 $\overline{8}$ 8-006-Q1-K1-E9

Method BLASTX NCBI GI g2129553



BLAST score 267 E value 4.0e-23

Match length 67 % identity 72

NCBI Description calcium-dependent protein kinase 6 - Arabidopsis thaliana

Seq. No. 268238

Contig ID 15445_1.R1011

5'-most EST LIB30 $\overline{6}$ 9-025-Q1-K1-H6

Method BLASTX
NCBI GI g4204265
BLAST score 754
E value 7.0e-80
Match length 322
% identity 49

NCBI Description (AC005223) 45643 [Arabidopsis thaliana]

Seq. No. 268239

Contig ID 15445 3.R1011 5'-most EST ypc700803711.h1

Method BLASTX
NCBI GI g3152559
BLAST score 263
E value 7.0e-28
Match length 74
% identity 82

NCBI Description (AC002986) Similarity to A. thaliana gene product

F21M12.20, gb_AC000132. EST gb Z25651 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 268240

Contig ID 15446_1.R1011 5'-most EST kem700612028.h1

Seq. No. 268241

Contig ID 15447 1.R1011 5'-most EST cjh700195394.h1

Seq. No. 268242

Contig ID 15448 1.R1011

5'-most EST LIB3088-006-Q1-K1-F6

Seq. No. 268243

Contig ID 15449_1.R1011 5'-most EST uC-zmflb73123h02a1

Seq. No. 268244

Contig ID 15453_1.R1011

5'-most EST LIB3136-013-Q1-K1-F8

Seq. No. 268245

Contig ID 15464 1.R1011

5'-most EST LIB3158-017-Q1-K1-C4

Seq. No. 268246

Contig ID 15472 1.R1011

5'-most EST LIB3088-006-Q1-K1-B1



268247 Seq. No. 15478 1.R1011 Contig ID uC-zmflb73156a09b1 5'-most EST BLASTN Method q2564049 NCBI GI 43 BLAST score 2.0e-14 E value 217 Match length 85 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MLE2, complete sequence [Arabidopsis thaliana] 268248 Seq. No. 15480 1.R1011 Contig ID uC-zmflmo17108g03b1 5'-most EST BLASTX Method q1808694 NCBI GI BLAST score 834 2.0e-89 E value 171 Match length 93 % identity (Y10787) hypothetical protein [Sporobolus stapfianus] NCBI Description 268249 Seq. No. 15482 1.R1011 Contig ID uC-zmflmo17070f07b1 5'-most EST BLASTX Method q4204303 NCBI GI BLAST score 235 4.0e-19 E value 146 Match length % identity (AC003027) lcl_prt_seq No definition line found NCBI Description [Arabidopsis thaliana] 268250 Seq. No. 15482 2.R1011 Contig ID nbm700468853.h1 5'-most EST 268251 Seq. No. 15482 3.R1011 Contig ID ceu700434525.hl 5'-most EST 268252 Seq. No. 15484 1.R1011 Contig ID uC-zmroteosinte092f06b2 5'-most EST 268253 Seq. No. 15486 1.R1011 Contig ID $\mathtt{cat70}\overline{\mathtt{0}}\mathtt{021141.r1}$ 5'-most EST

Method BLASTX
NCBI GI g3786009
BLAST score 390
E value 1.0e-37
Match length 107

% identity

70



NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 268254

Contig ID 15489_1.R1011 5'-most EST fwa700101421.h1

Method BLASTX
NCBI GI g3322278
BLAST score 489
E value 2.0e-48
Match length 634
% identity 27

NCBI Description (AE001187) conserved hypothetical protein [Treponema

pallidum]

Seq. No. 268255

Contig ID 15492_1.R1011

5'-most EST LIB3088-005-Q1-K1-H5

Method BLASTX
NCBI GI g3551257
BLAST score 266
E value 3.0e-23
Match length 103
% identity 52

NCBI Description (AB012708) 98b [Daucus carota]

Seq. No. 268256

Contig ID 15493_1.R1011 5'-most EST LIB36-001-Q1-E1-F7

Method BLASTX
NCBI GI g2213600
BLAST score 354
E value 2.0e-33
Match length 147

% identity 47

NCBI Description (AC000348) T7N9.20 [Arabidopsis thaliana]

Seq. No. 268257

Contig ID 15495 1.R1011

5'-most EST LIB143-019-Q1-E1-H10

Method BLASTX
NCBI GI g2246376
BLAST score 418
E value 1.0e-40
Match length 158
% identity 65

NCBI Description (Z86093) b-Zip DNA binding protein [Arabidopsis thaliana]

Seq. No. 268258

Contig ID 15496_1.R1011

5'-most EST uC-zmflmo17293d11b1

Seq. No. 268259

Contig ID 15504 1.R1011

5'-most EST LIB189-003-Q1-E1-H3

Seq. No. 268260

Contig ID 15509_1.R1011



5'-most EST uC-zmflb73194c03b2 BLASTX Method NCBI GI q3560264 BLAST score 336 E value 7.0e-31 Match length 261 % identity 34 NCBI Description (AL031535) soll family protein [Schizosaccharomyces pombe] 268261 Seq. No. 15509 2.R1011 Contig ID uC-zmflmo17116e11b1 5'-most EST Seq. No. 268262 Contig ID 15510 1.R1011 5'-most EST $xjt70\overline{0}095320.h1$ Method BLASTX NCBI GI q1778147 BLAST score 1535 E value 1.0e-171 Match length 322 % identity 95 NCBI Description (U66403) phosphate/phosphoenolpyruvate translocator precursor [Zea mays] Seq. No. 268263 Contig ID 15510_2.R1011 5'-most EST uC-zmroteosinte075c08b1 Method BLASTX g1778147 NCBI GI BLAST score 316 5.0e-29 E value Match length 64 % identity 100 NCBI Description (U66403) phosphate/phosphoenolpyruvate translocator precursor [Zea mays] 268264 Seq. No. Contig ID 15517 1.R1011 5'-most EST uC-zmflb73151f06a2 268265 Seq. No. Contig ID 15520 1.R1011 5'-most EST LIB189-003-Q1-E1-A5 Method BLASTX NCBI GI q3024491 BLAST score 199 E value 6.0e-15 Match length 126 % identity 37 NCBI Description PEROXISOMAL FARNESYLATED PROTEIN >gi 627824 pir A54090 PxF

protein - Chinese hamster >gi 529146 (U05959) PxF

[Cricetulus griseus]

268266 Seq. No.

Contig ID 15520 2.R1011 5'-most EST pwr700448834.hl

E value

Match length

2.0e-31



```
BLASTX
Method
NCBI GI
                  q3461849
BLAST score
                  542
E value
                  3.0e-55
                  132
Match length
% identity
                  72
NCBI Description (AC005315) putative cytochrome P450 [Arabidopsis thaliana]
                  268267
Seq. No.
                  15520 3.R1011
Contig ID
5'-most EST
                  LIB3136-039-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  q4506339
                  196
BLAST score
                  9.0e-15
E value
Match length
                  116
                  38
% identity
NCBI Description peroxisomal farnesylated protein
                  >gi 729723 sp P40855 PXF HUMAN PEROXISOMAL FARNESYLATED
                  PROTEIN (33 KD HOUSEKEEPING PROTEIN)
                  >gi_551250_emb_CAA53225_ (X75535) house keeping gene 33
                  [Homo sapiens] >gi 2570023 emb CAA70257
                                                           (Y09048) PxF
                  protein [Homo sapiens] >gi 4521235 dbj BAA76291.1
                  (AB018541) PEX19 [Homo sapiens]
                  268268
Seq. No.
Contig ID
                  15522 1.R1011
5'-most EST
                  LIB189-016-Q1-E1-H2
Method
                  BLASTX
NCBI GI
                  q4263519
BLAST score
                  470
                  7.0e-47
E value
Match length
                  96
                  93
% identity
NCBI Description (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis
                  thaliana]
                  268269
Seq. No.
                  15522 2.R1011
Contig ID
5'-most EST
                  fdz701163481.hl
Method
                  BLASTX
                  g4263519
NCBI GI
BLAST score
                  145
E value
                  2.0e-09
Match length
                  32
% identity
NCBI Description (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis
                  thaliana]
                  268270
Seq. No.
Contig ID
                  15522 4.R1011
5'-most EST
                  LIB3067-006-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  q4263519
BLAST score
                  336
```



```
% identity
                   (ACO04044) small nuclear riboprotein Sm-D1 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   268271
                  15523 1.R1011
Contig ID
5'-most EST
                  uC-zmroteosinte075b12b1
Seq. No.
                   268272
                  15523 2.R1011
Contig ID
5'-most EST
                  uC-zmflmo17117d12a1
                  268273
Seq. No.
                  15526 1.R1011
Contig ID
5'-most EST
                  gct701176117.h1
                  268274
Seq. No.
Contig ID
                  15531 1.R1011
5'-most EST
                  pwr700449207.h1
Method
                  BLASTX
                  g4406814
NCBI GI
BLAST score
                   434
                   1.0e-42
E value
                  115
Match length
% identity
                  72
NCBI Description (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis
                  thaliana]
Seq. No.
                   268275
Contig ID
                   15536 1.R1011
5'-most EST
                  hvj700623615.h1
                   BLASTX
Method
NCBI GI
                   q4557647
                   150
BLAST score
                   2.0e-09
E value
                   64
Match length
% identity
                   44
NCBI Description heat shock factor binding protein 1 >gi_3283409 (AF068754)
                  heat shock factor binding protein 1 HSBP1 [Homo sapiens]
Seq. No.
                   268276
                   15537 1.R1011
Contig ID
                   cat700018470.rl
5'-most EST
                   268277
Seq. No.
                   15542 1.R1011
Contig ID
                   LIB3069-032-Q1-K1-B4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4490756
BLAST score
                   159
```

E value 3.0e-10 Match length 97 % identity

NCBI Description (AL035708) hypothetical protein [Arabidopsis thaliana]

268278 Seq. No.

Contiq ID 15543 1.R1011



```
uC-zmflmo17176g06b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2982293
                  287
BLAST score
                  2.0e-25
E value
                  65
Match length
                  85
% identity
                  (AF051231) ISP42-like protein [Picea mariana]
NCBI Description
                  268279
Seq. No.
                  15543 2.R1011
Contig ID
                  LIB3059-030-Q1-K1-H1
5'-most EST
                  BLASTX
Method
                  g2982293
NCBI GI
                  285
BLAST score
                  3.0e-25
E value
                  61
Match length
                  89
% identity
                  (AF051231) ISP42-like protein [Picea mariana]
NCBI Description
                  268280
Seq. No.
                  15545 1.R1011
Contig ID
                  LIB3088-004-Q1-K1-G8
5'-most EST
                  268281
Seq. No.
                  15545 2.R1011
Contig ID
                  uC-zmflb73351h12a1
5'-most EST
                   268282
Seq. No.
Contig ID
                   15562 1.R1011
                   uC-zmrob73060g06a1
5'-most EST
                   268283
Seq. No.
                   15571 1.R1011
Contig ID
5'-most EST
                   qmh700026440.fl
                   BLASTX
Method
                   q4510406
NCBI GI
BLAST score
                   536
                   3.0e-54
E value
Match length
                   325
                   39
% identity
NCBI Description (AC006587) putative protein kinase [Arabidopsis thaliana]
                   268284
Seq. No.
                   15571 2.R1011
Contig ID
                   LIB3069-006-Q1-K1-C6
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3135253
BLAST score
                   423
                   2.0e-41
E value
                   187
Match length
```

49 % identity

(AC003058) putative receptor protein kinase [Arabidopsis NCBI Description

thaliana]

268285 Seq. No.

15579 1.R1011 Contig ID

Method

NCBI GI

BLASTX

g549750



```
uC-zmflm017205b11b1
 5'-most EST
                    268286
 Seq. No.
                    15583 1.R1011
 Contig ID
                    uC-zm\overline{f}lmo17314d09a1
 5'-most EST
                    268287
 Seq. No.
                    15586 1.R1011
 Contig ID
 5'-most EST
                    wty700173037.hl
 Method
                    BLASTX
 NCBI GI
                    q3757522
 BLAST score
                    152
 E value
                    2.0e-09
                    102
 Match length
                    36
 % identity
 NCBI Description
                    (AC005167) putative splicing factor [Arabidopsis thaliana]
                    268288
 Seq. No.
 Contig ID
                    15589 1.R1011
 5'-most EST
                    LIB3115-025-P1-K1-B11
                    268289
 Seq. No.
 Contig ID
                    15590 1.R1011
 5'-most EST
                    uC-zm\overline{f}1b73239d01b2
- Method
                    BLASTX
 NCBI GI
                    q3426037
                    1375
 BLAST score
                    1.0e-152
 E value
 Match length
                    382
 % identity
                    65
 NCBI Description
                    (AC005168) putative ABC transporter protein [Arabidopsis
                    thaliana]
                    268290
 Seq. No.
 Contig ID
                    15591 1.R1011
 5'-most EST
                    cjh700196021.hl
                    268291
 Seq. No.
 Contig ID
                    15594 1.R1011
 5'-most EST
                    LIB3088-003-Q1-K1-E12
 Method
                    BLASTX
 NCBI GI
                    g1708107
 BLAST score
                    292
                    6.0e-31
 E value
                    90
 Match length
 % identity
                    87
 NCBI Description
                   HISTONE H2B >gi 473605 (U08226) histone H2B [Zea mays]
 Seq. No.
                    268292
                    15597 1.R1011
 Contig ID
 5'-most EST
                    LIB3088-003-Q1-K1-F11
                    268293
 Seq. No.
                    15601 1.R1011
 Contig ID
 5'-most EST
                    ymt700224031.h1
```



BLAST score 335 E value 8.0e-31 Match length 196 % identity 39

NCBI Description HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION >gi_539221_pir__S38045 hypothetical protein YKL207w - yeast

(Saccharomyces cerevisiae) >gi_486369_emb_CAA82052_(Z28207) ORF YKL207w [Saccharomyces cerevisiae]

Seq. No. 268294

Contig ID 15611 1.R1011 5'-most EST uC-zmflb73034a12b2

Seq. No. 268295

Contig ID 15611_2.R1011

5'-most EST LIB3088-003-Q1-K1-C9

Seq. No. 268296

Contig ID 15614 1.R1011

5'-most EST LIB3088-003-Q1-K1-D12

Seq. No. 268297

Contig ID 15615_1.R1011

5'-most EST LIB3088-003-Q1-K1-D9

Seq. No. 268298

Contig ID 15616 1.R1011

5'-most EST LIB3150-110-P2-K1-C1

Seq. No. 268299

Contig ID 15618_1.R1011 5'-most EST uC-zmflb73011a12b1

Method BLASTX

NCBI GI g2769566

BLAST score 358

E value 4.0e-38 Match length 112

Macchi Tengchi II2

% identity 70

NCBI Description (Y10477) chloroplast thylakoidal processing peptidase

[Arabidopsis thaliana]

Seq. No. 268300

Contig ID 15618_3.R1011 5'-most EST ceu700431581.h1

Method BLASTX
NCBI GI g1946373
BLAST score 462
E value 5.0e-46
Match length 120
% identity 72

NCBI Description (U93215) leader peptidase I isolog [Arabidopsis thaliana]

Seq. No. 268301

Contig ID 15622 1.R1011

5'-most EST LIB3088-003-Q1-K1-A1

Method BLASTX NCBI GI g115577



574 BLAST score 2.0e-59 E value 114 Match length % identity PHOSPHOENOLPYRUVATE CARBOXYLASE, HOUSEKEEPING ISOZYME NCBI Description (PEPCASE) >gi_348536_pir__S28614 phosphoenolpyruvate carboxylase (EC 4.1.1.31) - sugarcane hybrid H32-8560 >gi_169844 (M86661) phosphoenolpyruvate carboxylase [Saccharum sp.] 268302 Seq. No. 15628 1.R1011 Contig ID 5'-most EST uwc700152520.h1 268303 Seq. No. 15631 1.R1011 Contig ID wty700169969.h1 5'-most EST BLASTX Method g1575752 NCBI GI 339 BLAST score 3.0e-31 E value 258 Match length 31 % identity (U70672) glutathione S-transferase [Arabidopsis thaliana] NCBI Description 268304 Seq. No. 15631 2.R1011 Contig ID $dyk70\overline{0}105323.h1$ 5'-most EST BLASTX Method NCBI GI q1575752 212 BLAST score 6.0e-17 E value 108 Match length 44 % identity (U70672) glutathione S-transferase [Arabidopsis thaliana] NCBI Description 268305 Seq. No. 15635_1.R1011 Contig ID uC-zmflmo17065g10b1 5'-most EST Method BLASTX q4406372 NCBI GI 178 BLAST score 9.0e-13 E value 49 Match length 61 % identity (AF109156) thiosulfate sulfurtransferase [Datisca NCBI Description glomerata] 268306 Seq. No. 15635 2.R1011 Contig ID $uC-zm\overline{f}1b73027e02b1$ 5'-most EST BLASTX Method q4406372 NCBI GI

37329

1387

302

82

1.0e-154

BLAST score

Match length

% identity

E value



```
(AF109156) thiosulfate sulfurtransferase [Datisca
NCBI Description
                  glomerata]
                  268307
Seq. No.
Contig ID
                  15639 1.R1011
                  uC-zmflmo17306h04a1
5'-most EST
                  268308
Seq. No.
Contig ID
                  15643 1.R1011
                  hbs701185478.h1
5'-most EST
                  BLASTX
Method
                  q3582333
NCBI GI
BLAST score
                  358
                  8.0e-34
E value
                  195
Match length
% identity
                  (AC005496) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   268309
                   15651 1.R1011
Contig ID
                   uC-zmflb73124a12a1
5'-most EST
Seq. No.
                   268310
                   15653 1.R1011
Contig ID
                   fC-zmro700573093a1
5'-most EST
Method
                   BLASTX
                   q132909
NCBI GI
                   149
BLAST score
                   3.0e-09
E value
Match length
                   43
                   65
% identity
                   50S RIBOSOMAL PROTEIN L34 >gi_71360_pir__R6PS34 ribosomal
NCBI Description
                   protein L34 - Pseudomonas putīda >gī_45706_emb_CAA44414_
                   (X62540) homologous to E.coli rpmH [Pseudomonas putida]
                   268311
Seq. No.
                   15656 1.R1011
Contig ID
                   LIB3088-002-Q1-K1-F12
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2735839
BLAST score
                   227
                   1.0e-124
E value
                   524
Match length
                   91
% identity
                   Sorghum bicolor ADP-glucose pyrophosphorylase subunit SH2,
NCBI Description
                   transcriptional regulator, NADPH-dependent reductase A1-a
                   and NADPH-dependent reductase A1-b genes, complete cds
                   268312
Seq. No.
                   15659 1.R1011
Contig ID
```

 $uC-zm\overline{f}lMo17007e03b1$ 5'-most EST BLASTX

Method g4160354 NCBI GI BLAST score 269 4.0e-23 E value 180 Match length 36 % identity



```
NCBI Description (Z64354) unknown [Schizosaccharomyces pombe]
                  268313
Seq. No.
                  15661 1.R1011
Contig ID
                  bdu700382069.h1
5'-most EST
                  268314
Seq. No.
                  15668 1.R1011
Contig ID
                  gct701168213.h1
5'-most EST
                  BLASTX
Method
                  q4454464
NCBI GI
                  330
BLAST score
                  1.0e-30
E value
                  82
Match length
                  71
% identity
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   268315
Seq. No.
                   15669 1.R1011
Contig ID
                  LIB3088-002-Q1-K1-D1
5'-most EST
Seq. No.
                   268316
                   15670 1.R1011
Contig ID
                   LIB3088-002-Q1-K1-D11
5'-most EST
                   BLASTX
Method
                   q4538935
NCBI GI
                   185
BLAST score
                   2.0e-13
E value
                   48
Match length
                   65
% identity
                  (AL049483) putative protein [Arabidopsis thaliana]
NCBI Description
                   268317
Seq. No.
                   15703 1.R1011
Contig ID
5'-most EST
                   uC-zmroteosinte058e08b2
Method
                   BLASTX
                   g3193292
NCBI GI
                   468
BLAST score
                   2.0e-46
E value
                   137
Match length
                   67
% identity
                   (AF069298) similar to ATPases associated with various
NCBI Description
                   cellular activites (Pfam: AAA.hmm, score: 230.91)
                   [Arabidopsis thaliana]
                   268318
Seq. No.
                   15703 2.R1011
Contig ID
                   LIB3088-001-Q1-K1-H4
 5'-most EST
                   BLASTX
Method
                   g3193292
NCBI GI
 BLAST score
                   608
                   3.0e-63
 E value
 Match length
                   159
                   74
 % identity
                   (AF069298) similar to ATPases associated with various
 NCBI Description
                    cellular activites (Pfam: AAA.hmm, score: 230.91)
```

[Arabidopsis thaliana]



Seq. No. 268319

Contig ID 15705_1.R1011 5'-most EST uC-zmflb73206e06b1

Method BLASTX
NCBI GI g3281853
BLAST score 811
E value 2.0e-86
Match length 264
% identity 61

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 268320

Contig ID 15705_2.R1011 5'-most EST uwc700153872.h1

Seq. No. 268321

Contig ID 15705 3.R1011

5'-most EST LIB3180-036-P2-M2-E5

Seq. No. 268322

Contig ID 15705_4.R1011 5'-most EST uC-zmflb73116b05b2

Method BLASTX
NCBI GI g3281853
BLAST score 246
E value 2.0e-29
Match length 115
% identity 57

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 268323

Contig ID 15706_1.R1011 5'-most EST fdz701164935.h1

Method BLASTX
NCBI GI g3860321
BLAST score 1469
E value 1.0e-171
Match length 413

% identity 71

NCBI Description (AJ012687) beta-galactosidase [Cicer arietinum]

Seq. No. 268324

Contig ID 15706_2.R1011 5'-most EST hbs701181044.h1

Method BLASTX
NCBI GI g4006924
BLAST score 1332
E value 1.0e-147
Match length 372
% identity 63

NCBI Description (Z99708) beta-galactosidase like protein [Arabidopsis

thaliana]

Seq. No. 268325

Contig ID 15706 4.R1011

5'-most EST LIB3059-007-Q1-K1-F1

BLAST score

Match length

E value

8.0e-55

154



Method BLASTX NCBI GI g4006924 BLAST score 331 1.0e-30 E value Match length 94 % identity (Z99708) beta-galactosidase like protein [Arabidopsis NCBI Description thaliana] 268326 Seq. No. 15707 1.R1011 Contig ID uC-zmflMo17091f04b1 5'-most EST Method BLASTX g2129636 NCBI GI 779 BLAST score 1.0e-82 E value Match length 338 46 % identity lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase NCBI Description [Arabidopsis thaliana] Seq. No. 268327 15709 1.R1011 Contig ID 5'-most EST LIB189-012-Q1-E1-A5 BLASTX Method g4160579 NCBI GI BLAST score 198 7.0e-15 E value Match length 114 % identity 35 (AL035218) hypothetical protein [Schizosaccharomyces pombe] NCBI Description 268328 Seq. No. 15712 1.R1011 Contig ID $uC\text{-}zm\overline{\texttt{f}}\texttt{1}b73083\texttt{f}05b2$ 5'-most EST BLASTX Method g1709007 NCBI GI BLAST score 175 5.0e-12 E value 165 Match length 36 % identity O-SUCCINYLHOMOSERINE SULFHYDRYLASE (OSH SULFHYDRYLASE) NCBI Description >qi 607830 (U10904) O-succinylhomoserine sulfhydrylase [Pseudomonas aeruginosa] 268329 Seq. No. 15714 1.R1011 Contig ID 5'-most EST LIB3088-001-Q1-K1-F2 268330 Seq. No. 15717 1.R1011 Contig ID ypc700803940.hl 5'-most EST Method BLASTX g2660677 NCBI GI 538

% identity



```
% identity
NCBI Description
                  (AC002342) unknown protein [Arabidopsis thaliana]
                  268331
Seq. No.
                  15719 1.R1011
Contig ID
                  LIB3059-059-Q1-K1-H3
5'-most EST
Method
                  BLASTX
NCBI GI
                  g123178
                  897
BLAST score
E value
                  8.0e-97
Match length
                  218
% identity
                  HISTIDINOL DEHYDROGENASE, CHLOROPLAST PRECURSOR (HDH)
NCBI Description
                  >gi_99844_pir__A39358 histidinol dehydrogenase (EC
                  1.1.1.23) precursor, chloroplast - cabbage >gi_167142
                  (M60466) histidinol dehydrogenase [Brassica oleracea]
                  268332
Seq. No.
                  15737 1.R1011
Contig ID
5'-most EST
                  LIB3088-001-Q1-K1-A9
                  268333
Seq. No.
                  15742 1.R1011
Contig ID
5'-most EST
                  qw1700613171.h1
Method
                  BLASTX
NCBI GI
                  q2129622
BLAST score
                  590
E value
                  6.0e-61
Match length
                  128
% identity
                  85
NCBI Description immunophilin FKBP15-1 - Arabidopsis thaliana >gi 1272406
                  (U52046) immunophilin [Arabidopsis thaliana]
                  268334
Seq. No.
Contig ID
                  15744_1.R1011
5'-most EST
                  LIB3150-045-Q1-N1-E3
Method
                  BLASTX
NCBI GI
                  q2988398
BLAST score
                  183
E value
                  3.0e-13
Match length
                  116
% identity
                  36
NCBI Description (AC004381) Unknown gene product [Homo sapiens]
Seq. No.
                  268335
                  15744 2.R1011
Contig ID
5'-most EST
                  LIB3069-047-Q1-K1-H7
Seq. No.
                  268336
Contig ID
                  15745 1.R1011
5'-most EST
                  uC-zmflmo17344g01b1
Method
                  BLASTX
NCBI GI
                  g2462759
BLAST score
                  214
                  3.0e-17
E value
Match length
                  55
```



(AC002292) Putative Cytochrome B5 [Arabidopsis thaliana] NCBI Description 268337 Seq. No. 15745 3.R1011 Contig ID ypc700801551.hl 5'-most EST BLASTX Method q2462759 NCBI GI BLAST score 312 3.0e-28 E value 92 Match length 61 % identity (AC002292) Putative Cytochrome B5 [Arabidopsis thaliana] NCBI Description 268338 Seq. No. 15746 1.R1011 Contig ID LIB3088-001-Q1-K1-C10 5'-most EST Method BLASTN q3821780 NCBI GI BLAST score 36 1.0e-10 E value 36 Match length 100 % identity Xenopus laevis cDNA clone 27A6-1 NCBI Description 268339 Seq. No. 15749 1.R1011 Contig ID LIB3136-059-Q1-K1-H2 5'-most EST BLASTX Method NCBI GI g2465151 217 BLAST score 4.0e-17 E value 124 Match length 43 % identity (Z99753) hypothetical protein [Schizosaccharomyces pombe] NCBI Description 268340 Seq. No. 15749 2.R1011 Contig ID $pmx70\overline{0}085160.h1$ 5'-most EST BLASTX Method g2407068 NCBI GI 207 BLAST score 3.0e-16 E value Match length 130 37 % identity (AF014955) TFAR19 [Homo sapiens] NCBI Description 268341 Seq. No. 15762 1.R1011 Contig ID qmh700029010.fl 5'-most EST

Seq. No. 268342 Contig ID 15766_1.R1011

5'-most EST LIB3062-023-Q1-K1-B9

Method BLASTX
NCBI GI g3135265
BLAST score 317
E value 6.0e-29



Match length 103 % identity 60

NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]

Seq. No. 268343

Contig ID 15767_1.R1011

5'-most EST LIB3088-001-Q1-K1-F6

Seq. No. 268344

Contig ID 15770_1.R1011 5'-most EST uC-zmflb73010d09a1

Seq. No. 268345

Contig ID 15778_1.R1011 5'-most EST uC-zmflb73233b04b1

Method BLASTX
NCBI GI g1703151
BLAST score 230
E value 2.0e-18
Match length 204
% identity 31

NCBI Description ACTIN >gi_2119319_pir__JC4612 actin - Chlamydomonas

reinhardtii >gi_915194_dbj_BAA09450_ (D50839) actin [Chlamydomonas reinhardtii] >gi_1526415_dbj_BAA09449_

(D50838) actin [Chlamydomonas reinhardtii]

Seq. No. 268346

Contig ID 15779_1.R1011

5'-most EST LIB3180-020-P2-M1-A6

Method BLASTX
NCBI GI 94263776
BLAST score 253
E value 2.0e-21
Match length 68
% identity 69

NCBI Description (AC006068) unknown protein [Arabidopsis thaliana]

>gi_4510390_gb_AAD21478.1_ (AC007017) unknown protein

[Arabidopsis thaliana]

Seq. No. 268347

Contig ID 15780_1.R1011

5'-most EST LIB3066-052-Q1-K1-A11

Seq. No. 268348

Contig ID 15780_2.R1011

5'-most EST uC-zmflb73369h11a1

Seq. No. 268349

Contig ID 15789_1.R1011

5'-most EST uC-zmflb73240a04a2

Seq. No. 268350

Contig ID 15799_1.R1011 5'-most EST ntr700074620.h1

Seq. No. 268351

Contig ID 15811_1.R1011



LIB3088-004-Q1-K1-E10 5'-most EST BLASTX Method NCBI GI q1708107 252 BLAST score 5.0e-31 E value 98 Match length 81 % identity HISTONE H2B >gi 473605 (U08226) histone H2B [Zea mays] NCBI Description 268352 Seq. No. 15815 1.R1011 Contig ID LIB3088-004-Q1-K1-E9 5'-most EST BLASTX Method NCBI GI g4314378 367 BLAST score 1.0e-34 E value 156 Match length 46 % identity (AC006232) putative lipase [Arabidopsis thaliana] NCBI Description 268353 Seq. No. 15818 1.R1011 Contig ID LIB3180-062-P2-M1-F10 5'-most EST BLASTX Method g4371296 NCBI GI 1054 BLAST score 1.0e-115 E value 341 Match length 64 % identity (AC006260) putative receptor protein kinase [Arabidopsis NCBI Description thaliana] 268354 Seq. No. 15827 1.R1011 Contig ID 5'-most EST wuj700282130.hl BLASTX Method q445613 NCBI GI BLAST score 360 6.0e-34 E value Match length 156 47 % identity NCBI Description ribosomal protein L7 [Solanum tuberosum] 268355 Seq. No. Contig ID 15833 1.R1011 5'-most EST ymt700220255.h1 BLASTX Method

Method BLASTX
NCBI GI g2809385
BLAST score 170
E value 5.0e-12
Match length 37
% identity 86

NCBI Description (AF024634) NADPH cytochrome P450 reductase [Petroselinum

crispum]

Seq. No. 268356

Contig ID 15838_1.R1011

E value

Match length



```
5'-most EST
                  uC-zmflmo17241a02a1
                  268357
Seq. No.
                  15841 1.R1011
Contig ID
                  LIB3088-005-Q1-K1-D11
5'-most EST
                  268358
Seq. No.
Contig ID
                  15846 1.R1011
5'-most EST
                  uC-zmflmo17340b06b1
                  268359
Seq. No.
                  15846 2.R1011
Contig ID
5'-most EST
                  LIB143-021-Q1-E1-D6
                  BLASTX
Method
                  q3249105
NCBI GI
BLAST score
                  159
E value
                   3.0e-10
                  131
Match length
% identity
                   31
                   (AC003114) Contains similarity to protein phosphatase 2C
NCBI Description
                   (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]
                   268360
Seq. No.
Contig ID
                   15848 1.R1011
                  LIB3059-005-Q1-K1-H4
5'-most EST
                   268361
Seq. No.
                   15851 1.R1011
Contig ID
5'-most EST
                   ceu700422255.h1
Method
                   BLASTX
NCBI GI
                   g1652452
BLAST score
                   203
                   1.0e-15
E value
Match length
                   103
% identity
                   40
                  (D90905) hypothetical protein [Synechocystis sp.]
NCBI Description
                   268362
Seq. No.
Contig ID
                   15853 1.R1011
                   LIB3069-051-Q1-K1-D3
5'-most EST
Method
                   BLASTX
                   g4191789
NCBI GI
                   845
BLAST score
                   1.0e-173
E value
                   427
Match length
                   77
% identity
                   (AC005917) putative transmembrane transport protein
NCBI Description
                   [Arabidopsis thaliana]
                   268363
Seq. No.
                   15853 3.R1011
Contig ID
                   pmx700091781.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4191789
BLAST score
                   422
                   1.0e-41
```



% identity 80

NCBI Description (AC005917) putative transmembrane transport protein

[Arabidopsis thaliana]

Seq. No. 268364

Contig ID 15854_1.R1011

5'-most EST LIB3088-006-Q1-K1-D7

Seq. No. 268365

Contig ID 15856_1.R1011

5'-most EST LIB3279-050-P1-K1-B10

Method BLASTN
NCBI GI g2645165
BLAST score 65
E value 6.0e-28

E value 6.0 Match length 85 % identity 94

NCBI Description Oryza sativa mRNA, similar to ribosomal protein

Seq. No. 268366

Contig ID 15859_1.R1011

5'-most EST LIB3066-034-Q1-K1-F1

Method BLASTX
NCBI GI g3122234
BLAST score 1082
E value 1.0e-118
Match length 267
% identity 80

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT

(EIF-2-BETA) (P38) >gi_2306768 (U87163) eIF-2 beta subunit

[Triticum aestivum]

Seq. No. 268367

Contig ID 15859 2.R1011 5'-most EST xmt700262104.h1

Method BLASTX
NCBI GI g3122234
BLAST score 379
E value 2.0e-36
Match length 132
% identity 61

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT

(EIF-2-BETA) (P38) >gi 2306768 (U87163) eIF-2 beta subunit

[Triticum aestivum]

Seq. No. 268368

Contig ID 15859_3.R1011

5'-most EST uC-zmroteosinte019e10b1

Method BLASTX
NCBI GI g3122234
BLAST score 575
E value 3.0e-59
Match length 111
% identity 99

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT

(EIF-2-BETA) (P38) >gi_2306768 (U87163) eIF-2 beta subunit

[Triticum aestivum]

NCBI GI

BLAST score

g3821794 38



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268369
Seq. No.
                  15860 1.R1011
Contig ID
                  LIB3062-014-Q1-K1-F2
5'-most EST
                  268370
Seq. No.
                  15862 1.R1011
Contig ID
                  LIB83-004-Q1-E1-G9
5'-most EST
                  BLASTX
Method
                  q2244806
NCBI GI
                  322
BLAST score
                  3.0e-29
E value
                  228
Match length
                   38
% identity
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
                   268371
Seq. No.
                   15862 2.R1011
Contig ID
                   LIB189-023-Q1-E1-G3
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2244806
                   309
BLAST score
                   8.0e-28
E value
                   144
Match length
                   48
% identity
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
                   268372
Seq. No.
                   15866 1.R1011
Contig ID
                   LIB3060-043-Q1-K1-D8
5'-most EST
                   268373
Seq. No.
                   15870 1.R1011
Contig ID
                   uC-zmflmo17267c03a1
5'-most EST
                   268374
Seq. No.
                   15870 2.R1011
Contig ID
5'-most EST
                   uC-zmflmo17078a11b1
                   BLASTN
Method
                   g1518674
NCBI GI
                   44
BLAST score
                   4.0e-15
E value
                   119
Match length
% identity
                  Zea mays beta-D-glucosidase (glu1) gene, intron 10
NCBI Description
                   transposon 2, complete sequence
                   268375
Seq. No.
                   15879 1.R1011
Contig ID
                   wty700162619.hl
5'-most EST
 Seq. No.
                   268376
                   15886 1.R1011
 Contig ID
                   LIB3088-008-Q1-K1-D1
 5'-most EST
                   BLASTN
Method
```

E value 7.0e-12 Match length 78 % identity 87

NCBI Description Zea mays gene encoding protein kinase CK2 alpha subunit

Seq. No. 268377

Contig ID 15886_2.R1011 5'-most EST ceu700431227.h1

Method BLASTN
NCBI GI g3821794
BLAST score 38
E value 1.0e-11

Match length 78 % identity 87

NCBI Description Zea mays gene encoding protein kinase CK2 alpha subunit

Seq. No. 268378

Contig ID 15890_1.R1011 5'-most EST LIB83-010-Q1-E1-C10

Method BLASTX
NCBI GI g1171866
BLAST score 746
E value 5.0e-79
Match length 158
% identity 85

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR

(COMPLEX I-20KD) (CI-20KD) >gi_629601_pir__S48826 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain PSST - wild cabbage >gi_56282 emb_CAA57725_ (X82274) PSST subunit of

NADH: ubiquinone oxidoreductase [Brassica oleracea]

Seq. No. 268379

Contig ID 15890 2.R1011

5'-most EST LIB3279-015-P1-K1-G8

Method BLASTX
NCBI GI g2499327
BLAST score 320
E value 4.0e-29
Match length 78
% identity 76

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi 1084345 pir_S52286 NADH

dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_643090 emb_CAA58887.1 (X84078) NADH dehydrogenase

[Arabidopsis thaliana]

Seq. No. 268380

Contig ID 15916_1.R1011 5'-most EST xsy700208074.h1

Seq. No. 268381

Contig ID 15918 1.R1011

5'-most EST LIB3088-009-Q1-K1-G5

Seq. No. 268382

Contig ID 15923_1.R1011 5'-most EST uC-zmflb73272h06a1



```
BLASTX
Method
NCBI GI
                   q169363
                   238
BLAST score
                   9.0e-20
E value
                   54
Match length
                   76
% identity
NCBI Description (M75856) PVPR3 [Phaseolus vulgaris]
                   268383
Seq. No.
                   15923 2.R1011
Contig ID
                   uC-zmflmo17071c03b1
5'-most EST
                   BLASTX
Method
                   q169363
NCBI GI
                   274
BLAST score
                   5.0e-24
E value
                   61
Match length
                   75
% identity
                   (M75856) PVPR3 [Phaseolus vulgaris]
NCBI Description
                   268384
Seq. No.
                   15923 3.R1011
Contig ID
                   LIB3088-009-Q1-K1-H6
5'-most EST
                   BLASTX
Method
NCBI GI
                    q169363
BLAST score
                    160
                    1.0e-10
E value
                    39
Match length
% identity
NCBI Description (M75856) PVPR3 [Phaseolus vulgaris]
                    268385
Seq. No.
                    15923 5.R1011
Contig ID
                    LIB30<del>6</del>8-007-Q1-K1-G1
5'-most EST
                    268386
Seq. No.
                    15926 1.R1011
Contig ID
                    LIB3088-010-Q1-K1-B1
5'-most EST
                    268387
Seq. No.
                    15926 2.R1011
Contig ID
                    uC-zmflmo17154f02a1
5'-most EST
                    268388
Seq. No.
                    15928 1.R1011
Contig ID
                    uC-zm\overline{f}1b73131d06a1
 5'-most EST
                    BLASTX
Method
                    g3914239
NCBI GI
                    478
 BLAST score
                    5.0e-93
E value
                    324
Match length
                    57
 % identity
NCBI Description PROTEIN PHOSPHATASE 2C ABI2 (PP2C)
                    >gi_1945140_emb_CAA70163_ (Y08966) ABI2 protein phosphatase
2C [Arabidopsis thaliana] >gi_1945142_emb_CAA70162_
                    (Y08965) ABI2 protein phosphatase 2C [Arabidopsis thaliana]
                    >gi_2564213_emb_CAA72538 (Y11840) ABI2 [Arabidopsis
```

thaliana]



```
268389
Seq. No.
                  15928 2.R1011
Contig ID
                  uC-zmflb73175c03a2
5'-most EST
                  BLASTX
Method
                  g3242077
NCBI GI
                  144
BLAST score
                  8.0e-09
E value
                  37
Match length
                  76
% identity
                  (AJ003119) protein phosphatase 2C [Arabidopsis thaliana]
NCBI Description
                  268390
Seq. No.
                  15929 1.R1011
Contig ID
5'-most EST
                  uC-zmroteosinte066d04b1
                  BLASTX
Method
                  g3334490
NCBI GI
                  181
BLAST score
                  4.0e-13
E value
                  54
Match length
% identity
                  54
                  DNA-DIRECTED RNA POLYMERASES I, II, AND III 7.3 KD
NCBI Description
                  POLYPEPTIDE (ABC10-ALPHA) >gi 2529253 dbj BAA22807
                   (D89634) RNA polymarase II subunit Rpb12
                   [Schizosaccharomyces pombe] >gi 2625015 (AF027819) RNA
                   polymerases I, II and III subunīt Rpc10
                   [Schizosaccharomyces pombe]
                   268391
Seq. No.
                   15929 2.R1011
Contig ID
                  LIB3066-045-Q1-K1-H10
5'-most EST
                   BLASTX
Method
                   q3334490
NCBI GI
                   158
BLAST score
                   2.0e-10
E value
                   39
Match length
                   64
% identity
NCBI Description DNA-DIRECTED RNA POLYMERASES I, II, AND III 7.3 KD
                   POLYPEPTIDE (ABC10-ALPHA) >gi_2529253_dbj_BAA22807
                   (D89634) RNA polymarase II subunit Rpb12
                   [Schizosaccharomyces pombe] >gi_2625015 (AF027819) RNA
                   polymerases I, II and III subunit Rpc10
                   [Schizosaccharomyces pombe]
                   268392
Seq. No.
                   15929 3.R1011
Contig ID
                   nwy700445085.h1
5'-most EST
                   BLASTX
Method
                   g3334490
NCBI GI
BLAST score
                   186
E value
                   3.0e-14
Match length
                   50
 % identity
                   58
NCBI Description DNA-DIRECTED RNA POLYMERASES I, II, AND III 7.3 KD
                   POLYPEPTIDE (ABC10-ALPHA) >gi_2529253_dbj_BAA22807_
```

[Schizosaccharomyces pombe] >gi_2625015 (AF027819) RNA

(D89634) RNA polymarase II subunit Rpb12



268393

polymerases I, II and III subunit Rpc10
[Schizosaccharomyces pombe]

Contig ID 15937_1.R1011
5'-most EST LIB3062-035-Q1-K1-A10
Method BLASTX
NCBI GI g4454480
BLAST score 736
E value 9.0e-78

Match length 237 % identity 59

Seq. No.

NCBI Description (AC006234) putative (1-4)-beta-mannan endohydrolase

[Arabidopsis thaliana]

Seq. No. 268394

Contig ID 15938_1.R1011

5'-most EST LIB3088-010-Q1-K1-D8

Method BLASTX
NCBI GI g4454012
BLAST score 240
E value 5.0e-20
Match length 74
% identity 59

NCBI Description (AL035396) Pollen-specific protein precursor like

[Arabidopsis thaliana]

Seq. No. 268395

Contig ID 15941_1.R1011

5'-most EST LIB3279-050-P1-K1-B11

Method BLASTX
NCBI GI g2267597
BLAST score 451
E value 1.0e-44
Match length 98
% identity 92

NCBI Description (AF009413) 10 kDa chaperonin [Oryza sativa]

Seq. No. 268396

Contig ID 15941_2.R1011 5'-most EST qmh700026609.f1

Method BLASTX
NCBI GI g2267597
BLAST score 441
E value 2.0e-43
Match length 98
% identity 91

NCBI Description (AF009413) 10 kDa chaperonin [Oryza sativa]

Seq. No. 268397

Contig ID 15941_4.R1011

5'-most EST LIB3088-010-Q1-K1-E11

Method BLASTN
NCBI GI g2267596
BLAST score 73
E value 8.0e-33
Match length 113



% identity NCBI Description Oryza sativa 10 kDa chaperonin mRNA, complete cds 268398 Seq. No. 15943 1.R1011 Contig ID LIB3088-010-Q1-K1-E8 5'-most EST BLASTN Method g22204 NCBI GI 53 BLAST score 5.0e-21 E value 53 Match length 100 % identity Maize Bz-McC gene for UDPglucose flavonoid NCBI Description glycosyl-transferase 268399 Seq. No. 15955 1.R1011 Contig ID uC-zmroteosinte033f05b1 5'-most EST 268400 Seq. No. 15955 2.R1011 Contig ID dyk700102651.hl 5'-most EST 268401 Seq. No. 15955 4.R1011 Contig ID uC-zmflmo17289c04a1 5'-most EST 268402 Seq. No. Contig ID 15955 5.R1011 uC-zmflmo17234e03a1 5'-most EST 268403 Seq. No. 15969 1.R1011 Contig ID rvt700550166.hl 5'-most EST BLASTX Method g1946355 NCBI GI 179 BLAST score 2.0e-19 E value Match length 175 35 % identity (U93215) maize transposon MuDR mudrA protein isolog NCBI Description [Arabidopsis thaliana] >gi_2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana] 268404 Seq. No. 15971 1.R1011 Contig ID xmt700268017.hl 5'-most EST BLASTX Method q1706328 NCBI GI 2504 BLAST score 0.0e + 00E value

Match length 522 92 % identity

NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC) >gi 1009710 (U27350)

pyruvate decarboxylase 2 [Oryza sativa] - ji_1777455 (U38199) pyruvate decarboxylase 2 [Oryza sativa]



268405 Seq. No. 15971 2.R1011 Contig ID uC-zmflb73211b05a2 5'-most EST Method BLASTN NCBI GI g22764 BLAST score 261 1.0e-145 E value 297 Match length % identity 98 Z.mays mRNA for pyruvate decarboxylase (partial) NCBI Description >gi 217971 dbj D14457 MZEPYRDE2 Zea mays mRNA for pyruvate decarboxylase Seq. No. 268406 15972 1.R1011 Contig ID qmh700026587.f1 5'-most EST BLASTX Method NCBI GI g2829918 BLAST score 785 E value 1.0e-83 295 Match length 62 % identity NCBI Description (AC002291) similar to "tub" protein gp U82468 2072162 [Arabidopsis thaliana] 268407 Seq. No. Contig ID 15972 5.R1011 5'-most EST uC-zmflmo17241c01b1 268408 Seq. No. 15979 1.R1011 Contig ID 5'-most EST LIB3151-006-Q1-K1-F11 Method BLASTX g3033397 NCBI GI BLAST score 1843 E value 0.0e + 00Match length 468 73 % identity NCBI Description (AC004238) unknown protein [Arabidopsis thaliana] Seq. No. 268409 15979 2.R1011 Contig ID 5'-most EST uC-zmflmo17115d10a1 Method BLASTX NCBI GI g3033397 BLAST score 382 E value 8.0e-37 82 Match length % identity

NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]

Seq. No. 268410

Contig ID 15979 3.R1011

5'-most EST LIB3279-003-P1-K1-E10

Method BLASTX NCBI GI q3033397 BLAST score 467



8.0e-47E value 112 Match length 79 % identity NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]

268411 Seq. No. 15983 1.R1011 Contig ID uC-zmflb73047d09b1 5'-most EST

268412 Seq. No. 15983 2.R1011 Contig ID ntr700076786.h1 5'-most EST

268413

Seq. No. 15983 3.R1011 Contig ID $xjt70\overline{0}095729.h1$ 5'-most EST BLASTN Method g3821780 NCBI GI 36 BLAST score

7.0e-11 E value 36 Match length 100 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

268414 Seq. No. 15983 6.R1011 Contig ID xyt700344129.h1 5'-most EST

268415 Seq. No. Contig ID 15986 1.R1011 fC-zmle700423860f2 5'-most EST BLASTX Method

q1872521 NCBI GI 226 BLAST score 3.0e-18E value 73 Match length 36 % identity

(U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] NCBI Description >gi 1872523 (U87834) zinc-finger protein Lsdl [Arabidopsis

thaliana]

268416 Seq. No.

15986 2.R1011 Contig ID uC-zmflmo17153b10a1 5'-most EST

268417 Seq. No.

15989 1.R1011 Contig ID $uC-zm\overline{f}lmo17242h04b1$ 5'-most EST

268418 Seq. No.

15989 2.R1011 Contig ID

LIB3088-013-Q1-K1-B4 5'-most EST

BLASTN Method g2062705 NCBI GI 38 BLAST score 9.0e-12 E value 42 Match length



% identity 98

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 268419

Contig ID 15997_1.R1011 5'-most EST tfd700572635.h1

Method BLASTX
NCBI GI g3913425
BLAST score 487
E value 5.0e-73
Match length 139
% identity 91

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE >gi_2275203 (AC002337) RNA helicase isolog

[Arabidopsis thaliana]

Seq. No. 268420

Contig ID 15997_2.R1011

5'-most EST LIB3088-013-Q1-K1-G2

Method BLASTX
NCBI GI g3913425
BLAST score 190
E value 3.0e-14
Match length 43
% identity 81

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE >gi_2275203 (AC002337) RNA helicase isolog

[Arabidopsis thaliana]

Seq. No. 268421

Contig ID 15997_3.R1011 5'-most EST uC-zmrob73024f09a1

Method BLASTX
NCBI GI g3913425
BLAST score 1474
E value 1.0e-164
Match length 518
% identity 90

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE >gi_2275203 (AC002337) RNA helicase isolog

[Arabidopsis thaliana]

Seq. No. 268422

Contig ID 15997_4.R1011 5'-most EST afb700380936.h1

Method BLASTX
NCBI GI g3913425
BLAST score 673
E value 5.0e-71
Match length 138
% identity 89

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE >gi_2275203 (AC002337) RNA helicase isolog

[Arabidopsis thaliana]

Seq. No. 268423

Contig ID 15998_1.R1011

Seq. No.

Contig ID

268430

16012 1.R1011



```
LIB3088-013-Q1-K1-G8
5'-most EST
                  268424
Seq. No.
                  16000 1.R1011
Contig ID
                  uC-zmroteosinte011b12b1
5'-most EST
                  BLASTX
Method
                  g4490319
NCBI GI
                  367
BLAST score
                  1.0e-34
E value
                  174
Match length
                   47
% identity
                   (AL035678) metal-transporting P-type ATPase [Arabidopsis
NCBI Description
                  thaliana]
                   268425
Seq. No.
                   16001 1.R1011
Contig ID
                   uC-zmroteosinte033c03b1
5'-most EST
                   {\tt BLASTX}
Method
                   g3201969
NCBI GI
                   1050
BLAST score
E value
                   1.0e-114
                   198
Match length
                   96
% identity
                  (AF068332) submergence induced protein 2A [Oryza sativa]
NCBI Description
                   268426
Seq. No.
                   16001 2.R1011
Contig ID
                   uC-zmrob73078c08b1
5'-most EST
                   BLASTX
Method
                   q3201969
NCBI GI
BLAST score
                   575
                   1.0e-64
E value
                   168
Match length
                   78
% identity
                  (AF068332) submergence induced protein 2A [Oryza sativa]
NCBI Description
                   268427
Seq. No.
                   16001 4.R1011
Contig ID
                   tfd700573243.h1
5'-most EST
                   BLASTX
Method
                   q3201969
NCBI GI
BLAST score
                   317
                   3.0e-29
E value
                   126
Match length
% identity
NCBI Description (AF068332) submergence induced protein 2A [Oryza sativa]
                   268428
Seq. No.
                   16002 1.R1011
Contig ID
5'-most EST
                   LIB3088-014-Q1-K1-B3
                   268429
Seq. No.
Contig ID
                   16008 1.R1011
                   LIB3088-014-Q1-K1-E1
5'-most EST
```



uC-zmroteosinte039e01b1 5'-most EST BLASTX Method g3132470 NCBI GI BLAST score 266 6.0e-23 E value 122 Match length 48 % identity (AC003096) unknown protein [Arabidopsis thaliana] NCBI Description 268431 Seq. No. 16016 1.R1011 Contig ID LIB143-066-Q1-E1-H1 5'-most EST BLASTX Method g2130105 NCBI GI 370 BLAST score 4.0e-35 E value 95 Match length 80 % identity histone H2A type 2 (clone wcH2A-4) - wheat NCBI Description >gi_536892_dbj_BAA07278_ (D38089) protein H2A [Triticum aestivum] $\overline{\text{gi}}$ $\overline{5}$ 36896_db $\overline{\text{j}}$ BAA07280_ (D38091) protein H2A [Triticum aestivum] 268432 Seq. No. 16016 2.R1011 Contig ID LIB3088-019-Q1-K1-A3 5'-most EST BLASTX Method q2130105 NCBI GI BLAST score 370 E value 3.0e - 3595 Match length 80 % identity histone H2A type 2 (clone wcH2A-4) - wheat NCBI Description >gi_536892_dbj_BAA07278_ (D38089) protein H2A [Triticum aestivum] >gi_536896_dbj_BAA07280_ (D38091) protein H2A [Triticum aestivum] 268433 Seq. No. 16023 1.R1011 Contig ID 5'-most EST LIB3088-019-Q1-K1-B5 268434 Seq. No. 16025 1.R1011 Contig ID LIB3088-019-Q1-K1-C1 5'-most EST Method BLASTX g1655536 NCBI GI 193 BLAST score 1.0e-14 E value 54 Match length % identity 67

NCBI Description (Y09095) chloride channel [Arabidopsis thaliana]

>gi_1742957_emb_CAA96059_ (Z71447) CLC-c chloride channel

protein [Arabidopsis thaliana]

Seq. No. 268435

Contig ID 16027_1.R1011

5'-most EST LIB3088-019-Q1-K1-C3

```
268436
Seq. No.
                  16030 1.R1011
Contig ID
                  LIB3088-019-Q1-K1-D2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2462753
                  381
BLAST score
                  1.0e-36
E value
Match length
                  124
                  58
% identity
                  (AC002292) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
                  268437
Seq. No.
                  16032 1.R1011
Contig ID
                  uC-zmflm017025b09b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q129232
BLAST score
                  1799
                  0.0e + 00
E value
                  435
Match length
                  79
% identity
NCBI Description ORYZAIN BETA CHAIN PRECURSOR >gi 67645 pir KHRZOB oryzain
                  (EC 3.4.22.-) beta precursor - rice
                  >gi 218183 dbj BAA14403 (D90407) oryzain beta precursor
                  [Oryza sativa]
Seq. No.
                  268438
                  16032 2.R1011
Contig ID
5'-most EST
                  uC-zmflMo17014c10b1
Method
                  BLASTX
                  g129232
NCBI GI
BLAST score
                  323
E value
                  7.0e-30
                  94
Match length
% identity
                  74
NCBI Description ORYZAIN BETA CHAIN PRECURSOR >gi 67645 pir KHRZOB oryzain
                  (EC 3.4.22.-) beta precursor - rice
                  >gi_218183_dbj_BAA14403_ (D90407) oryzain beta precursor
                  [Oryza sativa]
                  268439
Seq. No.
                  16032 3.R1011
Contig ID
                  fdz701163617.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g129232
BLAST score
                  288
E value
                  5.0e-26
Match length
                  55
% identity
                  91
```

NCBI Description ORYZAIN BETA CHAIN PRECURSOR >gi 67645 pir_ KHRZOB oryzain

(EC 3.4.22.-) beta precursor - rice

>gi 218183 dbj BAA14403 (D90407) oryzain beta precursor

[Oryza sativa]

268440 Seq. No.

16032 4.R1011 Contig ID



5'-most EST fdz701164512.h1

Method BLASTX
NCBI GI g129232
BLAST score 298
E value 3.0e-27
Match length 58
% identity 86

NCBI Description ORYZAIN BETA CHAIN PRECURSOR >gi_67645_pir__KHRZOB oryzain

(EC 3.4.22.-) beta precursor - rice

>gi 218183 dbj_BAA14403_ (D90407) oryzain beta precursor

[Oryza sativa]

Seq. No. 268441

Contig ID 16039_1.R1011

5'-most EST uC-zmflmo17073b04b1

Method BLASTX
NCBI GI g3319353
BLAST score 335
E value 5.0e-31
Match length 101
% identity 55

NCBI Description (AF077407) contains similarity to copper-binding proteins

[Arabidopsis thaliana]

Seq. No. 268442

Contig ID 16039_2.R1011

5'-most EST LIB3068-008-Q1-K1-D1

Method BLASTX
NCBI GI 93319353
BLAST score 254
E value 1.0e-21
Match length 82
% identity 54

NCBI Description (AF077407) contains similarity to copper-binding proteins

[Arabidopsis thaliana]

Seq. No. 268443

Contig ID 16044_1.R1011

5'-most EST LIB3150-059-Q1-N1-D4

Method BLASTX
NCBI GI g134613
BLAST score 803
E value 9.0e-86
Match length 151
% identity 100

NCBI Description SUPEROXIDE DISMUTASE-2 (CU-ZN) >gi_82727_pir__A29077 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 2 - maize

>gi_168620 (M54936) superoxide dismutase 2 [Zea mays]

>gi_168622 (M15175) SOD2 protein [Zea mays]

Seq. No. 268444

Contig ID 16044_2.R1011 5'-most EST wyr700236980.h1

Method BLASTX
NCBI GI g134613
BLAST score 665
E value 7.0e-70



129 Match length % identity SUPEROXIDE DISMUTASE-2 (CU-ZN) >gi_82727_pir__A29077 NCBI Description superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 2 - maize >gi 168620 (M54936) superoxide dismutase 2 [Zea mays] >gi_168622 (M15175) SOD2 protein [Zea mays] 268445 Seq. No. 16047 1.R1011 Contig ID uC-zmflMo17091b05b1 5'-most EST BLASTX Method q1705667 NCBI GI 2021 BLAST score 0.0e + 00E value 429 Match length 87 % identity SERINE CARBOXYPEPTIDASE-LIKE PRECURSOR NCBI Description >gi 409582 dbj_BAA04511_ (D17587) serine carboxypeptidase-like protein [Oryza sativa] 268446 Seq. No. 16047 3.R1011 Contig ID LIB3060-023-Q1-K1-D12 5'-most EST BLASTX Method q2851577 NCBI GI 367 BLAST score 1.0e-36 E value 139 Match length 64 % identity SERINE CARBOXYPEPTIDASE III PRECURSOR (CP-MIII) NCBI Description >gi 1877219 emb CAA70817_ (Y09604) serine carboxypeptidase III, CP-MIII [Hordeum vulgare] 268447 Seq. No. 16047 4.R1011 Contig ID uC-zmf1B73045h01b1 5'-most EST BLASTX Method g1705667 NCBI GI BLAST score 388 2.0e-37 E value 96 Match length 77 % identity SERINE CARBOXYPEPTIDASE-LIKE PRECURSOR NCBI Description >qi 409582 dbj BAA04511_ (D17587) serine carboxypeptidase-like protein [Oryza sativa] 268448 Seq. No. 16048 1.R1011 Contig ID LIB3088-019-Q1-K1-G7 5'-most EST BLASTX Method

Method BLASTX
NCBI GI 94567262
BLAST score 169
E value 1.0e-11
Match length 129
% identity 40

NCBI Description (AC006841) putative ubiquitin [Arabidopsis thaliana]



268449 Seq. No. 16048 2.R1011 Contig ID ypc700806833.hl 5'-most EST BLASTX Method g4567262 NCBI GI 917 BLAST score 3.0e - 99E value 216 Match length

% identity (AC006841) putative ubiquitin [Arabidopsis thaliana] NCBI Description

268450 Seq. No.

16048 3.R1011 Contig ID tfd700573003.h1 5'-most EST

268451 Seq. No.

16049 1.R1011 Contig ID

LIB3069-006-Q1-K1-E5 5'-most EST

79

BLASTX Method g2459420 NCBI GI 708 BLAST score 8.0e-75 E value 140 Match length 97 % identity

(AC002332) putative ribosomal protein L17 [Arabidopsis NCBI Description

thaliana]

268452 Seq. No.

16049 2.R1011 Contig ID

5'-most EST LIB3067-006-Q1-K1-G9

Method BLASTX q2459420 NCBI GI 213 BLAST score 5.0e-17 E value Match length 41 100 % identity

(AC002332) putative ribosomal protein L17 [Arabidopsis NCBI Description

thaliana]

Seq. No. 268453

16052 1.R1011 Contig ID

uC-zmroteosinte004h11b1 5'-most EST

Method BLASTX NCBI GI g2736290 BLAST score 208 E value 5.0e-1699 Match length 45 % identity

(AF031383) hMed7 [Homo sapiens] >gi 4220890 (AF104251) NCBI Description

transcriptional co-activator CRSP33 [Homo sapiens]

268454 Seq. No.

16052 2.R1011 Contig ID

LIB3088-019-Q1-K1-H6 5'-most EST

BLASTX Method g2736290 NCBI GI 215 BLAST score



8.0e-17 E value 119 Match length 40 % identity (AF031383) hMed7 [Homo sapiens] >gi 4220890 (AF104251) NCBI Description transcriptional co-activator CRSP33 [Homo sapiens] 268455 Seq. No. 16052 3.R1011 Contig ID xsy700214473.h1 5'-most EST BLASTX Method g2736290 NCBI GI 210 BLAST score 1.0e-16 E value 111 Match length 42 % identity (AF031383) hMed7 [Homo sapiens] >gi 4220890 (AF104251) NCBI Description transcriptional co-activator CRSP33 [Homo sapiens] 268456 Seq. No. Contig ID 16052 4.R1011 5'-most EST $pmx70\overline{0}083151.h1$ 268457 Seq. No. 16053 1.R1011 Contig ID rv1700456778.h1 5'-most EST 268458 Seq. No. 16054 1.R1011 Contig ID LIB3088-020-Q1-K1-A7 5'-most EST BLASTX Method g2130124 NCBI GI 378 BLAST score 2.0e-36 E value 66 Match length 98 % identity DNA-binding protein Dof2 - maize (fragment) NCBI Description >gi 1061306_emb_CAA56287_ (X79934) Dof2 [Zea mays] Seq. No. 268459 Contig ID 16057 1.R1011 $uC-zm\overline{f}lmo17137a05b1$ 5'-most EST Method BLASTX q2244865 NCBI GI 293 BLAST score 4.0e-26 E value Match length 154 45 % identity (297337) hypothetical protein [Arabidopsis thaliana] NCBI Description 268460 Seq. No. 16060 1.R1011 Contig ID uC-zmflb73141c12b1 5'-most EST

Seq. No. 268461

Contig ID 16062_1.R1011 5'-most EST uer700578570.h1

Method BLASTN



g1159876 NCBI GI 43 BLAST score 8.0e-15 E value 43 Match length 100 % identity NCBI Description A.fatua mRNA for DNA-binding protein (clone ABF1) 268462 Seq. No. 16065 1.R1011 Contig ID uC-zmflMo17010e08b1 5'-most EST BLASTX Method q2081612 NCBI GI 1425 BLAST score 0.0e+00E value 712 Match length 74 % identity (D49714) deltal-pyrroline-5-carboxylate synthetase [Oryza NCBI Description sativa] 268463 Seq. No. 16074 1.R1011 Contig ID LIB3088-020-Q1-K1-F9 5'-most EST 268464 Seq. No. 16076 1.R1011 Contig ID 5'-most EST rvt700548979.h1 268465 Seq. No. 16076 2.R1011 Contig ID uC-zmflb73177d12b1 5'-most EST 268466 Seq. No. 16082 1.R1011 Contig ID LIB3067-045-Q1-K1-D4 5'-most EST BLASTX Method g3063698 NCBI GI 172 BLAST score 6.0e-12 E value 67 Match length 52 % identity NCBI Description (AL022537) putative protein [Arabidopsis thaliana] 268467 Seq. No. 16091 1.R1011 Contig ID $uC-zm\overline{f}lmo17263h01b1$ 5'-most EST Method BLASTN g22382 NCBI GI

Method BLASTN
NCBI GI g22382
BLAST score 211
E value 1.0e-115
Match length 252
% identity 95

NCBI Description Z.mays mRNA for U5snRNA (U53)

Seq. No. 268468

Contig ID 16091_2.R1011

5'-most EST LIB3088-021-Q1-K1-B4

Method BLASTN



```
g22382
NCBI GI
BLAST score
                  140
                  1.0e-72
E value
                  309
Match length
% identity
                  94
NCBI Description Z.mays mRNA for U5snRNA (U53)
                  268469
Seq. No.
                  16094 1.R1011
Contig ID
                  LIB3062-010-Q1-K1-A8
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2208988
BLAST score
                  435
                  8.0e-43
E value
Match length
                  86
                  95
% identity
NCBI Description (Y10117) signal recognition particle subunit 9 [Zea mays]
Seq. No.
                  268470
Contig ID
                  16102 1.R1011
5'-most EST
                  uC-zmrob73060a03a1
Seq. No.
                  268471
                  16102 2.R1011
Contig ID
5'-most EST
                  uC-zmflb73222e06b1
                  BLASTX
Method
NCBI GI
                  g3831441
BLAST score
                  150
                  1.0e-09
E value
Match length
                  58
                  69
% identity
NCBI Description (AC005819) hypothetical protein [Arabidopsis thaliana]
                  268472
Seq. No.
Contig ID
                  16109 1.R1011
5'-most EST
                  fdz701158804.h1
Method
                  BLASTX
NCBI GI
                  g3513736
                  159
BLAST score
E value
                  4.0e-19
                  89
Match length
                  57
% identity
                  (AF080118) No definition line found [Arabidopsis thaliana]
NCBI Description
                  >gi_4539367_emb_CAB40061.1 (AL049525) putative protein
                  [Arabidopsis thaliana]
                  268473
Seq. No.
Contig ID
                  16110 1.R1011
5'-most EST
                  uC-zmflb73274e03b1
                  BLASTX
Method
NCBI GI
                  g2317905
BLAST score
                  255
```

E value 9.0e-22 Match length 151 % identity 38

NCBI Description (U89959) bZIP-like protein [Arabidopsis thaliana]



Seq. No. 268474

Contig ID 16122_1.R1011

5'-most EST LIB3088-022-Q1-K1-E8

Method BLASTX
NCBI GI g3860250
BLAST score 1366
E value 1.0e-151
Match length 302
% identity 86

% identity 86 NCBI Description (AC005824) putative chloroplast prephenate dehydratase

[Arabidopsis thaliana]

Seq. No. 268475

Contig ID 16122_3.R1011 5'-most EST wyr700242968.h1

Method BLASTX
NCBI GI g2392772
BLAST score 345
E value 2.0e-32
Match length 130
% identity 61

NCBI Description (AC002534) putative chloroplast prephenate dehydratase

[Arabidopsis thaliana]

Seq. No. 268476

Contig ID 16122_4.R1011 5'-most EST uC-zmflb73082g10a2

Seq. No. 268477

Contig ID 16127_1.R1011

5'-most EST LIB3069-029-Q1-K1-B9

Method BLASTX
NCBI GI g3004547
BLAST score 283
E value 3.0e-25
Match length 86
% identity 65

NCBI Description (AC003673) unknown protein [Arabidopsis thaliana]

>gi 4185150 (AC005724) unknown protein [Arabidopsis

thaliana]

Seq. No. 268478

Contig ID 16127 2.R1011 5'-most EST uC-zmflb73102b04a1

Method BLASTX
NCBI GI g3004547
BLAST score 166
E value 1.0e-11
Match length 35
% identity 91

NCBI Description (AC003673) unknown protein [Arabidopsis thaliana]

>gi_4185150 (AC005724) unknown protein [Arabidopsis

thaliana]

Seq. No. 268479

Contig ID 16128_1.R1011

5'-most EST LIB3088-022-Q1-K1-H4



```
268480
Seq. No.
                  16128 2.R1011
Contig ID
                  LIB3066-043-Q1-K1-G1
5'-most EST
                  BLASTX
Method
                  g3860250
NCBI GI
                  320
BLAST score
                  5.0e-51
E value
                  210
Match length
% identity
                   (AC005824) putative chloroplast prephenate dehydratase
NCBI Description
                   [Arabidopsis thaliana]
                  268481
Seq. No.
                  16131 1.R1011
Contig ID
                  uC-zmflb73139b04b1
5'-most EST
                  BLASTX
Method
                   g2129698
NCBI GI
                   1151
BLAST score
                   1.0e-126
E value
                   319
Match length
                   71
% identity
                  protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana
NCBI Description
                   >gi 1054633 emb_CAA63387_ (X92728) protein kinase
                   [Arabidopsis thaliana]
                   268482
Seq. No.
                   16132 1.R1011
Contig ID
                   LIB3088-023-Q1-K1-A4
5'-most EST
                   BLASTX
Method
                   q4406781
NCBI GI
                   190
BLAST score
                   8.0e-14
E value
                   276
Match length
                   27
% identity
                   (AC006532) putative Na+/H+ antiporter [Arabidopsis
NCBI Description
                   thaliana]
                   268483
Seq. No.
                   16139 1.R1011
Contig ID
                   dyk700104331.h1
5'-most EST
                   BLASTX
Method
                   q2809251
NCBI GI
BLAST score
                   518
                   2.0e-52
E value
Match length
                   167
                   59
 % identity
                  (AC002560) F21B7.20 [Arabidopsis thaliana]
 NCBI Description
                   268484
 Seq. No.
                   16144 1.R1011
 Contig ID
                   LIB3088-023-Q1-K1-F11
 5'-most EST
                   268485
 Seq. No.
```

37359

16156 1.R1011

BLASTX

qmh700026822.fl

Contig ID

Method

5'-most EST



NCBI GI g2132930 BLAST score 688 E value 4.0e-72 Match length 295 % identity 47

NCBI Description probable membrane protein YOR262w - yeast (Saccharomyces cerevisiae) >gi 1420591 emb CAA99484 (Z75170) ORF YOR262w

[Saccharomyces cerevisiae]

Seq. No. 268486

Contig ID 16160 1.R1011

5'-most EST LIB3156-012-Q1-K1-G8

Seq. No. 268487

Contig ID 16160_2.R1011 5'-most EST cat700019711.r1

Seq. No. 268488

Contig ID 16162 1.R1011

5'-most EST LIB3088-024-Q1-K1-D7

Method BLASTX
NCBI GI g1173194
BLAST score 484
E value 2.0e-48
Match length 123
% identity 72

NCBI Description 30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13)

>gi_2119093_pir__S59594 ribosomal protein S13 precursor,
chloroplast - Arabidopsis thaliana >gi_16767_emb_CAA79013_
(Z17611) chloroplast 30S ribosomal protein S13 [Arabidopsis

thaliana] >gi_662869_emb_CAA88028_ (Z47986) chloroplast

ribosomal protein S13 [Arabidopsis thaliana]

>gi_1107483_emb_CAA63021_ (X91955) 30S ribosomal protein
S13 [Arabidopsis thaliana] >gi_1515107_emb_CAA60413_
(X86734) plastid ribosomal protein S13 [Arabidopsis

thaliana]

Seq. No. 268489

Contig ID 16163_1.R1011

5'-most EST LIB3088-024-Q1-K1-F3
Method BLASTX
NCBI GI g4115383

BLAST score 408
E value 5.0e-40
Match length 118
% identity 67

NCBI Description (AC005967) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No. 268490

Contig ID 16170_1.R1011

5'-most EST $uC-zm\overline{f}lmo17257g02b1$

Method BLASTX
NCBI GI g4490310
BLAST score 683
E value 2.0e-71
Match length 304



% identity 46
NCBI Description (AL035678) somatic embryogenesis receptor-like kinase-like protein [Arabidopsis thaliana]

Seq. No. 268491
Contig ID 16178_1.R1011
5'-most EST cyk700049323.f1
Method BLASTX
NCBI GI g2809246
PLAST score 850

metnod BLASTX
NCBI GI g2809246
BLAST score 850
E value 5.0e-91
Match length 306
% identity 55

NCBI Description (AC002560) F2401.15 [Arabidopsis thaliana]

Seq. No. 268492

Contig ID 16178_2.R1011 5'-most EST uC-zmflb73167b09b2

Seq. No. 268493 Contig ID 16178_3.R1011

5'-most EST uC-zmflb73306c04a1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 8.0e-11
Match length 36

% identity 100 NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 268494

Contig ID 16180_1.R1011 5'-most EST uC-zmflmo17289c05b1

Method BLASTX
NCBI GI g542200
BLAST score 571
E value 1.0e-58
Match length 159

% identity 65
NCBI Description hypothetical protein - garden asparagus

>gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus

officinalis]

Seq. No. 268495

Contig ID 16180_2.R1011

5'-most EST uC-zmroteosinte024d01b1

Method BLASTX
NCBI GI g643469
BLAST score 181
E value 3.0e-13
Match length 44
% identity 70

NCBI Description (U19886) unknown [Lycopersicon esculentum]

Seq. No. 268496

Contig ID 16187_1.R1011

5'-most EST LIB3088-025-Q1-K1-D5



Seq. No. 268497

Contig ID 16188_1.R1011

5'-most EST LIB3088-025-Q1-K1-D6 Method BLASTX NCBI GI g3176684

BLAST score 318
E value 3.0e-29
Match length 86
% identity 70

% identity 70
NCBI Description (AC003671) Contains similarity to equilibratiave nucleoside

transporter 1 gb_U81375 from Homo sapiens. ESTs gb_N65317, gb_T20785, gb_AA586285 and gb_AA712578 come from this gene.

[Arabidopsis thaliana]

Seq. No. 268498

Contig ID 16195_1.R1011 5'-most EST tfd700575815.h1

Seq. No. 268499

Contig ID 16199 1.R1011

5'-most EST LIB3088-025-Q1-K1-F3

Seq. No. 268500

Contig ID 16210_1.R1011

5'-most EST LIB3088-026-Q1-K1-A11

Seq. No. 268501

Contig ID 16212 1.R1011

5'-most EST LIB3158-005-Q1-K1-F8

Seq. No. 268502

Contig ID 16213_1.R1011

5'-most EST LIB3116-004-Q1-K2-D8

Seq. No. 268503

Contig ID 16235 1.R1011

5'-most EST LIB3088-029-Q1-K1-D11

Seq. No. 268504

Contig ID 16247 1.R1011

5'-most EST LIB3088-030-Q1-K1-A1

Seq. No. 268505

Contig ID 16247 2.R1011 5'-most EST rvt700550751.h1

Seq. No. 268506

Contig ID 16249 1.R1011

5'-most EST LIB3067-058-Q1-K1-C2

Seq. No. 268507

Contig ID 16250 1.R1011

5'-most EST uC-zmroteosinte059e01b1

Method BLASTX
NCBI GI g4454032
BLAST score 344



```
4.0e-32
E value
Match length
                  168
% identity
                   41
                  (AL035394) putative protein [Arabidopsis thaliana]
NCBI Description
                   268508
Seq. No.
                   16250 2.R1011
Contig ID
                   LIB84-008-Q1-E1-H2
5'-most EST
                   BLASTX
Method
                   g3702332
NCBI GI
BLAST score
                   215
                   3.0e-17
E value
                   109
Match length
                   44
% identity
                   (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                   268509
Seq. No.
                   16250 3.R1011
Contig ID
                   wyr700243548.hl
5'-most EST
                   BLASTX
Method
                   q3702332
NCBI GI
                   216
BLAST score
                   3.0e-17
E value
Match length
                   93
                   49
% identity
                   (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                   268510
Seq. No.
                   16253 1.R1011
Contig ID
                   rvt700548568.h1
5'-most EST
                   BLASTX
Method
                   g1854378
NCBI GI
                   804
BLAST score
                   6.0e-86
E value
                   170
Match length
                   94
% identity
                   (AB001338) Sucrose-Phosphate Synthase [Saccharum
NCBI Description
                   officinarum]
                   268511
Seq. No.
                   16254 1.R1011
Contig ID
                   uwc700155751.h1
5'-most EST
                   BLASTX
Method
                   g4467147
NCBI GI
                   1288
BLAST score
                   1.0e-142
E value
                   371
Match length
 % identity
                   (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                   268512
 Seq. No.
                   16255_1.R1011
 Contig ID
```

Contig ID 16255_1.R1011
5'-most EST uC-zmflB73046g08b1
Method BLASTX

Method BLASTX
NCBI GI g2252841
BLAST score 494
E value 2.0e-49



Match length 246 % identity 45

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

Seq. No. 268513

Contig ID 16255_2.R1011 5'-most EST hbs701183550.h1

Seq. No. 268514

Contig ID 16260_1.R1011

5'-most EST LIB3088-030-Q1-K1-E1

Seq. No. 268515

Contig ID 16261_1.R1011 5'-most EST nwy700446268.h1

Method BLASTX
NCBI GI g2367392
BLAST score 678
E value 4.0e-71
Match length 284
% identity 49

NCBI Description (U82513) random slug cDNA25 protein [Dictyostelium

discoideum]

Seq. No. 268516

Contig ID 16262 1.R1011

5'-most EST LIB3088-030-Q1-K1-F11

Seq. No. 268517

Contig ID 16264_1.R1011

5'-most EST LIB3088-030-Q1-K1-F5

Method BLASTX
NCBI GI 9730558
BLAST score 475
E value 2.0e-47
Match length 99
% identity 93

NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi_1076636_pir__S48027 ribosomal

protein L34 - common tobacco >gi_2129964_pir__S48028 ribosomal protein L34.e, cytosolic - common tobacco >gi_436030 (L27089) 60S ribosomal protein L34 [Nicotiana tabacum] >gi_436032 (L27107) 60S ribosomal protein L34

[Nicotiana tabacum]

Seq. No. 268518

Contig ID 16272_1.R1011

5'-most EST LIB3088-031-Q1-K1-A11

Seq. No. 268519

Contig ID 16272_2.R1011 5'-most EST cat700018677.r1

Method BLASTX
NCBI GI g3123100
BLAST score 231
E value 3.0e-19
Match length 87
% identity 54



HYPOTHETICAL 15.9 KD PROTEIN C4A8.02C IN CHROMOSOME I NCBI Description >gi 4490640 emb CAB11472.1 (Z98762) SPAC4A8.02c, unknown, len:142aa, similar eg. to YJBQ _ECOLI, P32698, hypothetical 15.7 kd protein, (138aa), fast \overline{a} scores, opt:403, E(): 2.4e-32, (41.0% identity in 134 aa overlap) [Schizosaccharomyces pombe] 268520 Seq. No. 16281 1.R1011 Contig ID LIB3088-031-Q1-K1-F9 5'-most EST BLASTX Method q2827553 NCBI GI BLAST score 187 1.0e-13 E value Match length 136 32 % identity (AL021635) predicted protein [Arabidopsis thaliana] NCBI Description Seq. No. 268521 Contig ID 16283 1.R1011 xsy700212777.hl 5'-most EST BLASTX Method q2980770 NCBI GI BLAST score 287 3.0e-25E value 218 Match length 32 % identity (AL022198) putative protein kinase [Arabidopsis thaliana] NCBI Description Seq. No. 268522 16283 2.R1011 Contig ID 5'-most EST uC-zmflmo17283a02a1 268523 Seq. No. Contig ID 16286 1.R1011 LIB3088-032-Q1-K1-A6 5'-most EST Seq. No. 268524 Contig ID 16287 1.R1011 5'-most EST LIB143-032-Q1-E1-A2 Method BLASTX q4309969 NCBI GI 273 BLAST score 1.0e-23 E value

Match length 128 % identity 45

(AC002983) putative phosphoglyceride transfer protein NCBI Description

[Arabidopsis thaliana]

268525 Seq. No.

16294 1.R1011 Contig ID uC-zmrob73051h05a1 5'-most EST

268526 Seq. No. 16294 2.R1011 Contig ID

LIB3088-032-Q1-K1-G7 5'-most EST



 Seq. No.
 268527

 Contig ID
 16294_3.R1011

 5'-most EST
 uC-zmflb73101g10a1

Seq. No. 268528 Contig ID 16295_1.R1011

5'-most EST LIB3088-033-Q1-K1-A1

Seq. No. 268529

Contig ID 16295_2.R1011

5'-most EST LIB3137-050-Q1-K1-G2

Seq. No. 268530

Contig ID 16295_3.R1011 5'-most EST rvt700552988.h1

Seq. No. 268531

Contig ID 16301_1.R1011 5'-most EST wen700333212.h1

Seq. No. 268532

Contig ID 16303_1.R1011 5'-most EST pmx700082906.h1

Method BLASTX
NCBI GI g3063459
BLAST score 376
E value 9.0e-36
Match length 93
% identity 70

NCBI Description (AC003981) F22013.21 [Arabidopsis thaliana]

Seq. No. 268533

Contig ID 16303_2.R1011 5'-most EST rvt700549594.h1

Seq. No. 268534

Contig ID 16307_1.R1011

5'-most EST LIB3088-033-Q1-K1-D8

Seq. No. 268535

Contig ID 16308_1.R1011

5'-most EST LIB3088-033-Q1-K1-E1

Method BLASTX
NCBI GI g3548815
BLAST score 239
E value 7.0e-20
Match length 72
% identity 58

NCBI Description (AC005313) similar to axoneme-associated protein mst101

[Arabidopsis thaliana]

Seq. No. 268536

Contig ID 16314_1.R1011

5'-most EST LIB3088-033-Q1-K1-F1

Method BLASTX
NCBI GI g4558548
BLAST score 251



4.0e-21 E value 119 Match length 45 % identity (AC007138) putative RNaseP-associated protein [Arabidopsis NCBI Description thaliana] 268537 Seq. No. 16318 1.R1011 Contig ID uC-zmroteosinte062c03b1 5'-most EST 268538 Seq. No. 16320 1.R1011 Contig ID clt700041947.f1 5'-most EST BLASTX Method g3877252 NCBI GI BLAST score 439 5.0e-43 E value 149 Match length 58 % identity NCBI Description (Z93382) F45G2.10 [Caenorhabditis elegans] 268539 Seq. No. 16320 2.R1011 Contig ID LIB3062-019-Q1-K1-F2 5'-most EST BLASTX Method g3877252 NCBI GI 158 BLAST score 2.0e-10 E value 65 Match length 52 % identity (Z93382) F45G2.10 [Caenorhabditis elegans] NCBI Description 268540 Seq. No. 16320 3.R1011 Contig ID 5'-most EST LIB3062-019-Q1-K1-F4 268541 Seq. No. 16328 1.R1011 Contig ID LIB3088-034-Q1-K1-C8 5'-most EST Method BLASTX q3080415 NCBI GI BLAST score 367 8.0e-35 E value Match length 88 77 % identity (AL022604) cysteine proteinase-like protein [Arabidopsis NCBI Description thaliana] 268542 Seq. No. Contig ID 16330 1.R1011 LIB3088-034-Q1-K1-D4 5'-most EST Method BLASTX q4220529 NCBI GI 404BLAST score

37367

4.0e-39

108

69

E value

Match length

% identity



```
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
                  268543
Seq. No.
                  16331 1.R1011
Contig ID
                  LIB3088-034-Q1-K1-E4
5'-most EST
                  268544
Seq. No.
                  16336 1.R1011
Contig ID
                  cjh700193490.h1
5'-most EST
                  BLASTX
Method
                  g2213600
NCBI GI
                  722
BLAST score
                  3.0e-76
E value
                  259
Match length
                  53
% identity
NCBI Description (AC000348) T7N9.20 [Arabidopsis thaliana]
                  268545
Seq. No.
                  16357 1.R1011
Contig ID
                  LIB3156-001-Q1-K1-F8
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3342802
                  1355
BLAST score
                  1.0e-150
E value
                  273
Match length
                  96
% identity
                  (AF061838) putative cytosolic 6-phosphogluconate
NCBI Description
                  dehydrogenase [Zea mays]
                  268546
Seq. No.
Contig ID
                  16358 1.R1011
                  ntr700072628.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q4262161
BLAST score
                   423
                  2.0e-41
E value
                  145
Match length
% identity
NCBI Description (AC005275) SYR1-like syntaxin [Arabidopsis thaliana]
                   268547
Seq. No.
Contig ID
                   16367 1.R1011
                   uC-zmflmo17366c10a1
5'-most EST
                   268548
Seq. No.
Contig ID
                   16375 1.R1011
                   LIB3088-036-Q1-K1-A6
5'-most EST
                   268549
Seq. No.
                   16388 1.R1011
Contig ID
                   wyr700241265.h1
```

5'-most EST BLASTN Method g531832 NCBI GI BLAST score 40 5.0e-13 E value Match length 64 91

% identity





NCBI Description Cloning vector pSport2, complete sequence

Seq. No. 268550

Contig ID 16391 1.R1011

5'-most EST LIB3115-009-Q1-K1-B9

Method BLASTX
NCBI GI g3980378
BLAST score 232
E value 7.0e-19
Match length 113
% identity 45

NCBI Description (AC004561) putative RNA binding protein [Arabidopsis

thaliana]

Seq. No. 268551

Contig ID 16393 1.R1011

5'-most EST uC-zmroteosinte049c06b1

Seq. No. 268552

Contig ID 16394 1.R1011

5'-most EST LIB3061-045-Q1-K1-B6

Seq. No. 268553

Contig ID 16400 1.R1011

5'-most EST LIB3088-039-Q1-K1-B1

Seq. No. 268554

Contig ID 16401_1.R1011 5'-most EST sem700930143.h1

Method BLASTX
NCBI GI g1778095
BLAST score 397

E value 3.0e-38 Match length 123 % identity 65

NCBI Description (U64903) putative sugar transporter; member of major

facilitative superfamily; integral membrane protein [Beta

vulgaris]

Seq. No. 268555

Contig ID 16408 1.R1011

5'-most EST LIB3088-039-Q1-K1-D5

Seq. No. 268556

Contig ID 16413_1.R1011 5'-most EST ceu700430202.h1

Seq. No. 268557

Contig ID 16413 2.R1011

5'-most EST uC-zmroteosinte086a04b1

Seq. No. 268558

Contig ID 16426 1.R1011

5'-most EST uC-zmflmo17020b08b1

Seq. No. 268559

Contig ID 16435 1.R1011

Match length

% identity

151 44



```
xyt700343413.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4006876
                  245
BLAST score
                  2.0e-20
E value
                  104
Match length
                  58
% identity
                 (Z99707) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  268560
Seq. No.
                  16435 2.R1011
Contig ID
                  uC-zmflB73010f09b1
5'-most EST
                  BLASTX
Method
                  g4006876
NCBI GI
                  226
BLAST score
                  3.0e-18
E value
                  92
Match length
                  59
% identity
                  (Z99707) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  268561
Seq. No.
                  16439 1.R1011
Contig ID
                  LIB3088-041-Q1-K1-B4
5'-most EST
                  BLASTX
Method
                  g481526
NCBI GI
BLAST score
                   642
                   3.0e-67
E value
                   138
Match length
                   94
% identity
NCBI Description probable ribosomal protein S1 - wheat mitochondrion
                   268562
Seq. No.
                   16440 1.R1011
Contig ID
                  hbs701183035.h1
5'-most EST
                   268563
Seq. No.
                   16445 1.R1011
Contig ID
                   uC-zmflb73225b11b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q120900
BLAST score
                   269
E value
                   4.0e-23
Match length
                   258
                   30
% identity
                   GALACTOKINASE >gi 421585 pir A47032 galactokinase galK -
NCBI Description
                   Lactobacillus helveticus >gi 44000 emb CAA40525 (X57248)
                   galactokinase [Lactobacillus helveticus]
                   268564
Seq. No.
Contig ID
                   16446 1.R1011
                   tzu700206502.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q629669
BLAST score
                   255
                   7.0e-24
E value
```



NCBI Description hypothetical protein - tomato

Seq. No. 268565

Contig ID 16451 1.R1011

5'-most EST LIB3115-018-P1-K1-E12

Seq. No. 268566

Contig ID 16452 1.R1011 5'-most EST uC-zmflb73039b01b1

Seq. No. 268567

Contig ID 16453 1.R1011

5'-most EST uC-zmflmo17163d09a1

Seq. No. 268568

Contig ID 16459_1.R1011 5'-most EST tzu700203027.h1

Seq. No. 268569

Contig ID 16464 1.R1011

5'-most EST LIB143-040-Q1-E1-B7

Seq. No. 268570

Contig ID 16464 2.R1011 5'-most EST xsy700214749.h1

Seq. No. 268571

Contig ID 16465_1.R1011 5'-most EST xsy700208083.h1

Method BLASTX
NCBI GI g2398829
BLAST score 430
E value 6.0e-42
Match length 106
% identity 81

NCBI Description (Y11220) mitochondrial uncoupling protein [Solanum

tuberosum]

Seq. No. 268572

Contig ID 16471_1.R1011 5'-most EST pmx700085105.h1

Method BLASTN
NCBI GI g1185553
BLAST score 87
E value 4.0e-41
Match length 227
% identity 63

NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)

gene, complete cds

Seq. No. 268573

Contig ID 16474_1.R1011 5'-most EST gwl700612479.h1

Seq. No. 268574

Contig ID 16476 1.R1011

5'-most EST uC-zmroteosinte019a03b1



BLASTX Method NCBI GI q113337 294 BLAST score 8.0e-26 E value Match length 320 28 % identity ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 NCBI Description ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) >gi 111367 pir_S11276 alpha-adaptin c - rat >gi 55729 emb CAA37791 (X53773) alpha-c large chain (AA 1-938) [Rattus norvegicus] 268575 Seq. No. 16476 2.R1011 Contig ID LIB3067-013-Q1-K1-G7 5'-most EST 268576 Seq. No. Contig ID 16477 1.R1011 ntr700075757.h1 5'-most EST Seq. No. 268577 16479 1.R1011 Contig ID 5'-most EST LIB3088-042-Q1-K1-H8 BLASTX Method q2961384 NCBI GI 292 BLAST score 3.0e-26 E value Match length 134 % identity 44 (AL022141) aldehyde dehydrogenase like protein [Arabidopsis NCBI Description thaliana] Seq. No. 268578 16480 1.R1011 Contig ID uC-zmrob73079c10b1 5'-most EST BLASTX Method g2982303 NCBI GI BLAST score 1211 1.0e-133 E value Match length 269 83 % identity (AF051236) hypothetical protein [Picea mariana] NCBI Description 268579 Seq. No. 16483 1.R1011 Contig ID LIB3136-055-Q1-K1-D12 5'-most EST BLASTX Method g4586058 NCBI GI 411 BLAST score 4.0e-40 E value

192 Match length 48 % identity

NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]

268580 Seq. No.

16487_1.R1011 Contig ID



```
dyk700102727.h1
5'-most EST
Seq. No.
                  268581
                  16493 1.R1011
Contig ID
5'-most EST
                  nbm700465228.h1
                  268582
Seq. No.
                  16502 1.R1011
Contig ID
                  LIB3068-016-Q1-K1-A9
5'-most EST
                  268583
Seq. No.
                  16502 2.R1011
Contig ID
                  uC-zm\overline{f}lmo17336c05b1
5'-most EST
                  268584
Seq. No.
                  16502 3.R1011
Contig ID
                  ceu700422641.h1
5'-most EST
Seq. No.
                  268585
                  16507 1.R1011
Contig ID
                  LIB3088-044-Q1-K1-F8
5'-most EST
                   268586
Seq. No.
                   16510 1.R1011
Contig ID
                   cyk70\overline{0}051156.f1
5'-most EST
                   BLASTX
Method
                   g544250
NCBI GI
                   746
BLAST score
                   3.0e-79
E value
Match length
                   200
                   71
% identity
                   ER LUMEN PROTEIN RETAINING RECEPTOR (HDEL RECEPTOR)
NCBI Description
                   >gi 541860 pir A49677 endoplasmic reticulum retention
                   receptor Erd2 - Arabidopsis thaliana
                   268587
Seq. No.
                   16513 1.R1011
Contig ID
5'-most EST
                   dyk700103981.h1
                   BLASTN
Method
NCBI GI
                   g2274996
BLAST score
                   70
                   1.0e-30
E value
                   200
Match length
                   84
% identity
NCBI Description Hordeum vulgare mRNA for expressed sequence tag
                   268588
Seq. No.
                   16537 1.R1011
Contig ID
                   LIB3137-049-Q1-K1-H4
5'-most EST
Method
                   BLASTX
```

Method BLASTX
NCBI GI g1351723
BLAST score 408
E value 1.0e-39
Match length 138
% identity 64

NCBI Description HYPOTHETICAL 35.0 KD PROTEIN C18G6.07C IN CHROMOSOME I



```
268589
Seq. No.
                  16541 1.R1011
Contig ID
                  LIB3088-047-Q1-K1-D3
5'-most EST
Seq. No.
                  268590
                  16543 1.R1011
Contig ID
                  LIB3088-047-Q1-K1-E12
5'-most EST
                  BLASTX
```

Method q4006872 NCBI GI 210 BLAST score 2.0e-16 E value 72 Match length

56 % identity

(Z99707) methionyl aminopeptidase-like protein [Arabidopsis NCBI Description

thaliana]

268591 Seq. No.

16545 1.R1011 Contig ID

5'-most EST LIB3088-047-Q1-K1-E3

268592 Seq. No.

16554 1.R1011 Contig ID

LIB3088-049-Q1-K1-C8 5'-most EST

BLASTN Method NCBI GI g2062705 BLAST score 36

1.0e-10 E value 36 Match length 100 % identity

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

268593 Seq. No.

16555 1.R1011 Contig ID

5'-most EST uC-zmflmo17163d12b1

Method BLASTX NCBI GI g2213592 BLAST score 245 2.0e-20 E value Match length 79 % identity

NCBI Description (AC000348) T7N9.12 [Arabidopsis thaliana]

268594 Seq. No.

16555 2.R1011 Contig ID 5'-most EST dyk700106661.hl

268595 Seq. No.

Contig ID 16555 3.R1011 5'-most EST wty700164661.h1

268596 Seq. No.

16556 1.R1011 Contig ID

LIB3137-011-Q1-K1-H12 5'-most EST

268597 Seq. No.

16556 2.R1011 Contig ID wty700170122.h1 5'-most EST

NCBI Description



```
268598
Seq. No.
Contig ID
                  16561 1.R1011
                  LIB3088-049-Q1-K1-G7
5'-most EST
                  BLASTX
Method
                  q1507699
NCBI GI
BLAST score
                  262
                  2.0e-22
E value
                  126
Match length
% identity
                  50
                  (L81119) COL2 [Arabidopsis thaliana] >gi 1507701 (L81120)
NCBI Description
                  COL2 [Arabidopsis thaliana]
                  268599
Seq. No.
                  16562 1.R1011
Contig ID
5'-most EST
                   xyt700345910.h1
Method
                   BLASTX
NCBI GI
                   g2245131
BLAST score
                   729
                   6.0e-77
E value
Match length
                   235
                   68
% identity
                  (Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   268600
Seq. No.
                   16562 2.R1011
Contig ID
                   LIB3067-025-Q1-K1-H9
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2245131
                   293
BLAST score
                   3.0e-26
E value
                   110
Match length
                   63
% identity
                  (Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   268601
Seq. No.
                   16564 1.R1011
Contig ID
5'-most EST
                   LIB3150-020-Q1-N1-F5
Method
                   BLASTX
                   q3885880
NCBI GI
                   810
BLAST score
                   1.0e-86
E value
                   178
Match length
% identity
                   8.5
                  (AF093628) protochlorophyllide reductase homolog [Oryza
NCBI Description
                   sativa]
                   268602
Seq. No.
                   16568_2.R1011
Contig ID
                   uC-zmrob73022h02a1
5'-most EST
                   BLASTX
Method
                   q1001630
NCBI GI
BLAST score
                   307
                   9.0e-28
E value
                   99
Match length
% identity
```

37375

(D64002) hypothetical protein [Synechocystis sp.]

E value

Match length

% identity

6.0e-46 181

NCBI Description (AC000348) T7N9.20 [Arabidopsis thaliana]

50



```
Seq. No.
                  268603
                  16583 1.R1011
Contig ID
5'-most EST
                  LIB3115-014-P1-K1-G2
Method
                  BLASTX
                  q2494116
NCBI GI
BLAST score
                  191
E value
                  2.0e-15
                  67
Match length
                  55
% identity
                  (AC002376) Similar to Synechocystis hypothetical protein
NCBI Description
                   (gb D90915). [Arabidopsis thaliana]
                  268604
Seq. No.
                  16594 1.R1011
Contig ID
                  LIB83-005-Q1-E1-A4
5'-most EST
Method
                  BLASTX
                  q2143290
NCBI GI
BLAST score
                  217
                   4.0e-17
E value
                  120
Match length
% identity
                 (Z95972) hypothetical protein Rv0669c [Mycobacterium
NCBI Description
                  tuberculosis]
                   268605
Seq. No.
                  16595 1.R1011
Contig ID
                  uC-zmflb73219d12b2
5'-most EST
Method
                  BLASTX
NCBI GI
                   q4138282
BLAST score
                   514
                   6.0e-52
E value
Match length
                   151
                   64
% identity
NCBI Description (AJ011576) RNA-directed RNA polymerase [Nicotiana tabacum]
                   268606
Seq. No.
                   16595 2.R1011
Contig ID
5'-most EST
                   rvt700552643.h1
Method
                   BLASTX
NCBI GI
                   q4138282
                   140
BLAST score
                   7.0e-09
E value
Match length
                   35
% identity
                   63
NCBI Description (AJ011576) RNA-directed RNA polymerase [Nicotiana tabacum]
                   268607
Seq. No.
                   16610 1.R1011
Contig ID
                   uC-zmflB73045b02b1
5'-most EST
                   BLASTX
Method
                   g2213600
NCBI GI
                   463
BLAST score
```



Seq. No. 268608 Contig ID 16624 1.R1011 uC-zmflb73285d02b1 5'-most EST Method BLASTN NCBI GI q3821780 BLAST score 35 E value 5.0e-10 Match length 35 % identity 100 Xenopus laevis cDNA clone 27A6-1 NCBI Description Seq. No. 268609 16624 2.R1011 Contig ID 5'-most EST uC-zmflb73199h12b1 Seq. No. 268610 Contig ID 16626 1.R1011 LIB3279-055-P1-K1-E4 5'-most EST 268611 Seq. No. 16627 1.R1011 Contig ID wyr700243535.hl 5'-most EST Method BLASTX g2055374 NCBI GI BLAST score 1449 1.0e-161 E value Match length 319 % identity 85 (U29095) serine-threonine protein kinase [Triticum NCBI Description aestivum] 268612 Seq. No. Contig ID 16628 1.R1011 uwc700154446.h1 5'-most EST BLASTX Method g4263507 NCBI GI BLAST score 519 1.0e-75 E value Match length 554 % identity 32 NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana] Seq. No. 268613 16629 1.R1011 Contig ID $uC-zm\overline{f}1b73224d01b2$ 5'-most EST BLASTX Method NCBI GI g4115379 358 BLAST score

E value 8.0e - 34155 Match length

(AC005967) putative carbonyl reductase [Arabidopsis NCBI Description

thaliana]

268614 Seq. No.

% identity

16629_2.R1011 Contig ID



LIB3115-006-Q1-K1-F2 5'-most EST Method BLASTX g4115379 NCBI GI BLAST score 295 3.0e-26 E value 183 Match length 37 % identity (AC005967) putative carbonyl reductase [Arabidopsis NCBI Description thaliana] 268615 Seq. No. 16631 1.R1011 Contig ID $uC-zm\overline{f}lmo17060e07b1$ 5'-most EST BLASTX Method q128350 NCBI GI BLAST score 2599 E value 0.0e + 00503 Match length % identity 98 NCBI Description FERREDOXIN--NITRITE REDUCTASE PRECURSOR 268616 Seq. No. 16645 1.R1011 Contig ID 5'-most EST ymt700220132.h1 Method BLASTX NCBI GI g2130099 BLAST score 943 E value 1.0e-102 Match length 252 76 % identity NCBI Description acetyl-CoA carboxylase (EC 6.4.1.2) - wheat >gi_514306 (U10187) acetyl-CoA carboxylase [Triticum aestivum] 268617 Seq. No. 16647 1.R1011 Contig ID LIB3115-034-P1-K2-B7 5'-most EST 268618 Seq. No. 16663 1.R1011 Contig ID LIB189-024-Q1-E1-D7 5'-most EST BLASTX Method g3800853 NCBI GI 2119 BLAST score 0.0e+00E value 429 Match length 96 % identity NCBI Description (AF084478) ribulose-1,5-bisphosphate carboxylase/oxygenase activase precursor [Zea mays]

268619 Seq. No.

16663 2.R1011 Contig ID

LIB3115-036-P1-K2-G10 5'-most EST

Method BLASTX g3800853 NCBI GI BLAST score 236 1.0e-19 E value 49 Match length



% identity

NCBI Description (AF084478) ribulose-1,5-bisphosphate carboxylase/oxygenase

activase precursor [Zea mays]

Seq. No.

268620

Contig ID

16665 1.R1011

5'-most EST

 $xmt70\overline{0}262287.h1$

Seq. No.

268621

Contig ID

16667 1.R1011

5'-most EST

 $uC-zm\overline{f}lmo17154e05b1$

Method NCBI GI BLASTX q399942

BLAST score

1037

E value

Match length

1.0e-113

% identity

245 86

NCBI Description

CHLOROPLAST STROMA 70 KD HEAT SHOCK-RELATED PROTEIN

PRECURSOR >gi_421881_pir S32818 heat shock protein, 70K, chloroplast - garden pea >gi 169023 (L03299) 70 kDa heat shock protein [Pisum sativum] >gi 871515 emb CAA49147 (X69213) Psst70 (stress 70 protein) [Pisum sativum]

Seq. No.

268622

Contig ID

16667 3.R1011

5'-most EST

LIB3060-006-Q1-K1-C8

Seq. No.

268623

Contig ID

16669 1.R1011

5'-most EST

fwa700100205.h1

Method NCBI GI BLASTX q4217999

BLAST score

695

E value

5.0e-73

Match length

156

% identity

NCBI Description

(AC006135) putative ubiquitin--protein ligase

(ubiquitin-conjugating enzyme) [Arabidopsis thaliana]

Seq. No.

268624

Contig ID

16687 1.R1011

5'-most EST

LIB189-010-Q1-E1-A5

Seq. No.

268625

Contig ID

16698 1.R1011

5'-most EST

LIB3067-032-Q1-K1-D9

Seq. No.

268626

Contig ID

16699 1.R1011

5'-most EST

uC-zmflmo17286f02b1

Seq. No.

268627

Contig ID

16704 1.R1011

5'-most EST

LIB3115-011-Q1-K1-F1

Seq. No.

268628

Contig ID

16713 1.R1011



5'-most EST LIB36-001-Q1-E1-G6 Method BLASTX NCBI GI q1780757 BLAST score 207 E value 3.0e-16 64 Match length 59 % identity (Y10291) highly expressed in proliferating cells NCBI Description [Arabidopsis thaliana] 268629 Seq. No. 16714 1.R1011 Contig ID 5'-most EST LIB3115-011-Q1-K1-G8 268630 Seq. No. 16722 1.R1011 Contig ID 5'-most EST LIB3069-048-Q1-K1-B7 BLASTX Method NCBI GI q3337435 BLAST score 149 4.0e-09 E value Match length 34 85 % identity (AF060198) PsbY precursor; putative photosytem II peptide NCBI Description [Spinacia oleracea] Seq. No. 268631 Contig ID 16722 2.R1011 5'-most EST LIB84-013-Q1-E1-A12 268632 Seq. No. Contig ID 16722 3.R1011 LIB84-028-Q1-E1-A8 5'-most EST Method BLASTX g3337435 NCBI GI BLAST score 154 4.0e-10 E value Match length 35 % identity 86 (AF060198) PsbY precursor; putative photosytem II peptide NCBI Description [Spinacia oleracea] 268633 Seq. No. 16722 5.R1011 Contig ID LIB3179-002-P1-K1-B12 5'-most EST BLASTX Method g3337435 NCBI GI

Method BLASTX
NCBI GI g3337435
BLAST score 160
E value 6.0e-11
Match length 49
% identity 34

NCBI Description (AF060198) PsbY precursor; putative photosytem II peptide

[Spinacia oleracea]

Seq. No. 268634

Contig ID 16722_6.R1011 5'-most EST ceu700423933.h1



```
268635
Seq. No.
Contig ID
                  16724 1.R1011
                  LIB3115-011-Q1-K1-C1
5'-most EST
                  268636
Seq. No.
Contig ID
                  16728 1.R1011
                  uC-zmflb73030d03b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2895276
BLAST score
                  172
                  1.0e-11
E value
Match length
                  176
                  32
% identity
                  (AF026029) poly(A) binding protein II [Homo sapiens]
NCBI Description
Seq. No.
                  268637
                  16728 2.R1011
Contig ID
5'-most EST
                  LIB3062-034-Q1-K1-D9
                  268638
Seq. No.
                  16736 1.R1011
Contig ID
                  mwy700442424.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q4469021
BLAST score
                   646
                   2.0e-67
E value
Match length
                   181
% identity
                   70
                  (AL035602) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   268639
Seq. No.
                   16737 1.R1011
Contig ID
5'-most EST
                   xsy700217258.h1
                   BLASTX
Method
                   g2673904
NCBI GI
                   221
BLAST score
                   1.0e-17
E value
Match length
                   154
% identity
                   38
                  (AC002561) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   268640
Seq. No.
                   16740 1.R1011
Contig ID
                   LIB3115-011-Q1-K1-A2
5'-most EST
                   268641
Seq. No.
                   16742_1.R1011
Contig ID
                   LIB3067-013-Q1-K1-A12
5'-most EST
```

Seq. No. 268642

Contig ID 16742_2.R1011 5'-most EST hbs701186021.h1

Seq. No. 268643 Contig ID 16744_1.R1011 5'-most EST fC-zmro700453286f1



Method BLASTX
NCBI GI g2947070
BLAST score 283
E value 6.0e-25
Match length 163
% identity 36

NCBI Description (AC002521) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 268644

Contig ID 16746 1.R1011

5'-most EST LIB189-026-Q1-E1-G1

Seq. No. 268645

Contig ID 16746_2.R1011 5'-most EST tzu700206362.h1

Seq. No. 268646

Contig ID 16765_1.R1011 5'-most EST nbm700475425.h1

Method BLASTX
NCBI GI g3913791
BLAST score 1976
E value 0.0e+00
Match length 436
% identity 83

NCBI Description GLUTAMATE--CYSTEINE LIGASE PRECURSOR

(GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi_2407615 (AF017983) gamma-glutamylcysteine synthetase

[Lycopersicon esculentum]

Seq. No. 268647

Contig ID 16765_2.R1011 5'-most EST ymt700221284.h1

Method BLASTX
NCBI GI g3913791
BLAST score 164
E value 3.0e-13
Match length 42
% identity 93

NCBI Description GLUTAMATE--CYSTEINE LIGASE PRECURSOR

(GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi_2407615 (AF017983) gamma-glutamylcysteine synthetase

[Lycopersicon esculentum]

Seq. No. 268648

Contig ID 16765_3.R1011

5'-most EST LIB3150-021-Q1-N1-D11

Method BLASTX
NCBI GI g3941322
BLAST score 324
E value 5.0e-30
Match length 86
% identity 73

NCBI Description (AF041340) gamma-glutamylcysteine synthetase [Medicago

truncatula]



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268649
Seq. No.
Contig ID
                  16766 1.R1011
                  uC-zmflb73232a01b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2723471
BLAST score
                  1154
                  1.0e-127
E value
Match length
                  255
                  81
% identity
                 (D87819) sucrose transporter [Oryza sativa]
NCBI Description
                  268650
Seq. No.
Contig ID
                  16766 2.R1011
                  LIB3068-011-Q1-K1-F4
5'-most EST
Method
                  BLASTX
                  g2723471
NCBI GI
BLAST score
                  434
                  5.0e-43
E value
Match length
                  103
                  77
% identity
NCBI Description (D87819) sucrose transporter [Oryza sativa]
                  268651
Seq. No.
                  16776 1.R1011
Contig ID
                  LIB3061-058-Q1-K1-G12
5'-most EST
                  BLASTX
Method
                  g3668087
NCBI GI
                   256
BLAST score
E value
                   8.0e-22
Match length
                   63
% identity
NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]
                   268652
Seq. No.
                   16786 1.R1011
Contig ID
                   LIB3115-009-Q1-K1-H8
5'-most EST
                   268653
Seq. No.
Contig ID
                   16788 1.R1011
5'-most EST
                   zla700379903.h1
                   268654
Seq. No.
                   16792 1.R1011
Contig ID
                   uwc700154343.h1
5'-most EST
Method
                   BLASTX
                   g2262100
NCBI GI
                   788
BLAST score
                   2.0e-84
E value
                   172
Match length
```

% identity 83

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

268655 Seq. No.

16797 1.R1011 Contig ID

uC-zmroteosinte015h07b1 5'-most EST

BLASTX Method NCBI GI g3790587



BLAST score 237 8.0e-20 E value Match length 94 53 % identity NCBI Description

(AF079182) RING-H2 finger protein RHF2a [Arabidopsis

thaliana]

268656

Seq. No. Contig ID 5'-most EST

16799 1.R1011 pmx700086359.h1

Method BLASTX NCBI GI g1652297 172 BLAST score 7.0e-12 E value Match length 124 % identity 33

(D90904) hypothetical protein [Synechocystis sp.] NCBI Description

Seq. No.

268657

Contiq ID 16801 1.R1011

LIB3115-009-Q1-K1-G10 5'-most EST

Method BLASTX NCBI GI q82080 BLAST score 316 7.0e-29 E value 119 Match length 52 % identity

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

>gi 226872 prf 1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

268658 Seq. No.

Contig ID 16808 1.R1011

5'-most EST LIB84-028-Q1-E1-G12

BLASTX Method NCBI GI g1652217 BLAST score 396 E value 4.0e-38 Match length 253 % identity

NCBI Description (D90903) hypothetical protein [Synechocystis sp.]

268659 Seq. No.

16813 1.R1011 Contig ID

LIB3115-009-Q1-K1-D11 5'-most EST

Seq. No. 268660

Contig ID 16826 1.R1011 5'-most EST uwc700150644.h1

268661 Seq. No.

16830 1.R1011 Contig ID 5'-most EST uC-zmflb73217e01b2

Method BLASTX NCBI GI g4324597 BLAST score 1338 E value 1.0e-148



Match length 406 % identity 64

NCBI Description (AF106324) sodium proton exchanger Nhx1 [Arabidopsis

thaliana]

Seq. No. 268662

Contig ID 16836_1.R1011 5'-most EST wyr700242304.h1

Method BLASTX
NCBI GI 94510395
BLAST score 1755
E value 0.0e+00
Match length 558
% identity 62

NCBI Description (AC006587) putative beta-galactosidase precursor

[Arabidopsis thaliana]

Seq. No. 268663

Contig ID 16837 1.R1011

5'-most EST uC-zmflmo17070b09a1

Seq. No. 268664

Contig ID 16858_1.R1011 5'-most EST xmt700266862.h1

Method BLASTX
NCBI GI g3150415
BLAST score 705
E value 3.0e-74
Match length 210
% identity 63

NCBI Description (AC004165) sec13-related protein [Arabidopsis thaliana]

>gi_3420046 (AC004680) sec13-related protein [Arabidopsis

thaliana]

Seq. No. 268665

Contig ID 16858_2.R1011 5'-most EST wyr700240675.h1

Seq. No. 268666

Contig ID 16861_1.R1011 5'-most EST uC-zmroB73013h09b1

Method BLASTX
NCBI GI g4337195
BLAST score 1173

BLAST score 1173 E value 1.0e-129 Match length 265 % identity 83

NCBI Description (AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No. 268667

Contig ID 16861 2.R1011

5'-most EST LIB3115-007-Q1-K1-H2

Method BLASTX
NCBI GI g4337195
BLAST score 190
E value 4.0e-14
Match length 46



% identity 72

NCBI Description (AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No. 268668

Contig ID 16861 3.R1011

5'-most EST LIB3116-018-P1-K1-F11

Seq. No. 268669

Contig ID 16872_1.R1011 5'-most EST xjt700094563.h1

Method BLASTX
NCBI GI g1086757
BLAST score 284
E value 5.0e-25
Match length 196
% identity 44

NCBI Description (U41037) coded for by C. elegans cDNA yk41a1.3; coded for

by C. elegans cDNA yk128e3.3; coded for by C. elegans cDNA yk37c8.3; coded for by C. elegans cDNA CEESB01F; coded for by C. elegans cDNA CEESG45F; coded for by C. elegans cDNA

CEESG45

Seq. No. 268670

Contig ID 16877 1.R1011

5'-most EST LIB189-022-Q1-E1-H10

Method BLASTX
NCBI GI g444344
BLAST score 565
E value 3.0e-58
Match length 101
% identity 100

NCBI Description thaumatin-like protein [Zea mays]

Seq. No. 268671

Contig ID 16883_1.R1011 5'-most EST LIB83-008-Q1-E1-A11

Method BLASTX
NCBI GI g3935169
BLAST score 286
E value 2.0e-25
Match length 68
% identity 81

NCBI Description (AC004557) F17L21.12 [Arabidopsis thaliana]

Seq. No. 268672

Contig ID 16883 2.R1011

5'-most EST LIB3181-007-P1-K2-E6

Method BLASTX
NCBI GI g3935169
BLAST score 157
E value 2.0e-10
Match length 33
% identity 91

NCBI Description (AC004557) F17L21.12 [Arabidopsis thaliana]

Seq. No. 268673

Contig ID 16883_3.R1011



5'-most EST uC-zmroteosinte100g01b2

Method BLASTX
NCBI GI g3935169
BLAST score 285
E value 2.0e-25
Match length 68
% identity 82

NCBI Description (AC004557) F17L21.12 [Arabidopsis thaliana]

Seq. No. 268674

Contig ID 16885_1.R1011 5'-most EST uC-zmrob73004e08b1

Method BLASTX
NCBI GI g1778093
BLAST score 858
E value 4.0e-92
Match length 301
% identity 59

NCBI Description (U64902) putative sugar transporter; member of major

facilitative superfamily; integral membrane protein [Beta

vulgaris]

Seq. No. 268675

Contig ID 16892_1.R1011 5'-most EST ymt700220061.h1

Method BLASTX
NCBI GI g4512651
BLAST score 767
E value 2.0e-81
Match length 245
% identity 55

NCBI Description (AC007048) putative tyrosine transaminase [Arabidopsis

thaliana]

Seq. No. 268676

Contig ID 16895_1.R1011 5'-most EST tzu700202409.h1

Method BLASTX
NCBI GI g3980402
BLAST score 327
E value 4.0e-30
Match length 170
% identity 44

NCBI Description (AC004561) putative tropinone reductase [Arabidopsis

thaliana]

Seq. No. 268677

Contig ID 16898_1.R1011

5'-most EST LIB3115-006-Q1-K1-C11

Seq. No. 268678

Contig ID 16905 1.R1011

5'-most EST uC-zmflmo17160g12b1

Method BLASTX
NCBI GI g4239845
BLAST score 1325
E value 1.0e-146



Match length 494 % identity 56

NCBI Description (AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No. 268679

Contig ID 16905 2.R1011

5'-most EST LIB3066-007-Q1-K1-H5

Seq. No. 268680

Contig ID 16905 3.R1011

5'-most EST uC-zmflmo17287b11b1

Seq. No. 268681

Contig ID 16905 4.R1011

5'-most EST LIB3136-033-Q1-K1-A1

Seq. No. 268682

Contig ID 16905_5.R1011

5'-most EST uC-zmflb73346h09a2

Seq. No. 268683

Contig ID 16905_10.R1011 5'-most EST nbm700465006.h1

Seq. No. 268684

Contig ID 16911 1.R1011

5'-most EST LIB3115-006-Q1-K1-B8

Seq. No. 268685

Contig ID 16920_1.R1011 5'-most EST fdz701167015.h1

Method BLASTX
NCBI GI g2809251
BLAST score 189
E value 5.0e-14
Match length 113
% identity 38

NCBI Description (AC002560) F21B7.20 [Arabidopsis thaliana]

Seq. No. 268686

Contig ID 16922 1.R1011

5'-most EST LIB3115-005-Q1-K1-E10

Seq. No. 268687

Contig ID 16922 2.R1011 5'-most EST vfk700404836.h1

Seq. No. 268688

Contig ID 16923_1.R1011

5'-most EST LIB3115-005-Q1-K1-E11

Method BLASTX
NCBI GI g1710503
BLAST score 225
E value 2.0e-18
Match length 63
% identity 67

NCBI Description PROBABLE 60S RIBOSOMAL PROTEIN L18 (RP28)



>gi_2130477_pir__S67377 ribosomal protein L18.e, cytosolic
- fission yeast (Schizosaccharomyces pombe)
>gi_3560198_emb_CAA20689_ (AL031528) 60s ribosomal protein
118 [Schizosaccharomyces pombe]

 Seq. No.
 268689

 Contig ID
 16930_1.R1011

 5'-most EST
 LIB143-042-Q1-E1-D11

 Method
 BLASTX

 NCBI GI
 g100883

 BLAST score
 618

BLAST score 618
E value 3.0e-64
Match length 134
% identity 90

NCBI Description heat shock protein 17.2 - maize >gi_22335_emb_CAA46641_

(X65725) heat shock protein 17.2 [Zea mays]

Seq. No. 268690 Contin ID 16930 2.F

Contig ID 16930 2.R1011 5'-most EST xmt700264021.h1

Method BLASTX
NCBI GI g100883
BLAST score 562
E value 2.0e-57
Match length 154
% identity 71

NCBI Description heat shock protein 17.2 - maize >gi_22335_emb_CAA46641_

(X65725) heat shock protein 17.2 [Zea mays]

Seq. No. 268691

Contig ID 16930_3.R1011

5'-most EST LIB143-063-Q1-E1-A7

Method BLASTX
NCBI GI g100883
BLAST score 348
E value 6.0e-64
Match length 153
% identity 90

NCBI Description heat shock protein 17.2 - maize >gi_22335_emb_CAA46641_

(X65725) heat shock protein 17.2 [Zea mays]

Seq. No. 268692

Contig ID 16930_4.R1011 5'-most EST nbm700467566.h1

Method BLASTX
NCBI GI g123543
BLAST score 597
E value 1.0e-61
Match length 155
% identity 77

NCBI Description 16.9 KD CLASS I HEAT SHOCK PROTEIN >gi_82480_pir__\$20874 heat shock protein - rice >gi_20265_emb_CAA43210_ (X60820)

16.9 KD low molecular weight heat shock protein [Oryza sativa] >gi_169797 (M80938) 16.9 kDa heat shock protein [Oryza sativa] >gi_445139_prf__1908439A heat shock protein

16.9A [Oryza sativa]



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Seq. No.
                  268693
                  16930 5.R1011
Contig ID
5'-most EST
                  LIB143-046-Q1-E1-D2
Method
                  BLASTX
NCBI GI
                  q100883
BLAST score
                  443
                  5.0e-44
E value
                  98
Match length
                  88
% identity
                  heat shock protein 17.2 - maize >gi 22335 emb CAA46641
NCBI Description
                  (X65725) heat shock protein 17.2 [Zea mays]
                  268694
Seq. No.
                  16930 6.R1011
Contig ID
5'-most EST
                  uC-zmflmo17132a12b1
Method
                  BLASTX
                  g2738511
NCBI GI
BLAST score
                  226
                  1.0e-18
E value
Match length
                  92
                  57
% identity
                  (AF007762) heat shock protein 16.5 [Agrostis stolonifera
NCBI Description
                  var. palustris]
                  268695
Seq. No.
Contig ID
                  16930 7.R1011
                  LIB143-065-Q1-E1-E4
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1122317
                  149
BLAST score
                  1.0e-09
E value
                  53
Match length
                  58
% identity
NCBI Description
                  (X94193) heat shock protein 17.9 [Pennisetum glaucum]
                  268696
Seq. No.
                  16944 1.R1011
Contig ID
5'-most EST
                  LIB3060-054-Q1-K1-C3
Method
                  BLASTX
NCBI GI
                  g4507711
BLAST score
                  191
                  4.0e-14
E value
Match length
                  102
                  41
% identity
                  tetratricopeptide repeat domain 1 >gi 1688074 (U46570)
NCBI Description
                  tetratricopeptide repeat protein [Homo sapiens]
Seq. No.
                  268697
Contig ID
                  16944 2.R1011
5'-most EST
                  LIB3115-003-Q1-K1-H7
                  268698
Seq. No.
```

Contig ID 16947 1.R1011

5'-most EST uC-zmflmo17218a07a1

BLASTX Method NCBI GI q2130082 BLAST score 168



E value 1.0e-11 Match length 108 % identity 33

NCBI Description protein kinase Xa21 (EC 2.7.1.-) - rice >gi_1122443 (U37133) receptor kinase-like protein [Oryza sativa] >gi 2586085 (U72723) receptor kinase-like protein [Oryza

longistaminata] >gi_1586408_prf__2203451A receptor

kinase-like protein [Oryza sativa]

Seq. No. 268699

Contig ID 16950 1.R1011

5'-most EST LIB $30\overline{6}0-020-Q1-K1-F8$

Method BLASTX
NCBI GI g114181
BLAST score 874
E value 2.0e-96
Match length 320
% identity 58

NCBI Description 3-DEHYDROQUINATE SYNTHASE >gi 68385_pir__SYECQ

3-dehydroquinate synthase (EC 4.6.1.3) - Escherichia coli >gi 40968 emb CAA27495 (X03867) 3-dehydroquinate synthase (aa 1-362) [Escherichia coli] >gi 41225 emb CAA79666 (Z19601) ORF, aroB. Millar G., Coggins J.R.; FEBS Lett. 200:11-17(1986) [Escherichia coli] >gi 606323 (U18997) 3-dehydroquinate synthase [Escherichia coli] >gi 1789791 (AE000414) 3-dehydroquinate synthase [Escherichia coli]

Seq. No. 268700

Contig ID 16954_1.R1011

5'-most EST LIB3115-005-Q1-K1-A2

Seq. No. 268701

Contig ID 16954_2.R1011 5'-most EST wty700162880.h1

Seq. No. 268702

Contig ID 16958 1.R1011

5'-most EST LIB3115-003-Q1-K1-G1

Seq. No. 268703

Contig ID 16959_1.R1011 5'-most EST LIB3180-048-P2-D1

Method BLASTX
NCBI GI g3928150
BLAST score 686
E value 3.0e-72
Match length 197
% identity 68

NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]

Seq. No. 268704

Contig ID 16959_2.R1011 5'-most EST wen700332167.h1

Method BLASTX NCBI GI g3928150 BLAST score 394 E value 4.0e-44



Match length 129
% identity 72
NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]
Seq. No. 268705

Contig ID 16962 1.R1011

5'-most EST LIB143-060-Q1-E1-C12

Method BLASTX
NCBI GI g3461820
BLAST score 594
E value 3.0e-61
Match length 182
% identity 63

NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]

 Seq. No.
 268706

 Contig ID
 16963_1.R1011

 5'-most EST
 uC-zmflmo17246g08b1

 Method
 BLASTX

NCBI GI g3063693
BLAST score 310
E value 1.0e-29
Match length 89
% identity 70

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 268707 Contig ID 16967_1.R1011

5'-most EST LIB3115-003-Q1-K1-E4

Method BLASTX
NCBI GI g166949
BLAST score 341
E value 9.0e-32
Match length 126
% identity 53

NCBI Description (M32885) cytochrome P-450LXXIA1 (cyp71A1) [Persea

americana]

Seq. No. 268708

Contig ID 16973_1.R1011

5'-most EST LIB3116-018-P1-K1-E12

Seq. No. 268709

Contig ID 16975_1.R1011

5'-most EST LIB3115-003-Q1-K1-B10

Method BLASTX
NCBI GI g2443857
BLAST score 802
E value 1.0e-85
Match length 148
% identity 96

NCBI Description (U79961) vacuolar sorting receptor homolog [Zea mays]

Seq. No. 268710

Contig ID 16977_1.R1011 5'-most EST uC-zmflb73126d11b1



Seq. No. 268711 Contig ID 16990 1.R1011 5'-most EST LIB3181-010-P1-K2-G1 Method BLASTX NCBI GI q3608139 BLAST score 242 2.0e-20 E value Match length 64 73 % identity

(AC005314) putative fibrillin [Arabidopsis thaliana] NCBI Description

Seq. No. 268712

Contig ID 16991 1.R1011 5'-most EST uC-zmflb73196f12b1

268713 Seq. No.

Contig ID 16995 1.R1011

5'-most EST LIB3279-015-P1-K1-C5

Method BLASTX q100099 NCBI GI BLAST score 288 3.0e-25 E value 114 Match length % identity 50

DNA-binding protein VBP1 - fava bean >gi 1372966 (M81827) NCBI Description

CREB-like protein [Vicia faba]

268714 Seq. No.

Contig ID 16995 3.R1011

5'-most EST LIB3061-002-Q1-K2-D5

Method BLASTN NCBI GI g2351061 BLAST score 35 E value 5.0e-10 59 Match length

90 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MAF19, complete sequence [Arabidopsis thaliana]

Seq. No. 268715

16995 4.R1011 Contig ID $uC-zm\overline{f}lmo17036h02a1$ 5'-most EST

268716 Seq. No.

17002 1.R1011 Contig ID 5'-most EST uC-zmflb73266a11b2

Method BLASTX NCBI GI q4006886 992 BLAST score E value 1.0e-108 261 Match length

% identity

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

268717 Seq. No.

17008 1.R1011 Contig ID 5'-most EST $nbm70\overline{0}468531.h1$



Method BLASTX
NCBI GI g2501021
BLAST score 504
E value 8.0e-51
Match length 195
% identity 58

NCBI Description LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS)

>gi 1652562 dbj BAA17483_ (D90906) lysyl-tRNA synthetase

[Synechocystis sp.]

Seq. No. 268718

Contig ID 17012 1.R1011

5'-most EST LIB3115-002-Q1-K1-C7

Method BLASTX
NCBI GI g2191197
BLAST score 335
E value 4.0e-31
Match length 105
% identity 66

NCBI Description (AF007271) contains similarity to Synechococcus PCC7942

chromosomal region used as basis of neutral siteII

recombinational cloning vector (PID:g1174192) [Arabidopsis

thaliana]

Seq. No. 268719

Contig ID 17012_2.R1011

5'-most EST LIB189-008-Q1-E1-B12

Method BLASTX
NCBI GI g2191197
BLAST score 487
E value 6.0e-49
Match length 175
% identity 58

NCBI Description (AF007271) contains similarity to Synechococcus PCC7942

chromosomal region used as basis of neutral siteII

recombinational cloning vector (PID:g1174192) [Arabidopsis

thaliana]

Seq. No. 268720

Contig ID 17016 1.R1011

5'-most EST LIB3115-002-Q1-K1-D4

Seq. No. 268721

Contig ID 17021_1.R1011 5'-most EST LIB83-005-Q1-E1-D1

Method BLASTX
NCBI GI g2344897
BLAST score 370
E value 5.0e-35
Match length 173
% identity 44

NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 268722

Contig ID 17022_1.R1011 5'-most EST wen700335196.h1



Seq. No. 268723

Contig ID 17023 1.R1011 gct701172412.h1 5'-most EST

Seq. No. 268724

17026 1.R1011 Contig ID

LIB3150-001-Q1-N1-D6 5'-most EST

Method BLASTX q1839589 NCBI GI BLAST score 1444 1.0e-160 E value 295 Match length 93 % identity

(S82314) PRm 3=chitinase {clone CHEM 5} [Zea mays=maize, NCBI Description

cv. INRA 258, mercuric chloride-treated, leaves, Peptide,

294 aa] [Zea mays]

268725 Seq. No.

Contig ID 17027 1.R1011

5'-most EST LIB3137-020-Q1-K1-G10

Seq. No. 268726

17033 1.R1011 Contig ID

5'-most EST uC-zmroteosinte008h02b1

Method BLASTX q799369 NCBI GI BLAST score 1156 1.0e-127 E value Match length 330 % identity

NCBI Description

(U25111) metalloendopeptidase [Pisum sativum]

Seq. No. 268727

Contig ID 17033 2.R1011

5'-most EST LIB3115-002-Q1-K1-C12

268728 Seq. No.

17034 1.R1011 Contig ID 5'-most EST $xmt70\overline{0}267546.h1$

Method BLASTX NCBI GI g2459445 BLAST score 460 2.0e-45 E value Match length 180 % identity 35

(AC002332) putative ribonucleoprotein [Arabidopsis NCBI Description

thaliana]

268729 Seq. No.

17034 2.R1011 Contig ID 5'-most EST xjt700092367.h1

268730 Seq. No.

17041 1.R1011 Contig ID

LIB3115-001-Q1-K1-H10 5'-most EST

268731 Seq. No.



Contig ID 17044 1.R1011

5'-most EST LIB3115-001-Q1-K1-H9

268732 Seq. No.

17045 1.R1011 Contig ID

uC-zmflmo17193g07b1 5'-most EST

268733 Seq. No.

17048 1.R1011 Contig ID

LIB3137-014-Q1-K1-A1 5'-most EST

Method BLASTX NCBI GI g4581163 BLAST score 242 2.0e-20 E value Match length 81 60 % identity

(AC006220) unknown protein [Arabidopsis thaliana] NCBI Description

268734 Seq. No.

17048 2.R1011 Contig ID

5'-most EST LIB189-021-Q1-E1-F11

Method BLASTX NCBI GI g4581163 BLAST score 304 2.0e-27 E value Match length 85 % identity 78

NCBI Description (AC006220) unknown protein [Arabidopsis thaliana]

268735 Seq. No.

17052 1.R1011 Contig ID 5'-most EST LIB36-008-Q1-E1-H1

Method BLASTX NCBI GI g1402889 BLAST score 221 E value 7.0e-18 Match length 58

% identity 71

NCBI Description (X98130) unknown [Arabidopsis thaliana]

268736 Seq. No.

Contig ID 17052 2.R1011 5'-most EST ceu700428938.h1

268737 Seq. No.

Contig ID 17055_1.R1011

5'-most EST LIB3115-001-Q1-K1-E8

Seq. No. 268738

17064_1.R1011 Contig ID 5'-most EST hvj700619188.h1

Seq. No. 268739

17065 1.R1011 Contig ID

LIB3115-001-Q1-K1-C3 5'-most EST

Method BLASTX NCBI GI g2827667



BLAST score 535 E value 2.0e-54 Match length 161 % identity 65

NCBI Description (AL021637) hypothetical protein [Arabidopsis thaliana]

>gi 2982430 emb CAA18238 (AL022224) hypothetical protein

[Arabidopsis thaliana]

Seq. No. 268740

Contig ID 17066 1.R1011

5'-most EST LIB3068-007-Q1-K1-F5

Method BLASTX
NCBI GI g1172861
BLAST score 1020
E value 1.0e-113
Match length 228
% identity 89

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR

(RUBISCO LARGE SUBUNIT) >gi 1363613 pir S58560

ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain

- maize chloroplast >gi_18036_emb_CAA78027_ (Z11973)

Ribulose bisphosphate carboxylase [Zea mays]

>gi_902230_emb_CAA60294 (X86563) rubisco large subunit

[Zea mays]

Seq. No. 268741

Contig ID 17066_2.R1011 5'-most EST uC-zmflb73136d12b1

Method BLASTX
NCBI GI g1172861
BLAST score 381
E value 2.0e-36
Match length 91
% identity 79

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN PRECURSOR

(RUBISCO LARGE SUBUNIT) >gi 1363613 pir S58560

ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain

- maize chloroplast >gi 18036 emb CAA78027 (Z11973)

Ribulose bisphosphate carboxylase [Zea mays]

>gi 902230 emb CAA60294 (X86563) rubisco large subunit

[Zea mays]

Seq. No. 268742

Contig ID 17082 1.R1011

5'-most EST LIB3115-001-Q1-K1-B7

Seq. No. 268743

Contig ID 17082 2.R1011

5'-most EST LIB189-025-Q1-E1-E12

Seq. No. 268744

Contig ID 17083_1.R1011

5'-most EST LIB3115-001-Q1-K1-A11

Seq. No. 268745

Contig ID 17084 1.R1011

5'-most EST LIB31 $\overline{1}$ 5-022-P1-K1-F8



Seq. No. 268746

Contig ID 17087_1.R1011 5'-most EST vux700162283.h1

Seq. No. 268747

Contig ID 17089 1.R1011

5'-most EST LIB3115-001-Q1-K1-D3

Method BLASTX
NCBI GI g4322327
BLAST score 280
E value 1.0e-29
Match length 130

% identity 47

NCBI Description (AF080545) peptide transporter [Nepenthes alata]

Seq. No. 268748

Contig ID 17099 1.R1011 5'-most EST xjt700093345.h1

Method BLASTN
NCBI GI g4140643
BLAST score 72
E value 3.0e-32
Match length 124
% identity 90

NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

Seq. No. 268749

Contig ID 17101_1.R1011

5'-most EST LIB3066-053-Q1-K1-A4

Method BLASTX
NCBI GI g1168607
BLAST score 402
E value 1.0e-38
Match length 191
% identity 49

NCBI Description AUXIN-INDUCED PROTEIN AUX2-11 >gi 16197 emb CAA37526

(X53435) Aux2-11 protein [Arabidopsis thaliana] >gi_454285 (L15450) auxin-responsive protein [Arabidopsis thaliana]

Seq. No. 268750

Contig ID 17101 2.R1011

5'-most EST LIB3150-048-Q1-N1-A3

Seq. No. 268751

Contig ID 17101_5.R1011 5'-most EST tzu700201489.h1

Seq. No. 268752

Contig ID 17101_6.R1011 5'-most EST wyr700243638.h1

Seq. No. 268753

Contig ID 17103_1.R1011 5'-most EST ceu700430366.h1

Method BLASTX



NCBI GI g4006915 BLAST score 162 E value 8.0e-11 Match length 117 % identity 32 (Z99708) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 268754 17109 1.R1011

Contig ID

LIB3059-025-Q1-K1-B8 5'-most EST

BLASTX Method NCBI GI g2098778 BLAST score 1253 1.0e-138 E value Match length 302

78 % identity

NCBI Description (U96045) APS reductase [Arabidopsis thaliana]

Seq. No. 268755

17111 2.R1011 Contia ID

LIB3059-033-Q1-K1-G12 5'-most EST

Seq. No. 268756

Contig ID 17111 3.R1011 5'-most EST LIB84-014-Q1-E1-E4

Seq. No. 268757

Contig ID 17121 1.R1011 5'-most EST ceu700423003.h1

268758 Seq. No.

17125 1.R1011 Contig ID

LIB3059-043-Q1-K1-B7 5'-most EST

Method BLASTX g4586265 NCBI GI 400 BLAST score 2.0e-38 E value Match length 163 % identity 46

(AL049640) putative protein [Arabidopsis thaliana] NCBI Description

268759 Seq. No.

17125 3.R1011 Contig ID tzu700207044.hl 5'-most EST

BLASTX Method g4586265 NCBI GI 219 BLAST score 6.0e-18E value 80 Match length % identity

(AL049640) putative protein [Arabidopsis tmaliana] NCBI Description

268760 Seq. No.

Contig ID 17126 1.R1011 pwr700451438.h1 5'-most EST

Method BLASTX g465820 NCBI GI



544 BLAST score 2.0e-55 E value Match length 161 58 % identity

HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III NCBI Description

>gi 280536 pir S28301 hypothetical protein C40H1.6 -Caenorhabditis elegans >gi_3874819_emb_CAA79557_ (Z19154)

C40H1.6 [Caenorhabditis elegans]

268761 Seq. No.

17126 2.R1011 Contig ID gw1700617946.h1 5'-most EST

Method BLASTX NCBI GI q465820 BLAST score 209 1.0e-16 E value 56 Match length 59 % identity

HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III NCBI Description

>gi_280536_pir__S28301 hypothetical protein C40H1.6 -Caenorhabditis elegans >gi_3874819_emb_CAA79557_ (Z19154)

C40H1.6 [Caenorhabditis elegans]

268762 Seq. No.

Contig ID 17127 1.R1011 5'-most EST uC-zmflb73297h03a1

Seq. No. 268763

17129 1.R1011 Contig ID

5'-most EST LIB3061-006-Q1-K1-E2

Method BLASTX NCBI GI q2623248 BLAST score 950 1.0e-103 E value Match length 173

% identity

NCBI Description (AF030882) SU1 isoamylase [Zea mays]

Seq. No. 268764

Contig ID 17131 1.R1011

5'-most EST uC-zmflMo17006d04b1

Method BLASTX NCBI GI q2088653 BLAST score 168 E value 2.0e-11 Match length 53 60 % identity

NCBI Description (AF002109) Hs1pro-1 related protein isolog [Arabidopsis

thaliana]

Seq. No. 268765

Contig ID 17164 1.R1011 5'-most EST ceu700430504.h1

Method BLASTX NCBI GI q2498397 BLAST score 286 2.0e-25 E value



Match length 53 100 % identity

FERREDOXIN-THIOREDOXIN REDUCTASE, VARIABLE CHAIN (FTR-V) NCBI Description

(FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT A) (FTR-A)

268766 Seq. No.

17165 1.R1011 Contig ID

LIB3115-008-Q1-K1-B6 5'-most EST

268767 Seq. No.

Contig ID 17168 1.R1011

LIB31<u>1</u>5-008-Q1-K1-C3 5'-most EST

268768 Seq. No.

17178_1.R1011 Contig ID

LIB3115-009-Q1-K1-A12 5'-most EST

BLASTX Method q1084453 NCBI GI BLAST score 424 9.0e-42E value Match length 117

71 % identity

NCBI Description calmodulin - rice

268769 Seq. No.

Contig ID 17191 1.R1011

5'-most EST LIB3115-014-P1-K1-H8

268770 Seq. No.

17191 2.R1011 Contig ID

5'-most EST uC-zmflmo17059d09b1

268771 Seq. No.

17195 1.R1011 Contig ID

5'-most EST uC-zmromo17011a04a1

Seq. No. 268772

17210 1.R1011 Contig ID uwc700149734.h1 5'-most EST

BLASTX Method NCBI GI q3080402 BLAST score 492 2.0e-49 E value 190 Match length % identity 56

(AL022603) putative NADPH quinone oxidoreductase NCBI Description

[Arabidopsis thaliana] >gi_4455266_emb_CAB36802.1_ (AL035527) putative NADPH quinone oxidoreductase

[Arabidopsis thaliana]

Seq. No. 268773

Contig ID 17215 1.R1011

5'-most EST LIB143-040-Q1-E1-F9

Method BLASTX NCBI GI g4220481 BLAST score 273 E value 1.0e-23

```
Match length 139
% identity 51
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
Seq. No. 268774
Contig ID 17215 2.R1011
```

5'-most EST LIB3060-023-Q1-K1-H12
Method BLASTX
NCBI GI g4220481
BLAST score 282
E value 7.0e-25
Match length 146
% identity 45

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

 Seq. No.
 268775

 Contig ID
 17215_3.R1011

 5'-most EST
 wen700333852.h1

 Method
 BLASTN

 NCBI GI
 g531828

BLAST score 42 E value 4.0e-14 Match length 98 % identity 86

NCBI Description Cloning vector pSport1, complete cds

Seq. No. 268776 Contig ID 17229 1.R1011

5'-most EST LIB3115-014-P1-K1-A5

Method BLASTX
NCBI GI g2642213
BLAST score 435
E value 8.0e-43
Match length 80

% identity 100

NCBI Description (AF030385) nitrate-induced NOI protein [Zea mays]

>gi_2895781 (AF045033) nitrate-induced NOI protein [Zea

mays]

Seq. No. 268777

Contig ID 17229_2.R1011 5'-most EST wyr700237257.h1

Method BLASTN
NCBI GI g2895780
BLAST score 228
E value 1.0e-125
Match length 343
% identity 92

NCBI Description Zea mays nitrate-induced NOI protein mRNA, complete cds

Seq. No. 268778

Contig ID 17229_3.R1011 5'-most EST xyt700344808.h1

Method BLASTX
NCBI GI g2642213
BLAST score 414
E value 3.0e-40



Match length 80 % identity 95

NCBI Description (AF030385) nitrate-induced NOI protein [Zea mays]

>gi 2895781 (AF045033) nitrate-induced NOI protein [Zea

mays]

Seq. No. 268779

Contig ID 17234_1.R1011

5'-most EST LIB3150-056-Q1-N1-H9

Method BLASTX
NCBI GI 94337197
BLAST score 422
E value 3.0e-41
Match length 143
% identity 56

NCBI Description (AC006403) putative AIG2 protein [Arabidopsis thaliana]

Seq. No. 268780

Contig ID 17240_1.R1011 5'-most EST ceu700432794.h1

Method BLASTX
NCBI GI g4371280
BLAST score 204
E value 9.0e-16
Match length 58

% identity 71
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]

Seq. No. 268781

Contig ID 17244_1.R1011 5'-most EST ceu700426274.h1

Seq. No. 268782

Contig ID 17246_1.R1011

5'-most EST LIB3115-015-P1-K1-A1

Seq. No. 268783

Contig ID 17253 1.R1011

5'-most EST LIB3062-011-Q1-K1-E12

Seq. No. 268784

Contig ID 17257 1.R1011

5'-most EST LIB3115-015-P1-K1-B7

Method BLASTX
NCBI GI g3805765
BLAST score 833
E value 3.0e-89
Match length 274
% identity 62

NCBI Description (AC005693) putative protein kinase [Arabidopsis thaliana]

Seq. No. 268785

Contig ID 17265_1.R1011 5'-most EST wty700172092.h1

Method BLASTX NCBI GI g2564249 BLAST score 215



E value 8.0e-17
Match length 91
% identity 48
NCRI Description (Y08686

NCBI Description (Y08686) serine palmitoyltransferase, subunit II [Homo sapiens] >gi_3043576_dbj_BAA25452_ (AB011098) KIAA0526 protein [Homo sapiens] >gi_4186182 (AF111168) serine

palmitoyl transferase, subunit II [Homo sapiens]

Seq. No. 268786

Contig ID 17267_1.R1011

5'-most EST uC-zmflmo17295g11b1

Method BLASTN
NCBI GI g454880
BLAST score 62
E value 5.0e-26

E value 5.0e-2 Match length 190 % identity 90

NCBI Description Rice mRNA for WSI724 protein induced by water stress,

complete cds

Seq. No. 268787

Contig ID 17267_2.R1011

5'-most EST LIB3067-026-Q1-K1-B9

Method BLASTN
NCBI GI 9454880
BLAST score 62
E value 6.0e-26
Match length 190
% identity 90

NCBI Description Rice mRNA for WSI724 protein induced by water stress,

complete cds

Seq. No. 268788

Contig ID 17269_1.R1011 5'-most EST nbm700468771.h1

Method BLASTX
NCBI GI 94206197
BLAST score 963
E value 1.0e-104
Match length 279
% identity 65

NCBI Description (AF071527) putative pre-mRNA splicing factor [Arabidopsis

thaliana]

Seq. No. 268789

Contig ID 17269 2.R1011

5'-most EST LIB3067-060-Q1-K1-A11

Method BLASTX
NCBI GI 94206197
BLAST score 183
E value 1.0e-13
Match length 46
% identity 67

NCBI Description (AF071527) putative pre-mRNA splicing factor [Arabidopsis

thaliana]

Seq. No. 268790



```
Contig ID
                  17269 3.R1011
5'-most EST
                  uC-zmflb73339g06a1
                  268791
Seq. No.
Contig ID
                  17271 1.R1011
                  LIB3115-015-P1-K1-D8
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2598589
BLAST score
                  216
                  5.0e-17
E value
                  76
Match length
                  55
% identity
NCBI Description
                  (Y15367) MtN19 [Medicago truncatula]
                  268792
Seq. No.
                  17273 1.R1011
Contig ID
5'-most EST
                  ntr700072003.h1
                  BLASTX
Method
NCBI GI
                  q4586246
BLAST score
                  271
                  1.0e-23
E value
Match length
                  77
                  60
% identity
NCBI Description
                 (AL049640) putative protein [Arabidopsis thaliana]
                  268793
Seq. No.
                  17277 1.R1011
Contig ID
5'-most EST
                  uC-zmflm017211a02b1
Method
                  BLASTX
NCBI GI
                  g2829911
BLAST score
                  476
                  1.0e-47
E value
Match length
                  182
% identity
                  53
                 (AC002291) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  268794
Seq. No.
                  17277 2.R1011
Contig ID
                  LIB3115-015-P1-K1-E4
5'-most EST
                  BLASTX
Method
                  g2829911
NCBI GI
BLAST score
                   411
                   8.0e-40
E value
                  170
Match length
                   49
% identity
NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]
                  268795
Seq. No.
                   17277 3.R1011
Contig ID
5'-most EST
                   uC-zmflmo17013d05b1
                  BLASTX
Method
NCBI GI
                   q2829911
BLAST score
                   194
E value
                   1.0e-14
                  87
Match length
                   45
% identity
```

NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]



```
268796
Seq. No.
                  17290 1.R1011
Contig ID
                  LIB3157-009-Q1-K1-H6
5'-most EST
                  268797
Seq. No.
                  17294 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73286b06b1
Method
                  BLASTX
                  g1652856
NCBI GI
BLAST score
                  410
                  1.0e-39
E value
Match length
                  247
                  38
% identity
                 (D90909) hypothetical protein [Synechocystis sp.]
NCBI Description
                  268798
Seq. No.
Contig ID
                  17295 1.R1011
5'-most EST
                  uC-zmflmo17037a11b1
Method
                  BLASTX
NCBI GI
                  q1346773
BLAST score
                  324
                  4.0e-30
E value
                  197
Match length
                  42
% identity
NCBI Description PHOSPHATIDYLINOSITOL TRANSFER PROTEIN ALPHA ISOFORM (PTDINS
                  TRANSFER PROTEIN ALPHA) (PTDINSTP) (PI-TP-ALPHA)
                  >gi_2137007_pir__JC4854 phosphatidylinositol transfer
                  protein - rabbit >gi_534829 (U12558) phosphatidylinositol
                  transfer protein [Oryctolagus cuniculus]
                  268799
Seq. No.
Contig ID
                  17295 3.R1011
5'-most EST
                  uer700581556.h1
                  268800
Seq. No.
Contig ID
                  17298 1.R1011
5'-most EST
                  uC-zmroB73017c03b1
Method
                  BLASTX
NCBI GI
                  g3080427
BLAST score
                  576
                  1.0e-59
E value
Match length
                  139
% identity
                  81
NCBI Description
                  (AL022604) putative protein [Arabidopsis thaliana]
                  268801
Seq. No.
Contig ID
                  17301 1.R1011
```

5'-most EST nbm700477714.hl

Method BLASTX NCBI GI g4186073 BLAST score 163 8.0e-11 E value Match length 175 % identity 33

(AJ010949) calcium channel alpha-2-delta-C subunit [Mus NCBI Description

musculus]

```
Seq. No.
                   268802
Contig ID
                   17306 1.R1011
5'-most EST
                   wty700163335.h1
                   268803
Seq. No.
Contig ID
                   17310 1.R1011
5'-most EST
                   tfd700571558.h1
                   268804
Seq. No.
Contig ID
                   17311 1.R1011
5'-most EST
                   uwc700150680.h1
Method
                   BLASTX
NCBI GI
                   q4455232
BLAST score
                   1726
E value
                   0.0e + 00
Match length
                   532
% identity
                   60
NCBI Description
                  (AL035523) putative protein [Arabidopsis thaliana]
                   268805
Seq. No.
Contig ID
                   17313 1.R1011
5'-most EST
                   uC-zmroteosinte020e02b1
Method
                   BLASTX
NCBI GI
                   q1931652
BLAST score
                   395
E value
                   4.0e-38
Match length
                   134
% identity
                   59
NCBI Description (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog
                   [Arabidopsis thaliana]
Seq. No.
                   268806
Contig ID
                   17314 1.R1011
5'-most EST
                  bdu700382101.h1
Method
                  BLASTX
NCBI GI
                   g2245394
BLAST score
                   285
E value
                   4.0e-25
Match length
                  103
% identity
                   52
NCBI Description (U89771) ARF1-binding protein [Arabidopsis thaliana]
Seq. No.
                  268807
Contig ID
                   17325 1.R1011
5'-most EST
                  LIB3279-015-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g3875246
BLAST score
                   306
E value
                   9.0e-28
Match length
                  133
% identity
                  43
NCBI Description
                  (Z81490) similar to WD domain, G-beta repeats (2 domains);
                   cDNA EST EMBL: T00482 comes from this gene; cDNA EST
                  EMBL: T00923 comes from this gene; cDNA EST yk449d4.3 comes
```

from this gene; cDNA EST yk449d4.5 comes from this gene;



Seq. No. 268808

Contig ID 17327 1.R1011

5'-most EST LIB3060-008-Q1-K1-A6

Method BLASTX
NCBI GI g2749939
BLAST score 571
E value 1.0e-58
Match length 210
% identity 60

NCBI Description (U70999) CCS1 [Chlamydomonas reinhardtii] >gi 2749941

(U71000) CCS1 [Chlamydomonas reinhardtii]

Seq. No. 268809

Contig ID 17330_1.R1011 5'-most EST fxb700397547.h1

Method BLASTX
NCBI GI g4508073
BLAST score 322
E value 1.0e-29
Match length 122
% identity 48

NCBI Description (AC005882) 43220 [Arabidopsis thaliana]

Seq. No. 268810

Contig ID 17337_1.R1011 5'-most EST clt700042049.f1

Method BLASTX
NCBI GI g1076360
BLAST score 1177
E value 1.0e-129
Match length 385
% identity 59

NCBI Description oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) -

Arabidopsis thaliana >gi_2129530_pir__S69195 acyl-(acyl carrier protein) thioesterase (clone TE 1-1) - Arabidopsis thaliana >gi_634003_emb_CAA85387_ (Z36910) acyl-(acyl carrier protein) thioesterase [Arabidopsis thaliana]

Seq. No. 268811

Contig ID 17337_3.R1011 5'-most EST tzu700205583.h1

Seq. No. 268812

Contig ID 17343_1.R1011 5'-most EST fwa700099992.h1

Method BLASTX
NCBI GI g118564
BLAST score 1540
E value 1.0e-172
Match length 356
% identity 80

NCBI Description GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE REDUCTASE) (HPR) (GDH) >gi_65955_pir__DEKVG glycerate

dehydrogenase (EC 1.1.1.29) - cucumber

>gi_18264_emb_CAA41434_ (X58542) NADH-dependent
hydroxypyruvate reductase [Cucumis sativus]
>gi_18275_emb_CAA32764_ (X14609) NAPH-dependent



hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]

268813 Seq. No.

17344 1.R1011 Contig ID

5'-most EST uC-zmflmo17140h09a1

268814 Seq. No.

17358 1.R1011 Contig ID

uC-zmflb73232a03b1 5'-most EST

BLASTX Method NCBI GI q4262152 BLAST score 441

2.0e-43E value Match length 114 68 % identity

(AC005275) putative frataxin-like protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 268815

17373 2.R1011 Contig ID

uC-zmflb73283h11b2 5'-most EST

BLASTX Method q549641 NCBI GI BLAST score 185 E value 2.0e-13 117 Match length 35 % identity

NCBI Description HYPOTHETICAL 35.8 KD PROTEIN IN PRP16-SRP40 INTERGENIC

REGION >gi 539282 pir__S38165 hypothetical protein YKR087c - yeast (Saccharomyces cerevisiae) >gi 415907 emb_CAA81638_

(Z27116) ORF YKR407 [Saccharomyces cerevisiae] >gi 486605 emb CAA82166 (Z28312) ORF YKR087c

[Saccharomyces cerevisiae]

268816 Seq. No.

Contig ID 17379 1.R1011 5'-most EST tzu700204790.h1

Seq. No. 268817

Contig ID 17381 1.R1011

5'-most EST LIB3115-017-P1-K1-D2

268818 Seq. No.

17386 1.R1011 Contig ID

uC-zmflmo17071b07b1 5'-most EST

Method BLASTX q3341688 NCBI GI 998 BLAST score 1.0e-108 E value Match length 259 % identity 72

NCBI Description (AC003672) putative casein kinase II beta subunit

[Arabidopsis thaliana]

268819 Seq. No.

17386 3.R1011 Contig ID

uC-zmflmo17274a01a1 5'-most EST



Method BLASTX
NCBI GI g3493611
BLAST score 149
E value 2.0e-09
Match length 34
% identity 76

NCBI Description (AF068318) regulatory subunit of protein kinase CK2; CK2

beta-subunit [Arabidopsis thaliana]

Seq. No. 268820

Contig ID 17386 4.R1011

5'-most EST LIB3136-014-Q1-K2-H3

Seq. No. 268821

Contig ID 17386_5.R1011

5'-most EST LIB3137-036-Q1-K1-E10

Seq. No. 268822

Contig ID 17386 8.R1011

5'-most EST LIB3060-028-Q1-K1-D8

Seq. No. 268823

Contig ID 17387_1.R1011

5'-most EST LIB3066-049-Q1-K1-C8

Method BLASTX
NCBI GI g2651307
BLAST score 353
E value 3.0e-33
Match length 112
% identity 58

NCBI Description (AC002336) putative uroporphyinogen decarboxylase

[Arabidopsis thaliana]

Seq. No. 268824

Contig ID 17387_2.R1011 5'-most EST xsy700210906.h1

Method BLASTX
NCBI GI g2501647
BLAST score 451
E value 8.0e-45
Match length 177
% identity 50

NCBI Description UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD)

>gi 1362120 pir S55732 uroporphyrinogen decarboxylase -

common tobacco gi_1009429_emb_CAA58040">gi_1009429_emb_CAA58040 (X82833) uroporphyrinogen decarboxylase [Nicotiana tabacum]

Seq. No. 268825

Contig ID 17387_3.R1011

5'-most EST uC-zmroteosinte057d02b1

Method BLASTX
NCBI GI g2501647
BLAST score 158
E value 3.0e-10
Match length 71
% identity 46

NCBI Description UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD)



>gi_1362120_pir__S55732 uroporphyrinogen decarboxylase common tobacco >gi_1009429_emb_CAA58040_ (X82833)
uroporphyrinogen decarboxylase [Nicotiana tabacum]

Seq. No. 268826

Contig ID 17387_4.R1011 5'-most EST fC-zmst700454413f1

Method BLASTX
NCBI GI g2501646
BLAST score 294
E value 2.0e-26
Match length 97
% identity 55

NCBI Description UROPORPHYRINOGEN DECARBOXYLASE (UPD)

>gi_1362169_pir__S55733 uroporphyrinogen decarboxylase barley >gi_1016347_emb_CAA58039_ (X82832) uroporphyrinogen

decarboxylase [Hordeum vulgare]

Seq. No. 268827

Contig ID 17389 1.R1011

5'-most EST LIB3136-015-Q1-K1-G12

Seq. No. 268828

Contig ID 17392_1.R1011 5'-most EST tfd700573237.h1

Method BLASTX
NCBI GI g699196
BLAST score 336
E value 4.0e-39
Match length 241
% identity 42

NCBI Description (U15181) 4-coumarate-coA ligase [Mycobacterium leprae]

Seq. No. 268829

Contig ID 17399 1.R1011

5'-most EST LIB3115-017-P1-K1-F10

Seq. No. 268830

Contig ID 17401 1.R1011

5'-most EST LIB3115-017-P1-K1-F12

Seq. No. 268831

Contig ID 17402_1.R1011 5'-most EST xsy700209866.h1

Method BLASTX
NCBI GI g4586116
BLAST score 473
E value 7.0e-49
Match length 193
% identity 49

NCBI Description (AL049638) putative C-4 sterol methyl oxidase [Arabidopsis

thaliana]

Seq. No. 268832

Contig ID 17403_1.R1011 5'-most EST hvj700623143.h1

Method BLASTX



NCBI GI g4586056 BLAST score 292 E value 7.0e-26 Match length 125 % identity 47

NCBI Description (AC007020) unknown protein [Arabidopsis thaliana]

Seq. No. 268833

Contig ID 17409_1.R1011 5'-most EST cyk700050338.f1

Seq. No. 268834

Contig ID 17415_1.R1011 5'-most EST ceu700434465.h1

Seq. No. 268835

Contig ID 17419_1.R1011

5'-most EST LIB18 $\overline{9}$ -014-Q1-E1-C5

Seq. No. 268836

Contig ID 17428_2.R1011 5'-most EST wyr700244108.h1

Method BLASTX
NCBI GI g3928543
BLAST score 339
E value 8.0e-32
Match length 92
% identity 68

NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 268837

Contig ID 17429 1.R1011

5'-most EST LIB3115-018-P1-K1-B9

Seq. No. 268838

Contig ID 17429 2.R1011 5'-most EST nwy700444337.h1

Seq. No. 268839

Contig ID 17434_1.R1011

5'-most EST LIB3068-002-Q1-K1-A4

Method BLASTX
NCBI GI g3790567
BLAST score 154
E value 7.0e-10
Match length 126
% identity 30

NCBI Description (AF078821) RING-H2 finger protein RHA1b [Arabidopsis

thaliana]

Seq. No. 268840

Contig ID 17434_2.R1011

5'-most EST LIB31 $\overline{1}$ 5-018-P1-K1-C7

Method BLASTX NCBI GI g4262223 BLAST score 162



E value 9.0e-11 Match length 55 % identity 53

(AC006200) RING-H2 finger protein RHA2b [Arabidopsis NCBI Description

thaliana]

Seq. No. 268841

17436 1.R1011 Contig ID

5'-most EST LIB3115-018-P1-K1-C9

268842 Seq. No.

Contig ID 17439 1.R1011

5'-most EST LIB3068-048-Q1-K1-H6

Seq. No. 268843

Contig ID 17440 1.R1011

5'-most EST fC-zmro700452115f1

Method BLASTX NCBI GI g4468993 BLAST score 247 E value 7.0e-21Match length 113 % identity 42

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 268844

17446 1.R1011 Contig ID

5'-most EST LIB3115-018-P1-K1-E4

Method BLASTN NCBI GI g2062705 BLAST score 34 1.0e-09 E value Match length 38

97 % identity

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 268845

Contig ID 17451 1.R1011 5'-most EST $dyk70\overline{0}104589.h1$

Method BLASTX q3184283 NCBI GI BLAST score 613 E value 1.0e-63 Match length 170 % identity 72

NCBI Description (AC004136) putative TBP-binding protein [Arabidopsis

thaliana]

Seq. No. 268846

17459_1.R1011 Contig ID 5'-most EST LIB36-015-Q1-E1-E11

Method BLASTX NCBI GI a4415940 BLAST score 273 E value 1.0e-23 Match length 84 % identity 62



NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No. 268847

Contig ID 17461 1.R1011

5'-most EST LIB3115-018-P1-K1-H1

Seq. No. 268848

Contig ID 17464 1.R1011

5'-most EST uC-zmromo17114e08a1

Method BLASTX
NCBI GI g1001253
BLAST score 187
E value 8.0e-18
Match length 128
% identity 44

NCBI Description (D64003) hypothetical protein [Synechocystis sp.]

Seq. No. 268849

Contig ID 17464 2.R1011

5'-most EST LIB3115-018-P1-K1-H12

Method BLASTX
NCBI GI g1001253
BLAST score 183
E value 3.0e-13
Match length 101
% identity 40

NCBI Description (D64003) hypothetical protein [Synechocystis sp.]

Seq. No. 268850

Contig ID 17468_1.R1011 5'-most EST tfd700574626.h1

Seq. No. 268851

Contig ID 17471 1.R1011

5'-most EST LIB31\overline{15}-019-P1-K1-A3

Method BLASTX
NCBI GI g2435522
BLAST score 352
E value 2.0e-33
Match length 112
% identity 62

NCBI Description (AF024504) contains similarity to other AMP-binding enzymes

[Arabidopsis thaliana]

Seq. No. 268852

Contig ID 17483 1.R1011 5'-most EST LIB36-009-Q1-E1-G6

Seq. No. 268853

Contig ID 17486 1.R1011

5'-most EST LIB3115-019-P1-K1-C6

Seq. No. 268854

Contig ID 17489_1.R1011 5'-most EST uC-zmflb73198f05b1

Seq. No. 268855



Contig ID 17491_1.R1011

5'-most EST LIB3115-019-P1-K1-D11

Method BLASTX
NCBI GI g2147484
BLAST score 1322
E value 1.0e-146
Match length 309
% identity 84

NCBI Description homeotic protein - Phalaenopsis sp >gi_1173622 (U34743)

homeobox protein [Phalaenopsis sp. 'hybrid SM9108']

Seq. No. 268856

Contig ID 17492 1.R1011

5'-most EST LIB3180-014-P2-M1-E9

Method BLASTX
NCBI GI g585551
BLAST score 762
E value 6.0e-81
Match length 149
% identity 94

NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)

>gi_629798_pir__S43330 nucleoside-diphosphate kinase (EC

2.7.4.6) - rice >gi_303849_dbj_BAA03798_ (D16292)

nucleoside diphosphate kinase [Oryza sativa]

Seq. No. 268857

Contig ID 17493 1.R1011

5'-most EST LIB189-034-Q1-E1-E1

Seq. No. 268858

Contig ID 17494 1.R1011 5'-most EST fdz701161124.h1

Seq. No. 268859

Contig ID 17494 2.R1011 5'-most EST fdz701161370.h1

Seq. No. 268860

Contig ID 17494_3.R1011 5'-most EST lhp700053487.r1

Seq. No. 268861

Contig ID 17505 1.R1011

5'-most EST uC-zmflmo17108c05b1

Method BLASTX
NCBI GI g3850585
BLAST score 480
E value 8.0e-48
Match length 217
% identity 47

NCBI Description (AC005278) ESTs gb_H36966, gb_R65511, gb_T42324 and

gb_T20569 come from this gene. [Arabidopsis thaliana]

Seq. No. 268862

Contig ID 17505 2.R1011

5'-most EST LIB3117-004-Q1-K1-E7



```
Seq. No.
                  268863
                  17505 3.R1011
Contig ID
5'-most EST
                  xyt700346264.h1
                  268864
Seq. No.
                  17511 1.R1011
Contig ID
                  LIB3115-019-P1-K1-G8
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1001955
BLAST score
                  162
E value
                  5.0e-11
Match length
                  48
% identity
                  67
NCBI Description (U19099) unknown protein [Lycopersicon chilense ]
Seq. No.
                  268865
                  17515 1.R1011
Contig ID
5'-most EST
                  LIB3115-019-P1-K1-H2
Seq. No.
                  268866
                  17517 1.R1011
Contig ID
                  rvt700550128.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2131767
BLAST score
                  149
E value
                  3.0e-09
                  95
Match length
                  40
% identity
NCBI Description hypothetical protein YLR074c - yeast (Saccharomyces
                  cerevisiae) >gi_1360432_emb_CAA97631_ (Z73246) ORF YLR074c
                  [Saccharomyces cerevisiae]
Seq. No.
                  268867
                  17517 2.R1011
Contig ID
                  nwy700445959.h1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4455246
BLAST score
                  432
E value
                  8.0e-80
                  334
Match length
                  49
% identity
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
Seq. No.
                  268868
Contig ID
                  17520 1.R1011
5'-most EST
                  LIB189-019-Q1-E1-G2
Seq. No.
                  268869
Contig ID
                  17521 1.R1011
                  LIB3115-020-P1-K1-A11
5'-most EST
Method
                  BLASTX
```

Contig ID 17521_1.R1011
5'-most EST LIB3115-020-P1-K1Method BLASTX
NCBI GI g112994
BLAST score 195
E value 6.0e-15
Match length 39

Match length 39 % identity 97

NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN



>gi_82685_pir__S04536 embryonic abundant protein, glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564) ABA-inducible gene protein [Zea mays]

>gi_226091_prf__1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 268870

Contig ID 17523 1.R1011

5'-most EST LIB3115-020-P1-K1-A3

Method BLASTX
NCBI GI g1620753
BLAST score 171
E value 7.0e-12
Match length 58
% identity 59

NCBI Description (U72942) proteinase inhibitor [Oryza sativa]

>gi 2829212 gb AAC00503 (AF044059) proteinase inhibitor

[Oryza sativa]

Seq. No. 268871

Contig ID 17523 2.R1011

5'-most EST LIB1 $4\overline{3}$ -014-Q1-E1-A4

Method BLASTN
NCBI GI 94337128
BLAST score 49
E value 3.0e-18
Match length 173
% identity 82

NCBI Description Oryza sativa proteinase inhibitor (Rgpi9) gene, complete

cds

Seq. No. 268872

Contig ID 17528_1.R1011 5'-most EST wty700168111.h1

Seq. No. 268873

Contig ID 17528_2.R1011

5'-most EST LIB3115-020-P1-K1-B5

Seq. No. 268874

Contig ID 17528_4.R1011 5'-most EST fC-zmle700444465d4

Seq. No. 268875

Contig ID 17533 1.R1011

5'-most EST LIB31<u>1</u>5-020-P1-K1-C11

Seq. No. 268876

Contig ID 17534_1.R1011

5'-most EST uC-zmflmo17320e10b1

Method BLASTX
NCBI GI g1946372
BLAST score 305
E value 2.0e-27
Match length 95
% identity 64

NCBI Description (U93215) yeast hypothetical protein YDB1 SCHPO isolog



[Arabidopsis thaliana]

Seq. No. 268877

Contig ID 17534 2.R1011

5'-most EST uC-zmroteosinte025c04b1

Method BLASTX
NCBI GI g1946372
BLAST score 215
E value 5.0e-17
Match length 52
% identity 79

NCBI Description (U93215) yeast hypothetical protein YDB1 SCHPO isolog

[Arabidopsis thaliana]

Seq. No. 268878

Contig ID 17535_1.R1011 5'-most EST uer700577209.h1

Seq. No. 268879

Contig ID 17535 2.R1011

5'-most EST LIB3116-014-Q1-K1-B9

Seq. No. 268880

Contig ID 17542 1.R1011

5'-most EST LIB3062-013-Q1-K1-G4

Seq. No. 268881

Contig ID 17542_2.R1011 5'-most EST wyr700244217.h1

Seq. No. 268882

Contig ID 17543_1.R1011 5'-most EST clt700045530.f1

Method BLASTX
NCBI GI g2494417
BLAST score 1661
E value 0.0e+00
Match length 327
% identity 96

NCBI Description FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC

(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_1364071_pir__S57717 fructose-1, 6-bisphosphatase (EC

3.1.3.11) - sugarcane hybrid H65-7052

>gi_895909_emb_CAA61409.1_ (X89006) fructose-1,

6-bisphosphatase [Saccharum hybrid cultivar H65-7052]

Seq. No. 268883

Contig ID 17543_3.R1011 5'-most EST fdz701158577.h1

Method BLASTX
NCBI GI g3913640
BLAST score 426
E value 6.0e-42
Match length 94
% identity 91

NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC

(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)



>gi_3041775_dbj_BAA25422_ (AB007193)
fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No. 268884

Contig ID 17544 2.R1011 5'-most EST nbm700472603.h1

Seq. No. 268885

Contig ID 17549 1.R1011 5'-most EST hbs701182836.h1

Method BLASTX
NCBI GI g3080375
BLAST score 380
E value 2.0e-36
Match length 118
% identity 65

NCBI Description (AL022580) putative protein [Arabidopsis thaliana]

Seq. No. 268886

Contig ID 17553_1.R1011 5'-most EST ceu700432672.h1

Seq. No. 268887

Contig ID 17558 1.R1011

5'-most EST LIB3069-009-Q1-K1-D11

Method BLASTX
NCBI GI g3892058
BLAST score 214
E value 4.0e-25
Match length 103
% identity 54

NCBI Description (AC002330) putative glutamate-/aspartate-binding peptide

[Arabidopsis thaliana]

Seq. No. 268888

Contig ID 17569_1.R1011 5'-most EST uC-zmflb73285e05b1

Seq. No. 268889

Contig ID 17570 1.R1011

5'-most EST uC-zmflmo17341f11b1

Method BLASTX
NCBI GI 94091806
BLAST score 297
E value 2.0e-26
Match length 305
% identity 33

NCBI Description (AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No. 268890

Contig ID 17571_1.R1011 5'-most EST LIB84-012-Q1-E12-E3

Seq. No. 268891

Contig ID 17572_1.R1011

5'-most EST LIB3115-029-P1-K1-E11



Seq. No. 268892

Contig ID 17574 1.R1011

5'-most EST LIB3115-021-P1-K1-A2

Method BLASTX
NCBI GI g3063392
BLAST score 397
E value 3.0e-38
Match length 100
% identity 75

NCBI Description (AB012932) Ca2+/H+ exchanger [Vigna radiata]

Seq. No. 268893

Contig ID 17576_1.R1011 5'-most EST nbm700471842.h1

Method BLASTX
NCBI GI g4206640
BLAST score 632
E value 1.0e-65
Match length 157
% identity 79

NCBI Description (AF072858) zinc transporter ZAT [Arabidopsis thaliana]

Seq. No. 268894

Contig ID 17576 2.R1011

5'-most EST uC-zmflmo17053c07a1

Method BLASTX
NCBI GI g3510254
BLAST score 210
E value 1.0e-16
Match length 51

Match length 51 % identity 78

NCBI Description (AC005310) putative zinc transporter [Arabidopsis thaliana]

Seq. No. 268895

Contig ID 17576_3.R1011

5'-most EST LIB1 $4\overline{3}$ -061-Q1-E1-F5

Method BLASTX
NCBI GI g3510254
BLAST score 295
E value 2.0e-26
Match length 140
% identity 64

NCBI Description (AC005310) putative zinc transporter [Arabidopsis thaliana]

Seq. No. 268896

Contig ID 17578 1.R1011

5'-most EST LIB3115-021-P1-K1-A7

Method BLASTX
NCBI GI g2398829
BLAST score 249
E value 3.0e-21
Match length 56
% identity 82

NCBI Description (Y11220) mitochondrial uncoupling protein [Solanum

tuberosum]

Seq. No. 268897



Contig ID 17585_1.R1011 5'-most EST ceu700430003.h1

Method BLASTX
NCBI GI g3894197
BLAST score 314
E value 5.0e-29
Match length 67
% identity 82

NCBI Description (AC005662) hypothetical protein [Arabidopsis thaliana]

Seq. No. 268898

Contig ID 17586_1.R1011

5'-most EST uC-zmflmo17209f05a1

Seq. No. 268899

Contig ID 17589 1.R1011

5'-most EST LIB3136-027-P1-K1-H8

Seq. No. 268900

Contig ID 17593_1.R1011 5'-most EST uC-zmroB73030h03b1

Method BLASTX
NCBI GI g1170745
BLAST score 518
E value 2.0e-52
Match length 148
% identity 62

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA14-A >gi 167326

(M88321) Group 4 late embryogenesis-abundant protein [Gossypium hirsutum] >gi_167328 (M88322) Group 4 late embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 268901

Contig ID 17593_4.R1011 5'-most EST nwy700444330.h1

Method BLASTX
NCBI GI g1922244
BLAST score 185
E value 6.0e-14
Match length 41
% identity 76

NCBI Description (Y10085) putative desication related protein LEA14

[Arabidopsis thaliana] >gi_2505882_emb CAA73311 (Y12776)

LEA protein [Arabidopsis thaliana]

Seq. No. 268902

Contig ID 17594 1.R1011

5'-most EST LIB3115-021-P1-K1-D6

Method BLASTX
NCBI GI g3212863
BLAST score 211
E value 1.0e-16
Match length 65
% identity 62

NCBI Description (AC004005) putative translation initiation factor

[Arabidopsis thaliana]

```
Seq. No.
                  268903
Contig ID
                  17599 1.R1011
5'-most EST
                  LIB3115-021-P1-K1-E4
                  268904
Seq. No.
                  17601 1.R1011
Contig ID
5'-most EST
                  vux700156487.h1
Method
                  BLASTX
NCBI GI
                  q4006899
BLAST score
                  628
E value
                  3.0e-65
Match length
                  226
% identity
                  53
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]
Seq. No.
                  268905
                  17603 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73307a03b1
Method
                  BLASTX
NCBI GI
                  q4091117
BLAST score
                  360
                  4.0e-34
E value
Match length
                  92
% identity
                  74
NCBI Description (AF047428) nucleic acid binding protein [Oryza sativa]
                  268906
Seq. No.
                  17603 2.R1011
Contig ID
5'-most EST
                  tzu700202841.hl
Method
                  BLASTN
NCBI GI
                  g2773153
BLAST score
                  55
E value
                  6.0e-22
Match length
                  246
% identity
                  84
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
Seq. No.
                  268907
                  17604 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17264a01a1
Method
                  BLASTX
NCBI GI
                  g1085476
BLAST score
                  233
E value
                  3.0e-19
Match length
                  96
% identity
                  25
                  lactase (EC 3.2.1.108) / glycosylceramidase (EC 3.2.1.62)
NCBI Description
                   (clone BL20) - rabbit (fragment)
Seq. No.
                  268908
                  17605 1.R1011
Contig ID
```

5'-most EST uC-zmflm017205h09b1

Seq. No. 268909

Contig ID 17609 1.R1011

5'-most EST LIB3067-009-Q1-K1-A3



```
Seq. No.
                   268910
Contig ID
                   17617 1.R1011
5'-most EST
                   uer700576705.h1
Method
                  BLASTX
NCBI GI
                   g4567263
BLAST score
                   385
E value
                   4.0e-37
Match length
                   96
% identity
                   73
NCBI Description
                  (AC006841) putative cell division inhibitor [Arabidopsis
                   thaliana]
Seq. No.
                   268911
                   17619 1.R1011
Contig ID
5'-most EST
                  hbs701183224.h1
Method
                  BLASTX
NCBI GI
                  g1652868
BLAST score
                  186
E value
                   1.0e-14
Match length
                  125
% identity
                   37
NCBI Description (D90909) hypothetical protein [Synechocystis sp.]
Seq. No.
                   268912
                   17622 1.R1011
Contig ID
5'-most EST
                  uC-zmf1b73234h05b2
Seq. No.
                   268913
                  17622 2.R1011
Contig ID
5'-most EST
                  LIB3115-022-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g1174853
BLAST score
                  207
E value
                   3.0e-16
Match length
                  88
% identity
                  49
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-18 KD (UBIQUITIN-PROTEIN
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42)
                  >gi 481811 pir S39483 ubiquitin-conjugating enzyme UBC2-1
                   - Arabidopsis thaliana >gi 22658 emb CAA48378 (X68306)
                  ubiquitin-conjugating enzyme [Arabidopsis thaliana]
Seq. No.
                  268914
                  17623_1.R1011
Contig ID
5'-most EST
                  qmh700027148.f1
Seq. No.
                  268915
Contig ID
                  17632 1.R1011
5'-most EST
                  xdb70\overline{0}337347.h1
Method
                  BLASTX
```

NCBI GI g4262162 BLAST score 172 E value 7.0e-12 Match length 89

% identity

NCBI Description (AC005275) putative glycosylation enzyme [Arabidopsis



thaliana]

Seq. No. 268916 Contig ID 17633 1.R1011 5'-most EST LIB3180-048-P2-A12 BLASTX Method NCBI GI q3935181 BLAST score 1623 E value 0.0e + 00Match length 341 % identity 86 NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana] 268917 Seq. No. Contig ID 17637 1.R1011 5'-most EST uwc700151069.h1 BLASTX Method q2655285 NCBI GI BLAST score 624 E value 6.0e-90 199 Match length 85 % identity

NCBI Description (AF032971) germin-like protein 1 [Oryza sativa]

Seq. No. 268918

Contig ID 17639 1.R1011

5'-most EST LIB1 $4\overline{3}$ -054-Q1-E1-F8

Method BLASTX
NCBI GI g3834325
BLAST score 983
E value 1.0e-106
Match length 298

Match length 298 % identity 60

NCBI Description (AC005679) Strong similarity to gb AF067141 gamma-glutamyl

hydrolase from Arabidopsis thaliana. ESTs gb_R83955, gb_T45062, gb_T22220, gb_AA586207, gb_AI099851 and gb_AI00672 come from this gene. [Arabidopsis thaliana]

Seq. No. 268919

Contig ID 17639_2.R1011 5'-most EST yyf700347437.h1

Method BLASTN
NCBI GI g2245648
BLAST score 175
E value 2.0e-93
Match length 276
% identity 94

NCBI Description Zea mays discolored-1 (mutant allele dsc1-Ref::Mu1) gene,

partial sequence

Seq. No. 268920

Contig ID 17639_3.R1011 5'-most EST zuv700354808.h1

Method BLASTX
NCBI GI g3169656
BLAST score 256
E value 1.0e-21



Match length 68 % identity

NCBI Description (AF067141) gamma-glutamyl hydrolase [Arabidopsis thaliana]

Seq. No.

268921

Contig ID

17641 1.R1011

5'-most EST Method

LIB3279-006-P1-K1-G10

NCBI GI

BLASTX q3335337

BLAST score E value

361

Match length

4.0e-34

% identity

88 81

NCBI Description

(AC004512) Similar to acyl carrier protein, mitochondrial

precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD subunit (MYACP-1), gb_L23574 from A. thaliana. ESTs gb Z30712, gb Z30713, gb Z26204, gb N37975 and gb N96330

come from this gene

Seq. No.

268922

Contig ID 5'-most EST 17643 1.R1011 fwa700098726.h1

Method

BLASTX

NCBI GI

g3386565

BLAST score

739

E value

1.0e-120

Match length

227

% identity

NCBI Description (AF079588) 1-aminocyclopropane-1-carboxylate oxidase

[Sorghum bicolor]

Seq. No.

268923

Contig ID

17649 1.R1011

5'-most EST

LIB3068-037-Q1-K1-H1

Method

BLASTX

NCBI GI

g4115379

BLAST score

211

E value

1.0e-16

Match length

115

% identity

42

NCBI Description

(AC005967) putative carbonyl reductase [Arabidopsis

thaliana]

Seq. No.

268924

Contig ID

17649 2.R1011

5'-most EST

uC-zmflb73387a07a1

Seq. No.

268925

Contig ID

17661 1.R1011

5'-most EST

LIB3115-022-P1-K1-H1

Seq. No.

268926

Contig ID

17662 1.R1011

5'-most EST

LIB3115-022-P1-K1-H10

Seq. No.

268927

Contig ID

17665 1.R1011



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5'-most EST
                   uC-zmflmo17194f08a1
                   268928
Seq. No.
Contig ID
                   17670 1.R1011
5'-most EST
                   LIB3067-018-Q1-K1-G9
                   268929
Seq. No.
                   17671_1.R1011
Contig ID
5'-most EST
                   xmt70\overline{0}266672.h1
Method
                   BLASTX
NCBI GI
                   q4584347
BLAST score
                   222
                   9.0e-18
E value
Match length
                   65
% identity
                   66
                  (AC007127) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   268930
                   17672 1.R1011
Contig ID
5'-most EST
                   uC-zmroteosinte017h03b1
Method
                   BLASTX
NCBI GI
                   g3901268
BLAST score
                   242
E value
                   7.0e-20
Match length
                   284
% identity
                   29
NCBI Description (AF060173) SV2 related protein [Rattus norvegicus]
Seq. No.
                   268931
Contig ID
                   17673 1.R1011
5'-most EST
                   ceu700425267.h1
Seq. No.
                   268932
Contig ID
                   17679 1.R1011
5'-most EST
                   xtj70\overline{0}377612.h1
Method
                   BLASTX
NCBI GI
                   g3063710
BLAST score
                   489
E value
                   5.0e-49
Match length
                   229
% identity
                   48
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
Seq. No.
                   268933
                   17679 2.R1011
Contig ID
5'-most EST
                   dyk700104506.h1
Method
                   BLASTX
NCBI GI
                   g3063710
BLAST score
                   420
E value
                   1.0e-41
                   93
Match length
% identity
NCBI Description
                  (AL022537) putative protein [Arabidopsis thaliana]
```

Contig ID 17681 1.R1011

268934

Seq. No.

5'-most EST fdz701163844.h1



```
268935
Seq. No.
                  17686 1.R1011
Contig ID
5'-most EST
                  LIB3115-029-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g464711
BLAST score
                  268
                  1.0e-47
E value
Match length
                  129
                  77
% identity
NCBI Description
                 40S RIBOSOMAL PROTEIN S15A (YS24) >gi_320167_pir__S30003
                  ribosomal protein S15a.e - yeast (Kluyveromyces marxianus)
                  >gi_263484_bbs_122433 (S53434) S24-1=ribosomal protein
                  [Kluyveromyces marxianus, Peptide, 130 aa] [Kluyveromyces
                  marxianus]
                  268936
Seq. No.
                  17691 1.R1011
Contig ID
5'-most EST
                  gct701167896.h1
Method
                  BLASTX
                  g4115913
NCBI GI
BLAST score
                  241
E value
                  4.0e-20
Match length
                  81
% identity
                  52
                  (AF118222) contains similarity to Iron/Ascorbate family of
NCBI Description
                  oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88,
                  N=1) [Arabidopsis thaliana] >gi_4539409_emb_CAB40042.1_
                  (AL049524) putative flavanone 3-beta-hydroxylase
                  [Arabidopsis thaliana]
                  268937
Seq. No.
                  17693 1.R1011
Contig ID
5'-most EST
                  LIB3069-041-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  q498707
BLAST score
                  338
E value
                  2.0e-31
Match length
                  125
% identity
NCBI Description (X78422) HYP1 [Arabidopsis thaliana]
Seq. No.
                  268938
                  17694 1.R1011
Contig ID
5'-most EST
                  qmh700028827.f1
Seq. No.
                  268939
                  17696 1.R1011
Contig ID
5'-most EST
```

uC-zmroteosinte048a08b1

BLASTX Method NCBI GI q2435522 BLAST score 418 E value 7.0e-51 Match length 182 % identity 54

NCBI Description (AF024504) contains similarity to other AMP-binding enzymes

[Arabidopsis thaliana]



Seq. No. 268940

Contig ID 17705 1.R1011

5'-most EST uC-zmflmo17342f09b1

Method BLASTX
NCBI GI g2462763
BLAST score 773
E value 4.0e-82
Match length 208
% identity 73

NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 268941

Contig ID 17706_1.R1011 5'-most EST LIB148-059-Q1-E1-H3

Method BLASTX
NCBI GI g2213629
BLAST score 837
E value 9.0e-90
Match length 254
% identity 65

NCBI Description (AC000103) F21J9.21 [Arabidopsis thaliana]

Seq. No. 268942

Contig ID 17713_1.R1011 5'-most EST ymt700220537.h1

Method BLASTX
NCBI GI g3894393
BLAST score 325
E value 7.0e-30
Match length 197
% identity 4

NCBI Description (AF053998) Hcr2-5D [Lycopersicon esculentum]

Seq. No. 268943

Contig ID 17716_1.R1011 5'-most EST cat700020732.r1

Seq. No. 268944

Contig ID 17716 2.R1011

5'-most EST uC-zmflmo17365a04a1

Seq. No. 268945

Contig ID 17718_1.R1011 5'-most EST dyk700103356.h1

Seq. No. 268946

Contig ID 17718 2.R1011

5'-most EST LIB143-039-Q1-E1-C2

Seq. No. 268947

Contig ID 17718_3.R1011

5'-most EST LIB3115-024-P1-K1-C1

Seq. No. 268948

Contig ID 17720_1.R1011

37428



5'-most EST uC-zmflb73166e01b2

Method BLASTX
NCBI GI g3885328
BLAST score 717
E value 1.0e-113

Match length 411 % identity 51

NCBI Description (AC005623) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 268949

Contig ID 17720_2.R1011 5'-most EST qmh700027456.f1

Method BLASTX
NCBI GI g3885328
BLAST score 563
E value 1.0e-57
Match length 269
% identity 43

NCBI Description (AC005623) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 268950

Contig ID 17720 4.R1011

5'-most EST uC-zmflmo170112e10b1

Method BLASTX
NCBI GI g3885328
BLAST score 303
E value 2.0e-27
Match length 92
% identity 61

NCBI Description (AC005623) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 268951

Contig ID 17732 1.R1011

5'-most EST LIB3066-031-Q1-K1-F1

Seq. No. 268952

Contig ID 17734 1.R1011

5'-most EST LIB1 $4\overline{3}$ -012-Q1-E1-E5

Method BLASTX
NCBI GI g2501555
BLAST score 376
E value 1.0e-35
Match length 279
% identity 38

NCBI Description POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi_549984 (U13148)

possible apospory-associated protein [Pennisetum ciliare]

Seq. No. 268953

Contig ID 17736_1.R1011 5'-most EST uC-zmflB73004b03b1

Method BLASTX
NCBI GI g3122952
BLAST score 204
E value 1.0e-15



Match length 182 % identity 34

NCBI Description TIPD PROTEIN >gi_2407788 (AF019236) TipD [Dictyostelium

discoideum]

Seq. No. 268954

Contig ID 17739_1.R1011 5'-most EST xsy700208804.h1

Method BLASTX
NCBI GI g1362490
BLAST score 367
E value 1.0e-34
Match length 179
% identity 44

NCBI Description hypothetical protein YFR024c-a - yeast (Saccharomyces

cerevisiae)

Seq. No. 268955

Contig ID 17742_1.R1011 5'-most EST ceu700425268.h1

Method BLASTX
NCBI GI g4127350
BLAST score 515
E value 5.0e-52
Match length 191
% identity 53

NCBI Description (AJ010450) glutathione transferase [Alopecurus myosuroides]

Seq. No. 268956

Contig ID 17751_1.R1011 5'-most EST xjt700094360.h1

Seq. No. 268957

Contig ID 17751_2.R1011 5'-most EST ceu700424571.h1

Seq. No. 268958

Contig ID 17753 1.R1011 5'-most EST uC-zmflb73053h09b2

Seq. No. 268959

Contig ID 17753_3.R1011 5'-most EST rvt700552750.h1

Seq. No. 268960

Contig ID 17754_1.R1011 5'-most EST ceu700433701.h1

Method BLASTX
NCBI GI g3367522
BLAST score 512
E value 9.0e-52
Match length 147
% identity 66

NCBI Description (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 268961

```
Contig ID
                  17761 1.R1011
5'-most EST
                  ypc700806773.hl
                  BLASTX
Method
NCBI GI
                  g3878105
BLAST score
                  390
                   3.0e-37
E value
                  232
Match length
% identity
                  (AL024499) cDNA EST EMBL:C10123 comes from this gene
NCBI Description
                   [Caenorhabditis elegans]
                   268962
Seq. No.
                  17762 1.R1011
Contig ID
                  xsy700208326.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g3426039
BLAST score
                   1138
                   1.0e-125
E value
                   327
Match length
                   67
% identity
NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]
                   268963
Seq. No.
                   17762 2.R1011
Contig ID
                   tzu700206909.h1
5'-most EST
                   BLASTX
Method
                   g3426039
NCBI GI
```

BLAST score 199 3.0e-15

E value Match length 88 % identity

NCBI Description (AC005168) unknown protein [Arabidopsis thaliana]

268964 Seq. No. Contig ID 17763 1.R1011 5'-most EST LIB3115-025-P1-K1-A7 Method BLASTX NCBI GI q4314401 181 BLAST score

3.0e-13 E value Match length 50 % identity 66

(AC006232) putative beta-1,3-glucanase [Arabidopsis NCBI Description

thaliana]

Seq. No. 268965

17778 1.R1011 Contig ID

LIB3115-025-P1-K1-C3 5'-most EST

Method BLASTX g3928097 NCBI GI BLAST score 634 E value 5.0e-66 Match length 256 51 % identity

(AC005770) unknown protein, 5' partial [Arabidopsis NCBI Description

thaliana]



Seq. No. 268966

Contig ID 17779_1.R1011

5'-most EST LIB3157-006-Q1-K1-E12

Method BLASTX
NCBI GI g3426064
BLAST score 209
E value 1.0e-16
Match length 74
% identity 46

NCBI Description (AJ007588) monooxygenase [Arabidopsis thaliana]

>gi_4467141_emb_CAB37510_ (AL035540) monooxygenase 2 (MO2)

[Arabidopsis thaliana]

Seq. No. 268967

Contig ID 17781_1.R1011 5'-most EST fwa700100038.h1

Seq. No. 268968

Contig ID 17784 1.R1011

5'-most EST LIB3115-025-P1-K1-D12

Seq. No. 268969

Contig ID 17797_1.R1011

5'-most EST LIB3062-002-Q1-K2-D10

Method BLASTX
NCBI GI g3434973
BLAST score 199
E value 2.0e-15
Match length 70
% identity 53

NCBI Description (AB008106) ethylene responsive element binding factor 4

[Arabidopsis thaliana]

Seq. No. 268970

Contig ID 17798_1.R1011 5'-most EST LIB83-003-Q1-E1-H1

Seq. No. 268971

Contig ID 17804_1.R1011 5'-most EST dyk700104165.h1

Seq. No. 268972

Contig ID 17804_2.R1011 5'-most EST uC-zmflb73258f04a2

Seq. No. 268973

Contig ID 17805_1.R1011

5'-most EST LIB3115-025-P1-K1-H2

Seq. No. 268974

Contig ID 17807_1.R1011

5'-most EST uC-zmflmo17055f09b1

Method BLASTX
NCBI GI g3540198
BLAST score 335
E value 5.0e-31
Match length 122



% identity (AC004260) Unknown protein [Arabidopsis thaliana] NCBI Description

268975 Seq. No.

17808 1.R1011 Contig ID yyf700350834.hl 5'-most EST

Method BLASTX g2245378 NCBI GI BLAST score 384 2.0e-36 E value Match length 192 % identity 46

(U83245) auxin response factor 1 [Arabidopsis thaliana] NCBI Description

Seq. No. 268976

Contig ID 17815 1.R1011

LIB3115-026-P1-K1-A5 5'-most EST

268977 Seq. No.

Contig ID 17829 1.R1011

LIB84-017-Q1-E1-C12 5'-most EST

268978 Seq. No.

Contig ID 17841 1.R1011 uC-zmflb73105c10a1 5'-most EST

Method BLASTX NCBI GI g113377 232 BLAST score 4.0e-19 E value 54 Match length % identity 85

NCBI Description ALCOHOL DEHYDROGENASE 2 >gi_82671_pir_A23084 alcohol dehydrogenase (EC 1.1.1.1) 2 - maize

>gi_22137_emb_CAA26001_ (X01965) Adh2-N (aa 1-379) [Zea

mays]

268979 Seq. No.

17851 1.R1011 Contig ID

LIB3116-006-Q1-K1-D7 5'-most EST

Method BLASTX NCBI GI g3831440 BLAST score 588 E value 1.0e-60 Match length 198 % identity 61

(AC005819) putative cytochrome P450 [Arabidopsis thaliana] NCBI Description

>qi 4415946 gb AAD20176 (AC006418) putative cytochrome

P450 [Arabidopsis thaliana]

268980 Seq. No.

17853 1.R1011 Contig ID

LIB189-026-Q1-E1-H2 5'-most EST

268981 Seq. No.

Contig ID 17857 1.R1011

LIB3115-026-P1-K1-G5 5'-most EST



Seq. No. 268982

Contig ID 17858_1.R1011

5'-most EST LIB3115-026-P1-K1-G6

Seq. No. 268983

Contig ID 17859_1.R1011 5'-most EST uC-zmflb73283b03b2

Method BLASTN
NCBI GI g22320
BLAST score 48
E value 1.0e-17
Match length 92
% identity 88

NCBI Description Maize H1 mRNA for H1 histone

Seq. No. 268984

Contig ID 17859 2.R1011

5'-most EST LIB3059-004-Q1-K1-F1

Seq. No. 268985

Contig ID 17860_1.R1011 5'-most EST LIB83-001-Q1-E1-F4

Method BLASTX
NCBI GI g4585994
BLAST score 657
E value 6.0e-69
Match length 173
% identity 73

NCBI Description (AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 268986

Contig ID 17874_1.R1011 5'-most EST wty700163071.h1

Method BLASTX
NCBI GI g2654212
BLAST score 1189
E value 1.0e-131

Match length 295 % identity 79

NCBI Description (AF035458) heat shock 70 protein [Spinacia oleracea]

>gi_2773052 (AF039084) heat shock 70 protein [Spinacia

oleracea]

Seq. No. 268987

Contig ID 17888 1.R1011

5'-most EST LIB3115-028-P1-K1-C6

Method BLASTX
NCBI GI g2316016
BLAST score 519
E value 3.0e-70
Match length 229
% identity 66

NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No. 268988

Contig ID 17898_1.R1011 5'-most EST ntr700074065.h1

37434



```
268989
Seq. No.
                    17899 1.R1011
Contig ID
5'-most EST
                    tfd700572122.h1
                    268990
Seq. No.
                    17900 1.R1011
Contig ID
                    LIB148-010-Q1-E1-C10
5'-most EST
Method
                    BLASTX
                    q2570523
NCBI GI
BLAST score
                    2049
E value
                    0.0e + 00
                    519
Match length
                    75
% identity
NCBI Description
                   (AF022873) inorganic phosphate transporter [Lycopersicon
                    esculentum]
                    268991
Seq. No.
                    17900 2.R1011
Contig ID
5'-most EST
                    cyk70\overline{0}047922.f1
Method
                    BLASTX
NCBI GI
                    q1502430
BLAST score
                    956
                    1.0e-104
E value
                    233
Match length
% identity
                    (U62331) phosphate transporter [Arabidopsis thaliana]
NCBI Description
                    >gi 2564661 (AF022872) phosphate transporter [Arabidopsis
                    thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate
Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770)
                    phosphate transporter, AtPT2 [Arabidopsis thaliana]
Seq. No.
                    268992
Contig ID
                    17900 3.R1011
5'-most EST
                    uC-zmrob73050a08b1
Method
                    BLASTX
NCBI GI
                    g1523798
BLAST score
                    528
E value
                    7.0e-54
                    130
Match length
                    77
% identity
NCBI Description (Y07682) phosphate transporter [Arabidopsis thaliana]
Seq. No.
                    268993
                    17900 4.R1011
Contig ID
5'-most EST
                    xyt70\overline{0}345689.h1
Method
                    BLASTX
                    g2208908
NCBI GI
                    495
BLAST score
E value
                    1.0e-70
                    181
Match length
                    76
% identity
```

Seq. No. 268994 Contig ID 17900

Contig ID 17900_5.R1011 5'-most EST qmh700029937.f1

NCBI Description (AB004809) phosphate transporter [Catharanthus roseus]



Method BLASTX
NCBI GI g1502430
BLAST score 296
E value 8.0e-27
Match length 70
% identity 83

NCBI Description (U62331) phosphate transporter [Arabidopsis thaliana] >gi_2564661 (AF022872) phosphate transporter [Arabidopsis thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770)

phosphate transporter, AtPT2 [Arabidopsis thaliana]

Seq. No. 268995

Contig ID 17901_1.R1011 5'-most EST fwa700101407.h1

Method BLASTX
NCBI GI g3882355
BLAST score 706
E value 1.0e-74
Match length 205
% identity 65

NCBI Description (U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis

thaliana]

Seq. No. 268996

Contig ID 17901_2.R1011

5'-most EST LIB3115-028-P1-K1-E2

Method BLASTX
NCBI GI g3882356
BLAST score 626
E value 3.0e-65
Match length 201
% identity 60

NCBI Description (U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis

thaliana]

Seq. No. 268997

Contig ID 17904_1.R1011

5'-most EST LIB3115-028-P1-K1-E5

Seq. No. 268998

Contig ID 17916_1.R1011 5'-most EST uC-zmflb73084e07b2

Seq. No. 268999

Contig ID 17918_1.R1011

5'-most EST uC-zmflm017016e02b1

Seq. No. 269000

Contig ID 17918_2.R1011 5'-most EST gwl700613751.h1

Method BLASTX
NCBI GI g4218121
BLAST score 178
E value 1.0e-12
Match length 148
% identity 34



```
(AL035353) putative protein [Arabidopsis thaliana]
NCBI Description
                  269001
Seq. No.
Contig ID
                  17918 3.R1011
                  uC-zmrob73080b02b1
5'-most EST
                   269002
Seq. No.
                  17930_1.R1011
Contig ID
                   xsy700213021.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                   g3298443
BLAST score
                   645
                   3.0e-67
E value
                   193
Match length
                   69
% identity
                   (AB010880) chloroplast ribosomal protein L17 [Nicotiana
NCBI Description
                   tabacum]
                   269003
Seq. No.
                   17930 2.R1011
Contig ID
5'-most EST
                   xsy700214915.h1
Method
                   BLASTX
                   g3298443
NCBI GI
                   226
BLAST score
                   1.0e-18
E value
                   52
Match length
% identity
                   85
                   (AB010880) chloroplast ribosomal protein L17 [Nicotiana
NCBI Description
                   tabacum]
                   269004
Seq. No.
                   17930 3.R1011
Contig ID
5'-most EST
                   pmx700083487.hl
                   269005
Seq. No.
                   17935 1.R1011
Contig ID
5'-most EST
                   xsy700208195.hl
                   269006
Seq. No.
                   17938 1.R1011
Contig ID
5'-most EST
                   LIB3115-029-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   q4455351
BLAST score
                   619
E value
                   5.0e-64
Match length
                   169
% identity
                  (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 269007

Contig ID 17940_1.R1011 5'-most EST xyt700343646.h1

Seq. No. 269008

Contig ID 17946_1.R1011 5'-most EST uC-zmflb73178h10b1

Method BLASTX



NCBI GI g3152595
BLAST score 1007
E value 1.0e-109
Match length 275
% identity 67

NCBI Description (AC002986) Similar to D. melanogaster sno gene gb_U95760.

EST gb N97148 and gb Z26221 come from this gene.

[Arabidopsis thaliana]

Seq. No. 269009

Contig ID 17953_1.R1011 5'-most EST cat700020854.r1

Method BLASTX
NCBI GI g4432857
BLAST score 172
E value 4.0e-12
Match length 80
% identity 49

NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No. 269010

Contig ID 17955_1.R1011 5'-most EST uC-zmflmo17125c10b1

Seq. No. 269011

Contig ID 17955_2.R1011 5'-most EST uC-zmflmo17023d11b1

Seq. No. 269012

Contig ID 17955_3.R1011

5'-most EST LIB3060-050-Q1-K1-C1

Seq. No. 269013

Contig ID 17955_4.R1011

5'-most EST uC-zmflmo17011d10b1

Seq. No. 269014

Contig ID 17955_5.R1011

5'-most EST uC-zmflmo17174e03b1

Method BLASTX
NCBI GI g2688824
BLAST score 143
E value 1.0e-08
Match length 58
% identity 55

NCBI Description (U93273) putative auxin-repressed protein [Prunus

armeniaca]

Seq. No. 269015

Contig ID 17955 8.R1011

5'-most EST LIB3137-013-Q1-K1-E9

Seq. No. 269016

Contig ID 17955_10.R1011 5'-most EST uC-zmflMo17003b11b1

Seq. No. 269017



```
17956 1.R1011
Contig ID
                  LIB3115-029-P1-K1-F11
5'-most EST
                  BLASTX
Method
                  q832876
NCBI GI
BLAST score
                  382
                  1.0e-36
E value
                  118
Match length
                  60
% identity
                  (L41345) ascorbate free radical reductase [Solanum
NCBI Description
                  lycopersicum] >gi_1097368_prf__2113407A ascorbate free
                  radical reductase [Lycopersicon esculentum]
                  269018
Seq. No.
                  17957_1.R1011
Contig ID
                  LIB83-008-Q1-E1-F11
5'-most EST
                  BLASTX
Method
                  g3080427
NCBI GI
                   375
BLAST score
                  7.0e-36
E value
                  80
Match length
                  85
% identity
                  (AL022604) putative protein [Arabidopsis thaliana]
NCBI Description
                  269019
Seq. No.
                  17959 1.R1011
Contig ID
                  xsy700208741.hl
5'-most EST
Method
                  BLASTX
                   g2245125
NCBI GI
                   171
BLAST score
                   6.0e-12
E value
                   43
Match length
                   72
% identity
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   269020
Seq. No.
Contig ID
                   17962 1.R1011
5'-most EST
                   ceu700426784.h1
                   BLASTX
Method
NCBI GI
                   q2194137
BLAST score
                   307
                   2.0e-27
E value
Match length
                   219
                   38
% identity
                   (AC002062) ESTs gb R29947, gb H76702 come from this gene.
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   269021
                   17962 2.R1011
Contig ID
5'-most EST
                   yne700378536.h1
                   269022
Seq. No.
Contig ID
                   17964 1.R1011
```

5'-most EST LIB3115-029-P1-K1-G7

Seq. No. 269023

Contig ID 18035 1.R1011

5'-most EST uC-zmroteosinte026a02b1



```
269024
Seq. No.
                  18038 1.R1011
Contig ID
                  LIB3115-031-P1-K1-C4
5'-most EST
                  BLASTX
Method
                  q4455180
NCBI GI
                  507
BLAST score
                  3.0e-51
E value
                  139
Match length
                  71
% identity
                  (AL035521) putative protein [Arabidopsis thaliana]
NCBI Description
                  269025
Seq. No.
                  18038 2.R1011
Contig ID
                  mwy700441606.hl
5'-most EST
                  BLASTX
Method
                   q1001532
NCBI GI
                   310
BLAST score
                   9.0e-29
E value
                   86
Match length
                   69
% identity
                  (D64000) hypothetical protein [Synechocystis sp.]
NCBI Description
                   269026
Seq. No.
                   18042 1.R1011
Contig ID
                   LIB3137-028-Q1-K1-C6
5'-most EST
Seq. No.
                   269027
                   18042 2.R1011
Contig ID
                   uC-zmflmo17240h05a1
5'-most EST
                   269028
Seq. No.
                   18045 1.R1011
Contig ID
                   LIB3115-031-P1-K1-D12
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4218150
BLAST score
                   158
                   3.0e-10
E value
                   64
Match length
                   45
% identity
NCBI Description (AJ132705) DnaJ2 protein [Anabaena variabilis]
                   269029
Seq. No.
                   18046 1.R1011
Contig ID
                   ntr700075811.h1
5'-most EST
Seq. No.
                   269030
                   18048 1.R1011
Contig ID
                   LIB3115-031-P1-K1-D4
 5'-most EST
                   269031
Seq. No.
                   18057 1.R1011
Contig ID
                   uwc700155338.h1
 5'-most EST
                   269032
 Seq. No.
```

18060_1.R1011

 $uC-zm\overline{f}lm017025g08b1$

Contig ID

5'-most EST

NCBI Description



```
Method
                   BLASTX
                   q3747111
NCBI GI
BLAST score
                   673
                   2.0e-70
E value
                   265
Match length
                   51
% identity
                  (AF095641) MTN3 homolog [Arabidopsis thaliana]
NCBI Description
                   269033
Seq. No.
                   18060 2.R1011
Contig ID
                   LIB3115-031-P1-K1-F3
5'-most EST
                   269034
Seq. No.
                   18060 3.R1011
Contig ID
                   uC-zm\overline{f}lmo17339f11b1
5'-most EST
                   BLASTX
Method
                   q3928090
NCBI GI
                   203
BLAST score
                   1.0e-15
E value
                   75
Match length
                   52
% identity
                  (AC005770) putative MTN3 protein [Arabidopsis thaliana]
NCBI Description
                   269035
Seq. No.
                   18060_4.R1011
Contig ID
                   LIB3060-008-Q1-K1-B3
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1619602
                   251
BLAST score
                   2.0e-21
E value
                   66
Match length
                   71
% identity
NCBI Description (Y08726) MtN3 [Medicago truncatula]
                   269036
Seq. No.
                   18060 5.R1011
Contig ID
5'-most EST
                   wyr700237914.h1
Method
                   BLASTX
                   g1619602
NCBI GI
                   367
BLAST score
                   5.0e-35
E value
                   100
Match length
                   65
 % identity
NCBI Description (Y08726) MtN3 [Medicago truncatula]
                   269037
Seq. No.
                   18068 1.R1011
Contig ID
 5'-most EST
                   uC-zmflb73261d03b3
                   BLASTX
Method
                   q4558661
NCBI GI
                   824
 BLAST score
                    1.0e-88
 E value
Match length
                    215
 % identity
```

[Arabidopsis thaliana]

(AC007063) putative malate oxidoreductase (NAD)



Seq. No. 269038

Contig ID 18068_2.R1011

5'-most EST LIB3115-031-P1-K1-G5

Method BLASTX
NCBI GI g585450
BLAST score 527
E value 1.0e-53
Match length 148
% identity 70

NCBI Description MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 65 KD ISOFORM

PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME) (NAD-ME) >gi_1076271_pir__A49983 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) precursor, mitochondrial -prince's feather >gi_437104 (U01162) C4 photosynthetic NAD-dependent malic enzyme subunit alpha precursor

[Amaranthus hypochondriacus]

Seq. No. 269039

Contig ID 18069 1.R1011

5'-most EST LIB3115-031-P1-K1-G7

Seq. No. 269040

Contig ID 18070 1.R1011 5'-most EST hbs701181658.h1

Method BLASTX
NCBI GI g4406820
BLAST score 352
E value 3.0e-33
Match length 108
% identity 68

NCBI Description (AC006201) putative ras superfamily member [Arabidopsis

thaliana]

Seq. No. 269041

Contig ID 18071_1.R1011

5'-most EST uC-zmflmo17215c06b1

Seq. No. 269042

Contig ID 18074_1.R1011 5'-most EST uC-zmflb73208b12b1

Method BLASTX
NCBI GI g4220534
BLAST score 1017
E value 1.0e-110
Match length 350
% identity 58

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 269043

Contig ID 18074_2.R1011 5'-most EST uC-zmflb73208b12a2

Seq. No. 269044

Contig ID 18074_3.R1011 5'-most EST nbm700470441.h1

Method BLASTX NCBI GI g4220534



```
BLAST score
                     404
  E value
                     3.0e - 39
  Match length
                     147
  % identity
                     56
  NCBI Description
                    (AL035356) putative protein [Arabidopsis thaliana]
  Seq. No.
                     269045
  Contig ID
                     18075 1.R1011
  5'-most EST
                     LIB3068-023-Q1-K1-C12
  Seq. No.
                     269046
  Contig ID
                     18079 2.R1011
  5'-most EST
                     clt700045575.f1
  Method
                     BLASTX
  NCBI GI
                     q1001355
  BLAST score
                     296
  E value
                     9.0e-27
  Match length
                     148
  % identity
                     45
  NCBI Description
                    (D64006) auxin-induced protein [Synechocystis sp.]
                     269047
  Seq. No.
  Contig ID
                     18082 1.R1011
  5'-most EST
                     LIB3115-032-P1-K1-A5
  Method
                     BLASTX
  NCBI GI
                     q3298542
A BLAST score
                     368
  E value
                     4.0e-35
  Match length
                     171
  % identity
                     42
  NCBI Description
                     (AC004681) putative cellulose synthase [Arabidopsis
                     thaliana]
  Seq. No.
                     269048
  Contig ID
                     18085 1.R1011
  5'-most EST
                     pmx700084633.h1
  Method
                     BLASTX
  NCBI GI
                     q2494162
  BLAST score
                     281
  E value
                     6.0e-25
  Match length
                     160
                     37
  % identity
                     HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II
  NCBI Description
                     PRECURSOR >gi 3879803 emb CAA87414 (Z47356) similar to
                     DNAJ [Caenorhabditis elegans]
                     269049
  Seq. No.
                     18088 1.R1011
  Contig ID
  5'-most EST
                     LIB3115-032-P1-K1-B4
  Seq. No.
                     269050
                     18090 1.R1011
  Contig ID
  5'-most EST
                     ceu700430518.h1
  Seq. No.
                     269051
```

37443

18094_1.R1011

LIB3115-032-P1-K1-C5

Contig ID 5'-most EST

Contig ID

Method

5'-most EST



```
BLASTX
Method
NCBI GI
                   q4581118
BLAST score
                   314
E value
                   1.0e-28
Match length
                   153
% identity
                   46
NCBI Description
                  (AC005825) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   269052
                  18095 1.R1011
Contig ID
                   ymt70\overline{0}221519.h1
5'-most EST
                  BLASTX
Method
                   g4586054
NCBI GI
BLAST score
                   372
E value
                   4.0e-35
Match length
                  175
% identity
                   46
NCBI Description
                  (AC007020) unknown protein [Arabidopsis thaliana]
                   269053
Seq. No.
                  18095 4.R1011
Contig ID
5'-most EST
                  pmx700087868.h1
                  269054
Seq. No.
Contiq ID
                  18099_1.R1011
5'-most EST
                  LIB36-003-Q1-E1-B2
Method
                  BLASTX
NCBI GI
                   q4220594
BLAST score
                   395
E value
                   3.0e-38
Match length
                   105
% identity
                   73
NCBI Description
                  (AB011264) nicochianamine synthase 3 [Hordeum vulgare]
Seq. No.
                   269055
Contig ID
                   18099 2.R1011
5'-most EST
                  LIB3060-048-Q1-K1-D5
Method
                  BLASTX
NCBI GI
                   g4220594
BLAST score
                   268
E value
                   1.0e-23
                  74
Match length
                  72
% identity
NCBI Description (AB011264) nicochianamine synthase 3 [Hordeum vulgare]
                  269056
Seq. No.
Contig ID
                  18100 1.R1011
5'-most EST
                  LIB3115-032-P1-K1-D8
Seq. No.
                  269057
Contig ID
                  18101 1.R1011
5'-most EST
                  LIB3115-032-P1-K1-E1
Seq. No.
                  269058
```

37444

18114 1.R1011

BLASTX

LIB3115-032-P1-K1-G7



q1707015 NCBI GI 589 BLAST score 7.0e-61 E value Match length 203 % identity 60

(U78721) protein phosphatase 2C isolog [Arabidopsis NCBI Description

thaliana]

269059 Seq. No.

Contig ID 18117_1.R1011

5'-most EST LIB3115-032-P1-K1-H10

269060 Seq. No.

18119 1.R1011 Contig ID

5'-most EST LIB3115-032-P1-K1-H3

269061 Seq. No.

Contig ID 18119 2.R1011

LIB3059-049-Q1-K1-E12 5'-most EST

Seq. No. 269062

Contig ID 18122_1.R1011

5'-most EST LIB3067-037-Q1-K1-F6

BLASTX Method NCBI GI q3915665 BLAST score 346 E value 2.0e-32 Match length 127 51 % identity

NCBI Description ELONGATION FACTOR G (EF-G) >gi 2688449 (AE001155)

translation elongation factor G (fus-1) [Borrelia

burgdorferi]

269063 Seq. No.

Contig ID 18126 1.R1011

5'-most EST uC-zmroteosinte049e03b1

Method BLASTX NCBI GI q3876299 BLAST score 217 E value 2.0e-17 Match length 113 % identity 42

(Z71180) similar to BPTI/KUNITZ inhibitor domain; cDNA EST NCBI Description

EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabdi... >gi 3880760 emb CAA16311 (AL021474) similar to BPTI/KUNITZ inhibitor domain; cDNA EST EMBL: D68293 comes from this

gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes

from this gene [Caenorhab

269064 Seq. No.

18138 1.R1011 Contig ID 5'-most EST uC-zmflb73194f06b2

Seq. No. 269065



```
18157 1.R1011
Contig ID
5'-most EST
                   xjt70\overline{0}094662.h1
                   269066
Seq. No.
                   18157 3.R1011
Contig ID
                   uC-zm\overline{f}lmo17201h04a1
5'-most EST
Seq. No.
                   269067
Contig ID
                   18162 1.R1011
5'-most EST
                   LIB3115-034-P1-K2-H11
Method
                   BLASTN
NCBI GI
                   q22192
BLAST score
                   43
E value
                   5.0e-15
Match length
                   79
                   89
% identity
NCBI Description
                  Z.mays B-I gene for B transcriptional activator
Seq. No.
                   269068
Contig ID
                   18165 1.R1011
                   LIB3115-034-P1-K2-H5
5'-most EST
Seq. No.
                   269069
Contig ID
                   18169 1.R1011
5'-most EST
                   uC-zmflb73345q12a2
Method
                   BLASTX
NCBI GI
                   q1655536
BLAST score
                   323
E value
                   7.0e-30
Match length
                   70
% identity
                   83
NCBI Description
                   (Y09095) chloride channel [Arabidopsis thaliana]
                   >gi 1742957 emb CAA96059 (Z71447) CLC-c chloride channel
                   protein [Arabidopsis thaliana]
Seq. No.
                   269070
                   18170 1.R1011
Contig ID
                   tfd700573585.h1
5'-most EST
Seq. No.
                   269071
                   18171 1.R1011
Contig ID
5'-most EST
                   gct701167814.h1
Method
                   BLASTX
NCBI GI
                   g4584524
BLAST score
                   442
E value
                   4.0e-48
                   159
Match length
% identity
NCBI Description
                  (AL049607) putative protein [Arabidopsis thaliana]
                   269072
Seq. No.
```

Contig ID 18176_1.R1011 5'-most EST hbs701183639.h1

Method BLASTX
NCBI GI g3779218
BLAST score 377
E value 2.0e-53



Match length 141 % identity 81

NCBI Description (AF030879) protein kinase CPK1 [Solanum tuberosum]

Seq. No. 269073

Contig ID 18178_1.R1011 5'-most EST fdz701161530.h1

Seq. No. 269074

Contig ID 18178_2.R1011 5'-most EST cyk700050037.f1

Method BLASTX
NCBI GI g3820648
BLAST score 329
E value 1.0e-30
Match length 86
% identity 69

NCBI Description (Y12636) allene oxide synthase [Arabidopsis thaliana]

Seq. No. 269075

Contig ID 18178_4.R1011 5'-most EST xsy700213289.h1

Method BLASTN
NCBI GI g2288968
BLAST score 37
E value 2.0e-11
Match length 41
% identity 98

NCBI Description Zea mays mRNA for glutathione transferase

Seq. No. 269076

Contig ID 18184_1.R1011 5'-most EST tzu700206319.h1

Seq. No. 269077

Contig ID 18184 2.R1011

5'-most EST LIB189-032-Q1-E1-C9

Seq. No. 269078

Contig ID 18185 1.R1011

5'-most EST uC-zmroteosinte120h07b2

Method BLASTX
NCBI GI g2529678
BLAST score 784
E value 2.0e-83
Match length 247
% identity 62

NCBI Description (AC002535) unknown protein [Arabidopsis thaliana]

Seq. No. 269079

Contig ID 18189_1.R1011 5'-most EST tfd700569475.h2

Method BLASTX
NCBI GI g3319354
BLAST score 410
E value 5.0e-40
Match length 102



% identity 83
NCBI Description (AF077407) contains similarity to sugar transporters (Pfam: sugar_tr.hmm, score: 395.39) [Arabidopsis thaliana]

Seq. No. 269080

Contig ID 18190 1.R1011

5'-most EST LIB3115-036-P1-K2-E4

Seq. No. 269081

Contig ID 18190_4.R1011 5'-most EST cat700017901.r1

Seq. No. 269082

Contig ID 18193 1.R1011

5'-most EST LIB3068-038-Q1-K1-G2

Method BLASTX
NCBI GI g1843440
BLAST score 208
E value 2.0e-16
Match length 152
% identity 38

NCBI Description (Z70521) unknown [Cucumis melo]

Seq. No. 269083

Contig ID 18203_1.R1011

5'-most EST uC-zmflmo17270e07b1

Method BLASTX
NCBI GI g3608137
BLAST score 466
E value 9.0e-46
Match length 399
% identity 31

NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]

Seq. No. 269084

Contig ID 18203_2.R1011 5'-most EST arm700460779.h1

Method BLASTX
NCBI GI g4056438
BLAST score 158
E value 5.0e-10
Match length 64
% identity 44

NCBI Description (AC005990) F508.11 [Arabidopsis thaliana]

Seq. No. 269085

Contig ID 18203_10.R1011 5'-most EST uC-zmflmo17133b08b1

Seq. No. 269086

Contig ID 18208_1.R1011

5'-most EST uC-zmflmo17263b10a2

Method BLASTX
NCBI GI g2494144
BLAST score 779
E value 3.0e-91
Match length 329

% identity (AC002329) predicted leucine-rich protein [Arabidopsis NCBI Description thalianal 269087 Seq. No. Contig ID 18213 1.R1011 LIB3115-038-P1-K2-B4 5'-most EST Seq. No. 269088 18217 1.R1011 Contig ID LIB143-039-Q1-E1-E12 5'-most EST BLASTX Method NCBI GI q3378650 BLAST score 659 E value 7.0e-69 Match length 180 % identity 68 (X97606) abscisic acid activated [Medicago sativa] NCBI Description Seq. No. 269089 Contig ID 18217 2.R1011 5'-most EST LIB189-016-Q1-E1-E1 Method BLASTX NCBI GI q3236259 BLAST score 793 E value 1.0e-84 Match length 198 75 % identity (AC004684) putative alcohol dehydrogenase [Arabidopsis NCBI Description thaliana] 269090 Seq. No. 18217_3.R1011 Contig ID 5'-most EST LIB3068-022-Q1-K1-G2 Seq. No. 269091 18218 1.R1011 Contig ID

Contig ID 18218_1.R1011 5'-most EST rvt700550649.h1

Method BLASTX
NCBI GI g3236247
BLAST score 918
E value 3.0e-99
Match length 289
% identity 57

NCBI Description (AC004684) SCARECROW-like protein [Arabidopsis thaliana]

Seq. No. 269092

Contig ID 18238_1.R1011 5'-most EST uC-zmflb73295a02b2

Seq. No. 269093

Contig ID 18238_2.R1011 5'-most EST wty700170196.h1

Seq. No. 269094

Contig ID 18239_1.R1011 5'-most EST fC-zmst700336272a5



```
BLASTX
Method
                  q1066163
NCBI GI
                  1267
BLAST score
E value
                  1.0e-140
Match length
                   333
                  73
% identity
                  (X93015) glyoxysomal beta-ketoacyl-thiolase [Brassica
NCBI Description
                  napus]
                  269095
Seq. No.
Contig ID
                  18245_1.R1011
5'-most EST
                  LIB189-003-Q1-E1-G10
Method
                  BLASTX
NCBI GI
                   q2980806
BLAST score
                   579
E value
                   3.0e-59
Match length
                  258
                   45
% identity
NCBI Description
                  (AL022197) putative protein [Arabidopsis thaliana]
Seq. No.
                   269096
Contig ID
                   18245 2.R1011
5'-most EST
                  rvt700549217.h1
                   269097
Seq. No.
                   18248 1.R1011
Contig ID
5'-most EST
                  uC-zmroteosinte024f05b1
                   269098
Seq. No.
Contig ID
                   18252 1.R1011
                  LIB3061-005-Q1-K1-C7
5'-most EST
Method
                  BLASTX
NCBI GI
                   g736721
BLAST score
                   263
E value
                   7.0e-23
                   90
Match length
                   59
% identity
                  (D49833) stearoyl-acyl carrier protein desaturse [Sesamum
NCBI Description
                   indicum]
                   269099
Seq. No.
                   18271 1.R1011
Contig ID
                   LIB3115-039-P1-K2-F1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g421845
BLAST score
                   411
                   2.0e-40
E value
Match length
                   110
                   74
% identity
NCBI Description RecA homolog - Arabidopsis thaliana (fragment) > gi 166841
```

Seq. No. 269100 Contig ID 18277 1.R1011

5'-most EST LIB3115-039-P1-K2-G1

Method BLASTX NCBI GI g4512703

(M98039) replicase [Arabidopsis thaliana]



```
BLAST score
                   192
                   2.0e-14
E value
                   49
Match length
                   71
% identity
                   (AC006569) unknown protein [Arabidopsis thaliana]
NCBI Description
                   269101
Seq. No.
                   18279 1.R1011
Contig ID
                   LIB3060-010-Q1-K1-A5
5'-most EST
                   BLASTX
Method
NCBI GI
                   g546037
                   622
BLAST score
                   1.0e-64
E value
Match length
                   118
                   100
% identity
                   (S69196) IRF170=rps operon [corn, seedlings, Peptide, 170
NCBI Description
                   aa] [Zea mays]
                   269102
Seq. No.
                   18279 3.R1011
Contig ID
                   LIB3060-006-Q1-K1-E7
5'-most EST
                   BLASTX
Method
                   g82231
NCBI GI
                   423
BLAST score
                   4.0e-41
E value
Match length
                   82
                   98
% identity
                   hypothetical protein 82 - common tobacco chloroplast
NCBI Description
                   >gi 225200 prf 1211235AE ORF 82 [Nicotiana tabacum]
                   269103
Seq. No.
                   18288 1.R1011
Contig ID
                   \mathtt{uC-zm}\overline{\mathtt{f}}\mathtt{lb73239d12b2}
5'-most EST
                   BLASTX
Method
                   g2244759
NCBI GI
BLAST score
                   1997
E value
                   0.0e + 00
Match length
                   467
                   75
% identity
                  (Z97335) selenium-binding protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   269104
                   18290 1.R1011
Contig ID
5'-most EST
                   LIB3116-014-Q1-K1-G9
Seq. No.
                   269105
Contig ID
                   18300 1.R1011
5'-most EST
                   LIB84-026-Q1-E1-F9
Method
                   BLASTX
NCBI GI
                   g1684851
BLAST score
                   211
E value
                   8.0e-17
                   109
Match length
% identity
                   (U77935) DnaJ-like protein [Phaseolus vulgaris]
NCBI Description
```

Seq. No. 269106



Contig ID 18307 1.R1011

5'-most EST LIB3279-059-P1-K1-F9

Method BLASTX
NCBI GI g2980784
BLAST score 227
E value 3.0e-18
Match length 67
% identity 64

NCBI Description (AL022198) puative protein [Arabidopsis thaliana]

Seq. No. 269107

Contig ID 18307_2.R1011 5'-most EST xdb700338325.h1

Seq. No. 269108

Contig ID 18307_3.R1011 5'-most EST wty700168837.h1

Method BLASTX
NCBI GI g2980784
BLAST score 212
E value 9.0e-17
Match length 75
% identity 59

NCBI Description (AL022198) puative protein [Arabidopsis thaliana]

Seq. No. 269109

Contig ID - 18308_1.R1011 5'-most EST wty700170377.h1

Method BLASTX
NCBI GI g2244856
BLAST score 191
E value 3.0e-18
Match length 133
% identity 42

NCBI Description (Z97337) unnamed protein product [Arabidopsis thaliana]

Seq. No. 269110

Contig ID 18326_1.R1011 5'-most EST uer700577440.h1

Seq. No. 269111

Contig ID 18327_1.R1011 5'-most EST pmx700086496.h1

Method BLASTX
NCBI GI g4321762
BLAST score 517
E value 2.0e-52
Match length 102
% identity 100

NCBI Description (AF061107) transcription factor MYC7E [Zea mays]

Seq. No. 269112

Contig ID 18332_1.R1011

5'-most EST uC-zmroteosinte007c10b1

Method BLASTX NCBI GI g1800147 BLAST score 553



```
2.0e-56
E value
                   174
Match length
                   64
% identity
                   (U83655) membrane associated protein [Arabidopsis thaliana]
NCBI Description
                   269113
Seq. No.
                   18332 2.R1011
Contig ID
                   LIB3137-041-Q1-K1-E11
5'-most EST
                   BLASTX
Method
                   g3080389
NCBI GI
                   436
BLAST score
                   7.0e-43
E value
                   118
Match length
                   76
% identity
                   (AL022603) putative membrane associated protein
NCBI Description
                   [Arabidopsis thaliana]
                   269114
Seq. No.
                   18333 1.R1011
Contiq ID
                   LIB3116-014-Q1-K1-C3
5'-most EST
                   269115
Seq. No.
                   18341 1.R1011
 Contig ID
                   LIB3116-013-Q1-K1-F7
5'-most EST
                   269116
 Seq. No.
                   18344 1.R1011
 Contig ID
                   clt700041647.fl
 5'-most EST
                   BLASTX
 Method
                   g4115925
 NCBI GI
                   572
 BLAST score
                   9.0e-59
 E value
                   144
 Match length
                    46
 % identity
                   (AF118222) contains similarity to RNA recognition motifs
 NCBI Description
                    (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
                    >qi 4539439 emb CAB40027.1 (AL049523) RNA-binding protein
                    [Arabidopsis thaliana]
                    269117
 Seq. No.
                    18344 2.R1011
 Contig ID
                    LIB3116-013-Q1-K1-G6
 5'-most EST
                    BLASTX
 Method
 NCBI GI
                    g4115925
 BLAST score
                    303
                    2.0e-27
 E value
```

Match length 82 % identity 71

(AF118222) contains similarity to RNA recognition motifs NCBI Description (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein [Arabidopsis thaliana]

269118 Seq. No.

18348 1.R1011 Contig ID $uC-zm\overline{f}lmo17059b11b1$ 5'-most EST

BLASTX Method



NCBI GI g128350 BLAST score 153 E value 2.0e-09 Match length 37 % identity 78

NCBI Description FERREDOXIN--NITRITE REDUCTASE PRECURSOR

Seq. No. 269119

Contig ID 18358_1.R1011 5'-most EST uC-zmrob73034d05a1

Method BLASTX
NCBI GI g1703447
BLAST score 247
E value 6.0e-21
Match length 75
% identity 64

NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi_496102

(L19141) L-asparaginase [Lupinus albus]

Seq. No. 269120

Contig ID 18360_1.R1011 5'-most EST cat700021121.r1

Seq. No. 269121

Contig ID 18365_1.R1011 5'-most EST rvt700549595.h1

Method BLASTX
NCBI GI g3024552
BLAST score 676
E value 4.0e-71
Match length 133
% identity 98

NCBI Description RAS-RELATED PROTEIN RGP2 (GTP-BINDING REGULATORY PROTEIN

RGP2) >gi_419797_pir__S30273 GTP-binding protein rgp2 - rice >gi_218204_dbj_BAA02437_ (D13152) GTP binding protein [Oryza sativa] >gi_446772_prf__1912297A rgp2 gene [Oryza

sativa]

 Seq. No.
 269122

 Contig ID
 18365_3.R1011

 5'-most EST
 pmx700084977.h1

Method BLASTX
NCBI GI g3024552
BLAST score 382
E value 5.0e-37
Match length 77
% identity 96

NCBI Description RAS-RELATED PROTEIN RGP2 (GTP-BINDING REGULATORY PROTEIN

RGP2) >gi_419797_pir__S30273 GTP-binding protein rgp2 - rice >gi_218204_dbj_BAA02437_ (D13152) GTP binding protein [Oryza sativa] >gi_446772_prf__1912297A rgp2 gene [Oryza

sativa]

Seq. No. 269123

Contig ID 18372_1.R1011

5'-most EST uC-zmroteosinte004f06b1

Method BLASTX



g2981475 NCBI GI 793 BLAST score 1.0e-84 E value 206 Match length 69 % identity (AF053084) putative cinnamyl alcohol dehydrogenase [Malus NCBI Description domestica] 269124 Seq. No. 18375 1.R1011 Contig ID LIB3116-013-Q1-K1-B12 5'-most EST BLASTX Method g3540181 NCBI GI 209 BLAST score 1.0e-16 E value 96 Match length 55 % identity (AC004122) Unknown protein [Arabidopsis thaliana] NCBI Description 269125 Seq. No. 18377_1.R1011 Contig ID LIB3279-059-P1-K1-A10 5'-most EST 269126 Seq. No. 18378 1.R1011 Contig ID LIB3136-020-Q1-K1-B3 5'-most EST 269127 Seq. No. 18384 1.R1011 Contig ID LIB3116-012-Q1-K1-F7 5'-most EST 269128 Seq. No. 18388_1.R1011 Contig ID LIB3151-045-Q1-K1-C7 5'-most EST BLASTX Method NCBI GI g2623248 BLAST score 1561 1.0e-174 E value 292 Match length 97 % identity NCBI Description (AF030882) SU1 isoamylase [Zea mays] 269129 Seq. No. 18388 2.R1011 Contig ID LIB3180-047-P2-B3 5'-most EST BLASTX Method NCBI GI q2623248 BLAST score 787 E value 2.0e-95 163 Match length 100 % identity NCBI Description (AF030882) SU1 isoamylase [Zea mays]

Seq. No. 269130

 Seq. No.
 269130

 Contig ID
 18390_1.R1011

 5'-most EST
 gwl700613831.h1

Method BLASTX



NCBI GI g3582339 BLAST score 502 E value 1.0e-50 Match length 136 % identity 71

NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]

Seq. No. 269131

Contig ID 18391 1.R1011

5'-most EST LIB3116-012-Q1-K1-C2

Seq. No. 269132

Contig ID 18392_1.R1011 5'-most EST tfd700572183.h1

Method BLASTX
NCBI GI g3287494
BLAST score 1575
E value 1.0e-176
Match length 371
% identity 84

NCBI Description (D78504) similar to yeast SRP1 [Oryza sativa]

Seq. No. 269133

Contig ID 18394_1.R1011

5'-most EST LIB3116-012-Q1-K1-D3

Seq. No. 269134

Contig ID 18395_1.R1011 5'-most EST xyt700344373.h1

Method BLASTX
NCBI GI g4587570
BLAST score 373
E value 6.0e-35
Match length 486
% identity 28

NCBI Description (AC006550) Strong similarity to gi_2244833 centromere

protein homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97337. ESTs gb_T20765 and gb_AA586277 come from

this gene

Seq. No. 269135

Contig ID 18395_2.R1011 5'-most EST tfd700570806.h1

Seq. No. 269136

Contig ID 18395 3.R1011

5'-most EST LIB3136-037-P1-K1-E3

Seq. No. 269137

Contig ID 18398 1.R1011

5'-most EST uC-zmflmo17158c09b1

Seq. No. 269138

Contig ID 18403 1.R1011

5'-most EST LIB3116-012-Q1-K1-A7

Seq. No. 269139

```
Contig ID
                   18404_1.R1011
5'-most EST
                   uC-zmflb73201e10b1
Seq. No.
                   269140
Contig ID
                   18412 1.R1011
5'-most EST
                   LIB3116-012-Q1-K1-C10
Method
                   BLASTX
NCBI GI
                   g3540197
BLAST score
                   320
E value
                   2.0e-29
Match length
                   136
% identity
                   53
NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]
                   269141
Seq. No.
Contig ID
                   18414 1.R1011
5'-most EST
                   LIB3116-011-Q1-K1-F2
Method
                   BLASTX
NCBI GI
                   g4506597
BLAST score
                   449
E value
                   7.0e-45
Match length
                   109
% identity
                   76
NCBI Description ribosomal protein L12 >gi_266921_sp_P30050 RL12 HUMAN 60S
                   RIBOSOMAL PROTEIN L12 >gi_479851 pir S35531 ribosomal
                   protein L12 - human >gi_1\overline{18}6800 (\overline{L}065\overline{05}) ribosomal protein
                   L12 [Homo sapiens]
                   269142
Seq. No.
Contig ID
                   18430 1.R1011
5'-most EST
                   wyr700241184.h1
Method
                   BLASTX
NCBI GI
                   q4510363
BLAST score
                   549
E value
                   6.0e-56
Match length
                   139
% identity
NCBI Description
                   (AC007017) putative DNA-binding protein [Arabidopsis
                   thaliana]
Seq. No.
                   269143
                   18430 2.R1011
Contig ID
5'-most EST
                   LIB3069-026-Q1-K1-F12
Method
                   BLASTX
NCBI GI
                   g4510363
BLAST score
                   214
E value
                   5.0e-17
Match length
                   66
% identity
                   (AC007017) putative DNA-binding protein [Arabidopsis
```

Seq. No. 269144

NCBI Description

Contig ID 18430 3.R1011 5'-most EST ypc700805472.h1

thaliana]

Seq. No. 269145



```
18432 1.R1011
Contig ID
5'-most EST
                   ceu700433803.h1
Seq. No.
                   269146
Contig ID
                   18433 1.R1011
5'-most EST
                  LIB189-015-Q1-E1-E3
Method
                  BLASTX
NCBI GI
                  g4097522
BLAST score
                   485
E value
                   8.0e-49
Match length
                  153
% identity
                   56
NCBI Description
                  (U63534) cinnamyl alcohol dehydrogenase [Fragaria x
                  ananassa]
                   269147
Seq. No.
Contig ID
                   18441 1.R1011
                  mwy70\overline{0}441605.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1703200
BLAST score
                  1468
E value
                   1.0e-163
Match length
                   354
% identity
                   74
NCBI Description PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase
                   [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353)
                  protein kinase [Arabidopsis thaliana]
                  >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2)
                   [Arabidopsis thaliana]
Seq. No.
                  269148
                  18441 3.R1011
Contig ID
                  uC-zmflb73278d05a2
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2911280
BLAST score
                  725
E value
                  2.0e-76
Match length
                  359
% identity
NCBI Description (U73937) PK12 protein kinase [Nicotiana tabacum]
Seq. No.
                  269149
Contig ID
                  18441 5.R1011
5'-most EST
                  uer700581504.h1
Method
                  BLASTX
NCBI GI
                  g1703200
BLAST score
                  248
E value
                  1.0e-20
Match length
                  138
% identity
NCBI Description
                  PROTEIN KINASE AFC2 >gi 601789 (U16177) protein kinase
                  [Arabidopsis thaliana] >gi 642130 dbj BAA08214 (D45353)
                  protein kinase [Arabidopsis thaliana]
```

Seq. No. 269150

[Arabidopsis thaliana]

>gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2)



Contig ID 18441_7.R1011 5'-most EST ceu700433455.h1

Seq. No. 269151

Contig ID 18441_11.R1011 5'-most EST pmx700085167.h1

Seq. No. 269152

Contig ID 18441_12.R1011 5'-most EST hbs701185916.h1

Seq. No. 269153

Contig ID 18443_1.R1011

5'-most EST LIB189-002-Q1-E1-A5

Seq. No. 269154

Contig ID 18446_1.R1011 5'-most EST uC-zmflb73418f08a1

Seq. No. 269155

Contig ID 18450 1.R1011

5'-most EST LIB3062-025-Q1-K1-H1

Method BLASTX
NCBI GI g114885
BLAST score 279
E value 2.0e-24
Match length 134
% identity 44

NCBI Description BACTERIOFERRITIN COMIGRATORY PROTEIN >gi_538729 pir B49749

bacterioferritin comigratory protein - Escherichia coli >gi_1788825 (AE000335) bacterioferritin comigratory protein [Escherichia coli] >gi_1799908_dbj_BAA16358_ (D90876) bacterioferritin comigratory protein [Escherichia coli] >gi_1805539_dbj_BAA16368_ (D90877) bacterioferritin

comigratory protein [Escherichia coli] >gi_2668495 (M63654) bacterioferritin comigratory protein [Escherichia coli]

Seq. No. 269156

Contig ID 18450 2.R1011

5'-most EST LIB3060-005-Q1-K1-B9

Seq. No. 269157

Contig ID 18453 1.R1011

5'-most EST LIB3116-011-Q1-K1-B2

Method BLASTX
NCBI GI g2341033
BLAST score 510
E value 9.0e-52
Match length 142

% identity 68

NCBI Description (AC000104) Similar to Babesia aldo-keto reductase

(gb_M93122). [Arabidopsis thaliana]

Seq. No. 269158

Contig ID 18458 1.R1011

5'-most EST LIB3060-014-Q1-K1-H3

Seq. No. 269159

Contig ID 18465 1.R1011 -

5'-most EST LIB3116-010-Q1-K1-G10

Method BLASTX
NCBI GI g3293559
BLAST score 540
E value 3.0e-55
Match length 149
% identity 68

NCBI Description (AF072694) germin-like protein 7 [Oryza sativa]

Seq. No. 269160

Contig ID 18470_1.R1011 5'-most EST vux700157572.h1

Method BLASTX
NCBI GI g4376203
BLAST score 435
E value 6.0e-43
Match length 150
% identity 57

NCBI Description (U35226) putative cytochrome P-450 [Nicotiana

plumbaginifolia]

Seq. No. 269161

Contig ID 18473 1.R1011

5'-most EST LIB3116-010-Q1-K1-D10

Method BLASTX
NCBI GI g2654226
BLAST score 654
E value 1.0e-68
Match length 74

NCBI Description (AJ003069) aminoacyl-t-RNA synthetase [Arabidopsis

thaliana]

Seq. No. 269162

Contig ID 18477 1.R1011 5'-most EST ceu700424574.h1

Seq. No. 269163

Contig ID 18478 1.R1011 5'-most EST uwc700154128.h1

Method BLASTX
NCBI GI g3548801
BLAST score 366
E value 2.0e-34
Match length 184
% identity 41

NCBI Description (AC005313) putative transmembrane protein [Arabidopsis

thaliana] >gi_4335768_gb_AAD17445_ (AC006284) putative

integral membrane protein [Arabidopsis thaliana]

Seq. No. 269164

Contig ID 18481_1.R1011

5'-most EST LIB189-010-Q1-E1-G8

Method BLASTX NCBI GI g4097585



BLAST score 308 E value 6.0e-28 Match length 144 % identity 45

NCBI Description (U64925) NTGP4 [Nicotiana tabacum]

Seq. No. 269165

Contig ID 18489_1.R1011

5'-most EST LIB3116-010-Q1-K1-A4

Seq. No. 269166

Contig ID 18490_1.R1011

5'-most EST LIB189-032-Q1-E1-B12

Method BLASTN
NCBI GI g3821780
BLAST score 35
E value 5.0e-10
Match length 35
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 269167

Contig ID 18496 1.R1011

5'-most EST LIB3136-005-Q1-K1-D12

Seq. No. 269168

Contig ID 18498 1.R1011

5'-most EST LIB3116-010-Q1-K1-C11

Seq. No. 269169

Contig ID 18504_1.R1011

5'-most EST uC-zmrob73055d09a1

Method BLASTX
NCBI GI g3025189
BLAST score 191
E value 4.0e-14
Match length 90

Match length 90 % identity 43

NCBI Description HYPOTHETICAL 67.1 KD PROTEIN SLL1770

>gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis

sp.]

Seq. No. 269170

Contig ID 18505_1.R1011 5'-most EST zuv700356672.h1

Method BLASTX
NCBI GI g3881760
BLAST score 222
E value 2.0e-17
Match length 160
% identity 34

NCBI Description (Z37093) alternative splicing in ZK669.1b; cDNA EST

EMBL:D36962 comes from this gene; cDNA EST EMBL:D67348 comes from this gene; cDNA EST EMBL:D33981 comes from this gene [Caenorhabditis elegans] >gi_3881778_emb_CAA86847_(Z46812) alternative splicing in ZK669.1b; cDNA EST EMBL:D36962 comes from this gene; cDNA EST EMBL:D67348



comes from this gene; cDNA EST EMBL:D33981 comes from this gene [Caenorhabditis elegans]

 Seq. No.
 269171

 Contig ID
 18505_2.R1011

 5'-most EST
 uC-zmflb73131c05b2

Seq. No. 269172

Contig ID 18511 1.R1011

5'-most EST LIB3116-008-Q1-K1-H12

Seq. No. 269173

Contig ID 18512_1.R1011 5'-most EST dyk700104180.h1

Seq. No. 269174

Contig ID 18518_1.R1011

5'-most EST LIB143-022-Q1-E1-D5

Seq. No. 269175

Contig ID 18523 1.R1011

5'-most EST uC-zmroteosinte030f07b1

Seq. No. 269176

Contig ID 18523_2.R1011 5'-most EST hbs701184576.h1

Seq. No. 269177

Contig ID 18526 1.R1011

5'-most EST LIB3181-008-P1-M1-H4

Method BLASTX
NCBI GI g4432850
BLAST score 358
E value 6.0e-34
Match length 150

% identity 45

NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

>gi_4567240_gb_AAD23654.1_AC007070_3 (AC007070)

hypothetical protein [Arabidopsis Thaliana]

Seq. No. 269178

Contig ID 18527_1.R1011 5'-most EST qmh700028112.f1

Seq. No. 269179

Contig ID 18528_1.R1011

5'-most EST LIB3060-019-Q1-K1-D4

Seq. No. 269180

Contig ID 18535_1.R1011

5'-most EST LIB3116-009-Q1-K1-D12

Method BLASTX
NCBI GI g2245125
BLAST score 151
E value 1.0e-09
Match length 45
% identity 62

37462



```
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
                   269181
Seq. No.
Contig ID
                   18537 1.R1011
                   LIB3116-009-Q1-K1-D4
5'-most EST
Method
                   BLASTX
                   q4510345
NCBI GI
                   319
BLAST score
E value
                   4.0e-29
Match length
                   149
                   46
% identity
                  (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                   269182
Seq. No.
Contig ID
                   18542 1.R1011
                   LIB3116-008-Q1-K1-C11
5'-most EST
                   269183
Seq. No.
                   18542 3.R1011
Contig ID
5'-most EST
                   LIB83-012-Q1-E1-B3
Method
                   BLASTN
                   g3821780
NCBI GI
BLAST score
                   36
E value
                   7.0e-11
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   269184
Seq. No.
                   18549 1.R1011
Contig ID
5'-most EST
                   mwy700440650.h1
                   BLASTX
Method
NCBI GI
                   q3367522
BLAST score
                   534
E value
                   3.0e-54
Match length
                   172
% identity
                   59
                   (AC004392) EST gb T04691 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   269185
                   18550 1.R1011
Contig ID
5'-most EST
                   nbm70\overline{0}475536.h1
Seq. No.
                   269186
Contig ID
                   18554 1.R1011
                   LIB83-012-Q1-E1-C6
5'-most EST
                   {\tt BLASTX}
Method
NCBI GI
                   g3123295
BLAST score
                   216
                   3.0e-17
E value
Match length
                   116
                   42
% identity
```

thaliana]

(AF026473) calmodulin-related protein [Arabidopsis

NCBI Description CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi 2583169

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 Seq. No.
 269187

 Contig ID
 18562_2.R1011

 5'-most EST
 fdz701163453.h1

 Seq. No.
 269188

 Contig ID
 18564_1.R1011

 5'-most EST
 xmt700258012.h1

Method BLASTX
NCBI GI g3108053
BLAST score 2585
E value 0.0e+00
Match length 510
% identity 97

NCBI Description (AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea

mays]

Seq. No. 269189

Contig ID 18564 2.R1011

5'-most EST LIB3150-006-Q1-N1-C10

Method BLASTX
NCBI GI g3108053
BLAST score 492
E value 1.0e-49
Match length 101
% identity 97

NCBI Description (AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea

mays]

Seq. No. 269190

Contig ID 18564_3.R1011 5'-most EST nbm700466493.h1

Method BLASTX
NCBI GI g3108053
BLAST score 657
E value 6.0e-69
Match length 133
% identity 95

NCBI Description (AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea

mays]

Seq. No. 269191

Contig ID 18564_5.R1011 5'-most EST xmt700262587.h1

Method BLASTX
NCBI GI g3108053
BLAST score 369
E value 2.0e-35
Match length 76
% identity 96

NCBI Description (AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea

mays]

Seq. No. 269192

Contig ID 18567_1.R1011

5'-most EST LIB3279-004-P1-K1-F1

Method BLASTX NCBI GI g4507311



BLAST score 222 E value 1.0e-17 Match length 90 % identity 47

NCBI Description suppressor of Ty (S.cerevisiae) 4 homolog 1

>gi 3122873 sp Q16550 SPT4 HUMAN TRANSCRIPTION INITIATION PROTEIN SPT4 HOMOLOG 1 >gi 1209779 (U43923) similar to Saccharomyces cerevisiae Spt4; protein has potential N-terminal zinc-finger [Homo sapiens] >gi 1401053 (U38818) SUPT4H [Homo sapiens] >gi 1401066 (U43154) Supt4h [Mus musculus] >gi 3779194 (U96809) chromatin structural protein homolog

[Mus musculus]

Seq. No. 269193

Contig ID 18567_2.R1011 5'-most EST ymy700282485.h2

Seq. No. 269194

Contig ID 18586 1.R1011

5'-most EST LIB3067-053-Q1-K1-B11

Seq. No. 269195

Contig ID 18586 2.R1011

5'-most EST LIB143-005-Q1-E1-B9

Seq. No. 269196

Contig ID 18594_1.R1011

5'-most EST LIB3060-008-Q1-K1-A8

Method BLASTX
NCBI GI g2342719
BLAST score 525
E value 6.0e-53

Match length 180 % identity 55

NCBI Description (AC002341) SF16 protein isolog [Arabidopsis thaliana]

Seq. No. 269197

Contig ID 18594_2.R1011 5'-most EST cyk700047765.f1

Seq. No. 269198

Contig ID 18601_1.R1011

5'-most EST LIB3116-008-Q1-K1-B12

Method BLASTX
NCBI GI g2765817
BLAST score 300
E value 4.0e-27
Match length 86
% identity 63

NCBI Description (Z95352) AtMlo-h1 [Arabidopsis thaliana]

>gi 3892049 gb AAC78258.1 AAC78258 (AC002330) AtMlo-h1

[Arabidopsis thaliana]

Seq. No. 269199

Contig ID 18602_1.R1011 5'-most EST wyr700236043.h1



 Seq. No.
 269200

 Contig ID
 18602_2.R1011

 5'-most EST
 uer700579973.h1

 Seq. No.
 269201

 Contig ID
 18603_1.R1011

 5'-most EST
 wty700169810.h1

 Seq. No.
 269202

 Contig ID
 18603_2.R1011

 5'-most EST
 hvj700621704.h1

Seq. No. 269203

Contig ID 18603_3.R1011

5'-most EST LIB3059-022-Q1-K1-G7

Seq. No. 269204

Contig ID 18605_1.R1011

5'-most EST LIB3116-008-Q1-K1-C10

Method BLASTX
NCBI GI g4581162
BLAST score 520
E value 1.0e-52
Match length 117
% identity 85

NCBI Description (AC006220) putative symbiosis-related protein [Arabidopsis

thaliana]

Seq. No. 269205

Contig ID 18608_1.R1011

5'-most EST LIB3116-007-Q1-K1-E4

Method BLASTX
NCBI GI g3445207
BLAST score 206
E value 6.0e-17
Match length 110
% identity 46

NCBI Description (AC004786) unknown protein [Arabidopsis thaliana]

Seq. No. 269206

Contig ID 18609_1.R1011 5'-most EST uC-zmflb73014c07b1

Method BLASTX
NCBI GI g4580517
BLAST score 399
E value 1.0e-38
Match length 104
% identity 71

NCBI Description (AF036302) scarecrow-like 5 [Arabidopsis thaliana]

Seq. No. 269207

Contig ID 18609_2.R1011 5'-most EST mwy700440340.h1

Method BLASTX NCBI GI g4580517 BLAST score 540



```
1.0e-65
E value
                   183
Match length
                   69
% identity
                   (AF036302) scarecrow-like 5 [Arabidopsis thaliana]
NCBI Description
                   269208
Seq. No.
                   18610 1.R1011
Contig ID
                   uC-zm\overline{f}lmo17161f07b1
5'-most EST
                   269209
Seq. No.
Contig ID
                   18618 1.R1011
                   LIB3066-051-Q1-K1-H1
5'-most EST
                   269210
Seq. No.
                   18627 1.R1011
Contig ID
                   LIB189-005-Q1-E1-E10
5'-most EST
                   269211
Seq. No.
                   18630 1.R1011
Contig ID
5'-most EST
                   LIB3116-007-Q1-K1-D3
                   BLASTX
Method
                   q2239203
NCBI GI
BLAST score
                   167
E value
                   9.0e-12
                   98
Match length
                   44
% identity
                  (Z97209) aldolase reductase [Schizosaccharomyces pombe]
NCBI Description
                   269212
Seq. No.
                   18633 1.R1011
Contig ID
5'-most EST
                   LIB189-009-Q1-E1-G3
                   BLASTX
Method
NCBI GI
                   q2558938
BLAST score
                   150
                   1.0e-09
E value
Match length
                   68
% identity
                   41
                  (AF024625) arm repeat containing protein [Brassica napus]
NCBI Description
Seq. No.
                   269213
                   18641 1.R1011
Contig ID
                   LIB3116-007-Q1-K1-A12
5'-most EST
                   269214
Seq. No.
                   18645 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73069e11a1
Method
                   BLASTX
                   g2245064
NCBI GI
                   259
BLAST score
```

3.0e-22 E value 77 Match length 61 % identity

NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]

269215 Seq. No.

Contig ID 18649 1.R1011 LIB36-022-Q1-E1-C5 5'-most EST



BLASTX Method NCBI GI q119194 472 BLAST score E value 4.0e-47102 Match length 86 % identity NCBI Description

ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_81607_pir__S09152 translation elongation factor Tu

precursor, chloroplast - Arabidopsis thaliana >gi_22565_emb_CAA36498_ (X52256) elongation factor Tu precursor [Arabidopsis thaliana] >gi_226817_prf__1607332A

elongation factor Tu [Arabidopsis thaliana]

269216 Seq. No.

18649 2.R1011 Contig ID pmx700083194.h1 5'-most EST

269217 Seq. No.

18651 1.R1011 Contig ID

5'-most EST LIB3153-012-Q1-K1-A12

269218 Seq. No.

Contig ID 18654_1.R1011 5'-most EST uwc700150312.h1

Method BLASTX g2982262 NCBI GI BLAST score 445 8.0e-44E value 203 Match length % identity 46

(AF051214) probable glutathione S-transferase [Picea NCBI Description

mariana]

269219 Seq. No.

Contig ID 18658 1.R1011

5'-most EST LIB3156-010-Q1-K1-H10

Method BLASTX NCBI GI q2344898 BLAST score 578 2.0e-59 E value Match length 134 79 % identity

(AC002388) 60S ribosomal protein L30 isolog [Arabidopsis NCBI Description

thaliana]

Seq. No. 269220

18659 1.R1011 Contig ID

5'-most EST LIB3116-006-Q1-K1-G5

269221 Seq. No.

18660 1.R1011 Contig ID 5'-most EST tfd700571245.hl

269222 Seq. No.

Contig ID 18677 1.R1011

LIB3116-006-Q1-K1-C3 5'-most EST

Method BLASTX



NCBI GI g2244799 181 BLAST score 3.0e-13E value 146 Match length 33 % identity (Z97336) carnitine racemase homolog [Arabidopsis thaliana] NCBI Description 269223 Seq. No. 18680 1.R1011 Contig ID $uC-zm\overline{f}1b73177b10b1$ 5'-most EST BLASTX Method g3702325 NCBI GI 387 BLAST score 2.0e-36 E value 566 Match length 26 % identity (AC005397) hypothetical protein [Arabidopsis thaliana] NCBI Description 269224 Seq. No. 18680 2.R1011 Contig ID uC-zmroteosinte119c05b1 5'-most EST BLASTN Method g2944039 NCBI GI 450 BLAST score 0.0e+00E value 491 Match length 98 % identity Zea mays indeterminate spikelet 1 (ids1) mRNA, complete cds NCBI Description 269225 Seq. No. 18682 1.R1011 Contig ID hvj700621996.hl 5'-most EST BLASTX Method g1197164 NCBI GI 290 BLAST score 1.0e-32 E value 173 Match length 43 % identity NCBI Description (D83069) ADT/ATP translocase [Halocynthia roretzi] 269226 Seq. No. 18688 1.R1011 Contig ID LIB3116-006-Q1-K1-B4 5'-most EST BLASTX Method q606751 NCBI GI BLAST score 165 E value 7.0e-11 Match length 134 33 % identity NCBI Description (L34934) RNA binding protein [Drosophila melanogaster] 269227 Seq. No. 18691 1.R1011 Contig ID

5'-most EST uC-zmflmo17333c07b1

Method BLASTX NCBI GI g3540188 BLAST score 299

37469



```
9.0e-27
E value
Match length
                  91
                  59
% identity
NCBI Description (AC004122) Hypothetical protein [Arabidopsis thaliana]
                  269228
Seq. No.
                  18693 1.R1011
Contig ID
5'-most EST
                  LIB143-048-01-E1-D3
                  269229
Seq. No.
Contig ID
                  18693 2.R1011
5'-most EST
                  LIB148-027-Q1-E1-G10
                  269230
Seq. No.
                  18698 1.R1011
Contig ID
5'-most EST
                  nwy700447222.hl
                  BLASTX
Method
NCBI GI
                  q1663724
                  376
BLAST score
                  3.0e-39
E value
                  123
Match length
% identity
                  66
NCBI Description (U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
                  269231
Seq. No.
                  18699 1.R1011
Contig ID
5'-most EST
                  LIB3116-005-Q1-K1-G3
Method
                  BLASTX
NCBI GI
                  q4191785
BLAST score
                  353
E value
                  3.0e-33
Match length
                  136
% identity
                  51
NCBI Description (AC005917) putative hydrolase [Arabidopsis thaliana]
                  269232
Seq. No.
                  18705 1.R1011
Contig ID
5'-most EST
                  wyr700240993.h1
Method
                  BLASTX
                  g2058498
NCBI GI
BLAST score
                  456
                  2.0e-45
E value
Match length
                  141
% identity
NCBI Description (U76029) hemoglobin 1 [Oryza sativa] >gi 2058500 (U76030)
                  hemoglobin 1 [Oryza sativa]
Seq. No.
                  269233
                  18706 1.R1011
Contig ID
5'-most EST
                  LIB3116-005-Q1-K1-F1
Method
                  BLASTX
                  g3878134
NCBI GI
BLAST score
                  211
                  9.0e-17
E value
```

Match length 75 % identity 52

NCBI Description (Z68218) K01H12.1 [Caenorhabditis elegans]



269234 Seq. No. 18706 2.R1011 Contig ID LIB3067-057-Q1-K1-H10 5'-most EST Method BLASTX g3878134 NCBI GI BLAST score 196 3.0e-15 E value 59 Match length % identity 56 (Z68218) K01H12.1 [Caenorhabditis elegans] NCBI Description 269235 Seq. No. 18710 1.R1011 Contig ID clt700044920.f1 5'-most EST BLASTX Method g3024871 NCBI GI BLAST score 323 8.0e-30 E value 163 Match length 40 % identity HYPOTHETICAL 77.3 KD PROTEIN SLL0005 NCBI Description >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.] 269236 Seq. No. 18713 1.R1011 Contig ID LIB3068-020-Q1-K1-F8 5'-most EST 269237 Seq. No. 18716 1.R1011 Contig ID LIB189-027-Q1-E1-D5 5'-most EST 269238 Seq. No. 18720 1.R1011 Contig ID nbm700466418.h1 5'-most EST 269239 Seq. No. 18733 1.R1011 Contig ID dyk700103839.h1 5'-most EST BLASTX Method g4098250 NCBI GI 190 BLAST score 5.0e-14E value 74 Match length 53 % identity (U76611) similar to Solanum tuberosum ci21A gene product NCBI Description encoded by the sequence presented in GenBank Accession Number U76610 [Solanum tuberosum]

Seq. No. 269240

Contig ID 18733_2.R1011 5'-most EST nwy700444187.h1

Method BLASTN
NCBI GI g2773153
BLAST score 33
E value 4.0e-09



Match length 77 % identity 86

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

Seq. No. 269241

Contig ID 18734_1.R1011 5'-most EST ceu700430050.h1

Method BLASTX
NCBI GI g730512
BLAST score 514
E value 4.0e-52
Match length 104
% identity 97

NCBI Description RAS-RELATED PROTEIN RIC2 >gi_481506_pir__S38741 GTP-binding

protein ric2 - rice >gi_2182 $\overline{2}$ 8_dbj_ $\overline{B}AA0\overline{29}04$ _ (D13758)

ras-related GTP binding protein [Oryza sativa]

Seq. No. 269242

Contig ID 18734 2.R1011

5'-most EST LIB3116-004-Q1-K2-F4

Method BLASTX
NCBI GI g730512
BLAST score 244
E value 8.0e-21
Match length 58
% identity 86

NCBI Description RAS-RELATED PROTEIN RIC2 >gi_481506_pir__S38741 GTP-binding

protein ric2 - rice >gi_218228_dbj_BAA02904_ (D13758)

ras-related GTP binding protein [Oryza sativa]

Seq. No. 269243

Contig ID 18736 1.R1011 5'-most EST uC-zmflb73055e12b1

Method BLASTX
NCBI GI g4455256
BLAST score 433
E value 1.0e-42
Match length 111

% identity 70
NCBI Description (AL035523) protein-methionine-S-oxide reductase

[Arabidopsis thaliana]

Seq. No. 269244

Contig ID 18751_1.R1011

5'-most EST LIB3180-045-P2-M2-G11

Method BLASTX
NCBI GI g1304227
BLAST score 396
E value 2.0e-38
Match length 131
% identity 52

NCBI Description (D63781) Epoxide hydrolase [Glycine max]

>gi 2764804 emb CAA55293 (X78547) epoxide hydrolase

[Glycine max]

Seq. No. 269245



18754 1.R1011 Contig ID fwa700097793.hl 5'-most EST

269246 Seq. No.

18761 1.R1011 Contig ID

uC-zmflmo17039f09b1 5'-most EST

269247 Seq. No.

Contig ID 18761 2.R1011

5'-most EST LIB3067-027-Q1-K1-D7

Seq. No. 269248

Contig ID 18761 3.R1011

5'-most EST uC-zmflmo17177c01a1

Method BLASTN NCBI GI q1840117 BLAST score 45 E value 4.0e-16 Match length 117 % identity 86

Zea mays PIF-12 transposable element in r-1 (r-p) locus, NCBI Description

complete sequence

Seq. No. 269249

Contig ID 18765 1.R1011

uC-zmroteosinte080h04b1 5'-most EST

Method BLASTX g1076758 NCBI GI BLAST score 2331 E value 0.0e+00Match length 585 % identity 81

heat-shock protein precursor - rye >gi_2130093_pir__\$65776 NCBI Description

heat-shock protein, 82K, precursor - rye

>gi 556673 emb CAA82945_ (Z30243) heat-shock protein

[Secale cereale]

269250 Seq. No.

18768 1.R1011 Contig ID pmx700088443.h1 5'-most EST

BLASTX Method g3080425 NCBI GI 802 BLAST score 8.0e-86 E value Match length 178 % identity

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

269251 Seq. No.

18781 1.R1011 Contig ID uC-zmflb73085h04a1 5'-most EST

269252 Seq. No.

Contig ID 18781 2.R1011 5'-most EST gw1700617061.h1

269253 Seq. No.



```
18787 1.R1011
Contig ID
                  LIB3116-004-Q1-K1-B10
5'-most EST
Seq. No.
                  269254
                  18787 2.R1011
Contig ID
                  uC-zmflb73356d02a2
5'-most EST
                  269255
Seq. No.
Contig ID
                  18789 1.R1011
                  fwa700099654.h1
5'-most EST
Seq. No.
                  269256
                  18790 1.R1011
Contig ID
                  LIB3116-002-Q1-K1-G6
5'-most EST
Method
                  BLASTX
                  q3924603
NCBI GI
BLAST score
                  420
                  4.0e-41
E value
Match length
                  105
% identity
                   68
                  (AF069442) putative WD-repeat protein [Arabidopsis
NCBI Description
                  thaliana]
                   269257
Seq. No.
Contig ID
                   18795 1.R1011
                  LIB3116-002-Q1-K1-F11
5'-most EST
                   269258
Seq. No.
                  18797 1.R1011
Contig ID
                  gct701169325.hl
5'-most EST
                   269259
Seq. No.
                   18798 1.R1011
Contig ID
                  uC-zmflb73117a12b2
5'-most EST
                   269260
Seq. No.
                   18804 1.R1011
Contig ID
                   LIB3062-003-Q1-K1-H8
5'-most EST
                  BLASTX
Method
NCBI GI
                   g4585991
                   364
BLAST score
                   5.0e - 34
E value
                   292
Match length
                   39
% identity
NCBI Description (AC005287) very similar to mouse Dhm1 and Dhm2 [Arabidopsis
                   thaliana]
                   269261
Seq. No.
                   18808 1.R1011
Contig ID
                   uC-zmflb73285b08b1
5'-most EST
                   BLASTX
Method
```

NCBI GI q4584343 BLAST score 448

E value 5.0e-44Match length 262 % identity 42

NCBI Description (AC007127) putative ubiquitin protein [Arabidopsis



thaliana]

Seq. No. 269262
Contig ID 18808_2.R1011
5'-most EST LIB3150-042-Q1-N1-F3
Seq. No. 269263
Contig ID 18812_1.R1011
5'-most EST LIB3116-002-Q1-K1-D9
Method BLASTX

Method BLASTX
NCBI GI g3236240
BLAST score 683
E value 7.0e-72
Match length 232
% identity 58

NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 269264

Contig ID 18814_1.R1011 5'-most EST uC-zmflb73206e07b1

Seq. No. 269265

Contig ID 18814_2.R1011

5'-most EST LIB3116-002-Q1-K1-E2

Method BLASTX
NCBI GI g1931638
BLAST score 398
E value 9.0e-39
Match length 103
% identity 76

NCBI Description (U95973) transcription factor RUSH-lalpha isolog

[Arabidopsis thaliana]

Seq. No. 269266

Contig ID 18816_1.R1011

5'-most EST LIB3136-007-Q1-K1-D11

Method BLASTX
NCBI GI g2245006
BLAST score 145
E value 6.0e-09
Match length 67
% identity 46

NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No. 269267

Contig ID 18817 1.R1011

5'-most EST LIB3062-013-Q1-K1-G8

Method BLASTX
NCBI GI g2829889
BLAST score 447
E value 5.0e-44
Match length 149
% identity 59

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 269268

Contig ID 18817 6.R1011



```
uC-zmflb73205f12b2
5'-most EST
                   BLASTX
Method
                   q2829889
NCBI GI
                   158
BLAST score
                   1.0e-10
E value
Match length
                   49
                    59
% identity
                   (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   269269
Seq. No.
                   18817 7.R1011
Contig ID
5'-most EST
                   LIB3116-002-Q1-K1-E4
                    269270
Seq. No.
                    18819 1.R1011
Contig ID
                    LIB3068-015-Q1-K1-D12
5'-most EST
                    BLASTX
Method
                    g1346863
NCBI GI
                    321
BLAST score
                    2.0e-29
E value
                    61
Match length
                    100
% identity
                    PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR
NCBI Description
                    >gi_1363582_pir__S58534 photosystem II protein psbK - maize
chloroplast >gi_902204_emb_CAA60268_ (X86563) PSII K
                    protein [Zea mays]
                    269271
Seq. No.
                    18822 1.R1011
Contig ID
                    xsy70\overline{0}213038.h1
5'-most EST
                    BLASTX
Method
                    g3128177
NCBI GI
                    343
BLAST score
                    7.0e-32
E value
                    128
Match length
                    56
% identity
                   (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
                    269272
Seq. No.
                    18826 1.R1011
Contig ID
                    LIB3116-002-Q1-K1-B12
5'-most EST
Method
                    BLASTX
                    q2160694
NCBI GI
                    687
BLAST score
                    1.0e-72
E value
                    154
Match length
% identity
                    (U73528) B' regulatory subunit of PP2A [Arabidopsis
NCBI Description
                    thaliana]
                    269273
Seq. No.
                    18827 1.R1011
Contig ID
                    nwy700443832.h1
5'-most EST
```

37476

BLASTX

526

g4586027

2.0e-53

Method

NCBI GI BLAST score

E value



Match length 124 % identity 83

NCBI Description (AC007109) putative ribosomal protein L14 [Arabidopsis

thaliana]

Seq. No. 269274

Contig ID 18829_1.R1011 5'-most EST uC-zmroB73030c01b1

Method BLASTX
NCBI GI g3287696
BLAST score 819
E value 7.0e-88
Match length 209
% identity 74

NCBI Description

(ACO03979) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region.

[Arabidopsis thaliana]

Seq. No. 269275

Contig ID 18830_1.R1011 5'-most EST tfd700570427.h1

Method BLASTN
NCBI GI g22176
BLAST score 75
E value 8.0e-34
Match length 91
% identity 49

NCBI Description Z.mays P gene

Seq. No. 269276

Contig ID 18835_2.R1011 5'-most EST uC-zmflb73121b02b2

Seq. No. 269277

Contig ID 18847_1.R1011 5'-most EST vux700160626.h1

Method BLASTX
NCBI GI g4539242
BLAST score 210
E value 9.0e-22
Match length 146
% identity 45

NCBI Description (AL049489) conserved hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 269278

Contig ID 18847_2.R1011

5'-most EST LIB3062-049-Q1-K1-B5

Method BLASTX
NCBI GI g4539242
BLAST score 226
E value 4.0e-18
Match length 161
% identity 38

NCBI Description (AL049489) conserved hypothetical protein

[Schizosaccharomyces pombe]



```
269279
Seq. No.
                  18847 3.R1011
Contig ID
                  uC-zmroteosinte103a06b2
5'-most EST
                  269280
Seq. No.
                  18848 1.R1011
Contig ID
                  wyr700241451.hl
5'-most EST
                  269281
Seq. No.
                  18857 1.R1011
Contig ID
                  LIB3116-001-Q1-K1-B5
5'-most EST
                   269282
Seq. No.
                   18866 1.R1011
Contig ID
                   LIB3116-001-Q1-K1-D3
5'-most EST
                   BLASTX
Method
                   g4567303
NCBI GI
                   376
BLAST score
                   8.0e-36
E value
                   83
Match length
                   77
% identity
                  (AC005956) unknown protein [Arabidopsis thaliana]
NCBI Description
                   269283
Seq. No.
                   18866 2.R1011
Contig ID
                   uC-zm\overline{f}lMo17062e08b1
5'-most EST
                   BLASTX
Method
                   q4467125
NCBI GI
                   419
BLAST score
                   1.0e-40
E value
                   186
Match length
                   44
% identity
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
                   269284
Seq. No.
                   18866 4.R1011
Contig ID
                   xsy700217311.h1
5'-most EST
                   BLASTX
Method
                   q2924781
NCBI GI
                   534
BLAST score
                   2.0e-54
E value
                   183
Match length
% identity
NCBI Description (AC002334) putative cellulose synthase [Arabidopsis
                   thaliana]
                   269285
 Seq. No.
                   18866 6.R1011
 Contig ID
                   LIB3118-013-Q1-K1-G11
 5'-most EST
                   BLASTX
Method
                   q4567303
 NCBI GI
 BLAST score
                   161
```

37478

NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]

6.0e-11

81

E value

Match length % identity



269286 Seq. No. 18871 1.R1011 Contig ID LIB3116-001-Q1-K1-A12 5'-most EST 269287 Seq. No. 18873 1.R1011 Contig ID LIB3116-001-Q1-K1-A3 5'-most EST BLASTX Method g3786004 NCBI GI BLAST score 260 1.0e-22 E value 111 Match length 50 % identity (AC005499) hypothetical protein [Arabidopsis thaliana] NCBI Description 269288 Seq. No. 18883 1.R1011 Contig ID ceu700431719.hl 5'-most EST 269289 Seq. No. 18895_1.R1011 Contig ID 5'-most EST uC-zmroteosinte057a02b1 BLASTX Method q3047114 NCBI GI BLAST score 458 2.0e-45 E value 210 Match length 49 % identity (AF058919) No definition line found [Arabidopsis thaliana] NCBI Description 269290 Seq. No. 18898 1.R1011 Contig ID 5'-most EST LIB3279-051-P1-K1-A5 Seq. No. 269291 18908 1.R1011 Contig ID LIB3116-004-Q1-K2-F8 5'-most EST 269292 Seq. No. Contig ID 18920 1.R1011 $uC-zm\overline{f}lmo17115a07a1$ 5'-most EST BLASTX Method g3450842 NCBI GI 175 BLAST score E value 1.0e-12 59 Match length 59 % identity (AF080436) mitogen activated protein kinase kinase [Oryza NCBI Description sativa]

Seq. No. 269293 Contig ID 18957 1.R1011

5'-most EST LIB3060-018-Q1-K1-E3

Method BLASTX NCBI GI g2497702

BLAST score 171

37479



6.0e-12 E value Match length 124 40 % identity OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR NCBI Description >gi_2121019_pir__I40710 outer membrane lipoprotein -Citrobacter freundii >gi_717136 (U21727) lipocalin precursor [Citrobacter freundii] 269294 Seq. No. 18957 2.R1011 Contig ID $wen70\overline{0}336344.h1$ 5'-most EST 269295 Seq. No. 18972 1.R1011 Contig ID $yyf70\overline{0}350268.h1$ 5'-most EST BLASTX Method g2252631 NCBI GI 838 BLAST score 9.0e-90 E value 302 Match length 60 % identity (U95973) hypothetical protein [Arabidopsis thaliana] NCBI Description 269296 Seq. No. 18974_1.R1011 Contig ID 5'-most EST LIB189-028-Q1-E1-H2 Method BLASTX a3063711 NCBI GI 211 BLAST score 8.0e-17 E value Match length 99 47 % identity NCBI Description (AL022537) hypothetical protein [Arabidopsis thaliana] 269297 Seq. No. Contig ID 18978 1.R1011 wyr700237682.hl 5'-most EST 269298 Seq. No. 18981 1.R1011 Contig ID 5'-most EST wty700164770.hl Method BLASTX NCBI GI g2191138 BLAST score 390 2.0e-37 E value Match length 115 % identity 66 (AF007269) A_IG002N01.18 gene product [Arabidopsis NCBI Description thaliana]

 Seq. No.
 269299

 Contig ID
 18982_1.R1011

 5'-most EST
 LIB3116-012-Q1-K1-E2

 Method
 BLASTX

 NCBI GI
 g3402675

 BLAST score
 143

E value

3.0e-17



Match length 100 % identity 48

(AC004697) hypothetical protein [Arabidopsis thaliana] NCBI Description

269300 Seq. No.

18984 1.R1011 Contig ID

LIB3116-012-Q1-K1-G12 5'-most EST

269301 Seq. No.

Contig ID 18988 1.R1011

LIB3116-018-P1-K1-C6 5'-most EST

BLASTX Method NCBI GI g4567225 BLAST score 208 4.0e-16 E value Match length 77 % identity 52

(AC007119) unknown protein [Arabidopsis thaliana] NCBI Description

269302 Seq. No.

18990 1.R1011 Contig ID xyt700345814.h1 5'-most EST

BLASTX Method NCBI GI g140499 BLAST score 498 5.0e-50 E value Match length 283 43 % identity

PUTATIVE 30.7 KD METHYLTRANSFERASE IN TSM1-ARE1 INTERGENIC NCBI Description REGION >gi_83229_pir__S19460 hypothetical protein YCR047c -

yeast (Saccharomyces cerevisiae) >gi_1907189_emb_CAA42295_

(X59720) YCR047c, len:275 [Saccharomyces cerevisiae]

269303 Seq. No.

18991 1.R1011 Contig ID

LIB148-063-Q1-E1-F8 5'-most EST

Seq. No. 269304

18992 1.R1011 Contig ID

5'-most EST LIB3116-013-Q1-K1-E6

BLASTX Method g3913510 NCBI GI BLAST score 276 7.0e-24E value 179 Match length 38 % identity

DNA POLYMERASE I, THERMOSTABLE (TFI POLYMERASE 1) NCBI Description

>gi 2739139 (AF030320) thermostable DNA polymerase [Thermus

filiformis]

269305 Seq. No.

18993 1.R1011 Contig ID

5'-most EST LIB3116-013-Q1-K1-F6

269306 Seq. No.

18993 2.R1011 Contig ID 5'-most EST wty700168374.h1

NCBI GI

E value

BLAST score

g3236248

1.0e-117

1072



269307 Seq. No. 18995 1.R1011 Contig ID LIB84-013-Q1-E1-A11 5'-most EST BLASTX Method g470373 NCBI GI 287 BLAST score 3.0e-25 E value 165 Match length 37 % identity (U00047) ZK418.5 gene product [Caenorhabditis elegans] NCBI Description 269308 Seq. No. 18995 2.R1011 Contig ID LIB3279-004-P1-K1-C1 5'-most EST 269309 Seq. No. 18997 1.R1011 Contig ID $uC-zm\overline{f}lmo17075f08b2$ 5'-most EST BLASTX Method g1076315 NCBI GI 1368 BLAST score 1.0e-151 E value 457 Match length 61 % identity cytochrome P450 - Arabidopsis thaliana NCBI Description >gi_853719_emb_CAA60793__(X87367) CYP90 protein [Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368) CYP90 protein [Arabidopsis thaliana] 269310 Seq. No. 18999_1.R1011 Contig ID LIB3060-010-Q1-K1-C3 5'-most EST BLASTX Method g2499488 NCBI GI 668 BLAST score E value 8.0e-95 Match length 214 81 % identity PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE NCBI Description ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_483547_emb_CAA83682 (Z32849) pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinus communis] Seq. No. 269311 Contig ID 19005 1.R1011 5'-most EST LIB3116-015-P1-K1-A3 269312 Seq. No. 19007 1.R1011 Contig ID xsy700212502.h1 5'-most EST BLASTX Method

37482



Match length 261 % identity 80

NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No. 269313

Contig ID 19007_2.R1011

5'-most EST LIB3151-017-Q1-K1-F4

Seq. No. 269314

Contig ID 19008_1.R1011

5'-most EST LIB3116-015-P1-K1-A6

Seq. No. 269315

Contig ID 19008_2.R1011

5'-most EST LIB84-005-Q1-E1-B10

Seq. No. 269316

Contig ID 19008_3.R1011 5'-most EST clt700045378.f1

Seq. No. 269317

Contig ID 19009 1.R1011 5'-most EST tzu700203568.h1

Seq. No. 269318

Contig ID 19012_1.R1011 5'-most EST pwr700452526.h1

Method BLASTX
NCBI GI 9422029
BLAST score 987
E value 1.0e-107
Match length 317
% identity 66

NCBI Description transcription factor OBF3.2, ocs element-binding - maize

>gi_297018_emb_CAA48904_ (X69152) ocs-element binding

factor 3.2 [Zea mays]

Seq. No. 269319

Contig ID 19012_2.R1011

5'-most EST LIB3060-003-Q1-K1-H5

Method BLASTX
NCBI GI g100099
BLAST score 526
E value 3.0e-53
Match length 193
% identity 58

NCBI Description DNA-binding protein VBP1 - fava bean >gi_1372966 (M81827)

CREB-like protein [Vicia faba]

Seq. No. 269320

Contig ID 19012 3.R1011

5'-most EST LIB3137-039-Q1-K1-D11

Seq. No. 269321

Contig ID 19012_6.R1011 5'-most EST pmx700091539.h1



```
269322
Seq. No.
                  19031 1.R1011
Contig ID
                  LIB84-030-Q1-E1-B12
5'-most EST
                  BLASTN
Method
                  g1185553
NCBI GI
                  37
BLAST score
                   4.0e-11
E value
                  77
Match length
                   87
% identity
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)
NCBI Description
                   gene, complete cds
                   269323
Seq. No.
                   19036 1.R1011
Contig ID
                   qmh70\bar{0}030418.f1
5'-most EST
                   BLASTX
Method
                   g4504495
NCBI GI
                   198
BLAST score
                   4.0e-22
E value
                   214
Match length
                   36
% identity
                   HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 1
NCBI Description
                   >qi 1857419 (U80213) protein arginine N-methyltransferase 2
                   [Homo sapiens]
                   269324
Seq. No.
Contig ID
                   19036 2.R1011
                   uC-zmflb73052e12b1
5'-most EST
                   269325
Seq. No.
                   19040 1.R1011
Contig ID
                   uC-zmf1b73341e08a2
5'-most EST
Method
                   BLASTX
                   q3367596
NCBI GI
                   194
BLAST score
E value
                   6.0e-15
Match length
                   68
% identity
                   51
NCBI Description (AL031135) putative protein [Arabidopsis thaliana]
                   269326
Seq. No.
Contig ID
                   19041 1.R1011
5'-most EST
                   uC-zmflb73276b03a1
                   BLASTX
Method
NCBI GI
                   q3184292
BLAST score
                   247
E value
                   1.0e-20
Match length
                   53
                   72
% identity
                  (AC004136) putative nucleic acid binding protein, 5'
NCBI Description
                   partial [Arabidopsis thaliana]
                   269327
Seq. No.
                   19041 2.R1011
Contig ID
```

gw1700617016.h1 5'-most EST

Method BLASTX NCBI GI g3894178



BLAST score 221 4.0e-18 E value Match length 49 71 % identity (AC005312) putative nucleic acid binding protein NCBI Description [Arabidopsis thaliana] 269328 Seq. No. 19050 1.R1011 Contig ID uC-zmflb73056h05b1 5'-most EST

269329 Seq. No. 19050 2.R1011 Contig ID LIB83-010-Q1-E1-C6 5'-most EST

269330 Seq. No. 19059 1.R1011 Contig ID LIB3116-016-P1-K1-B2 5'-most EST BLASTX Method q2618691 NCBI GI

490 BLAST score 3.0e-49E value Match length 167 % identity 57

(AC002510) putative chloroplast envelope Ca2+-ATPase NCBI Description

[Arabidopsis thaliana]

Seq. No. 269331 19059 2.R1011 Contig ID $xjt70\overline{0}094369.h1$ 5'-most EST

269332 Seq. No. 19064_1.R1011 Contig ID LIB3116-016-P1-K1-E5 5'-most EST

BLASTN Method

g3821780 NCBI GI BLAST score 36 E value 7.0e-11 36 Match length 100 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

269333 Seq. No. 19069 1.R1011 Contig ID

LIB3136-017-Q1-K1-A10 5'-most EST

Method BLASTX NCBI GI q3688598 BLAST score 1192 E value 1.0e-131 373 Match length

57 % identity

NCBI Description (AB009029) Cycloartenol Synthase [Panax ginseng]

269334 Seq. No. Contig ID

19069 2.R1011

LIB3116-016-P1-K1-D1 5'-most EST

Method BLASTN



g2062705 NCBI GI BLAST score 38 6.0e-12 E value 42 Match length 98 % identity

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

269335 Seq. No.

19075 1.R1011 Contig ID

5'-most EST LIB3136-054-Q1-K1-D7

Method BLASTX g2979560 NCBI GI **1**74 BLAST score 7.0e-17 E value Match length 84 % identity 64

(AC003680) unknown protein [Arabidopsis thaliana] NCBI Description

269336 Seq. No.

19078 1.R1011 Contig ID

5'-most EST LIB3059-022-Q1-K1-D10

Method BLASTX NCBI GI g4454010 599 BLAST score E value 9.0e-78 Match length 220

% identity 68

NCBI Description (AL035396) putative protein [Arabidopsis thaliana]

269337 Seq. No.

19085 1.R1011 Contig ID $uC-zm\overline{f}lmo17271e11b1$ 5'-most EST

BLASTX Method q3402682 NCBI GI 146 BLAST score E value 4.0e-09 Match length 56 45 % identity

NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 269338

19090 1.R1011 Contig ID

uC-zmflmo17048d05b1 5'-most EST

Method BLASTX NCBI GI g3023522 BLAST score 360 E value 1.0e-33 172 Match length % identity 44

NCBI Description COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)

(P102) >qi 2454309 (AF002705) beta prime COP [Rattus

norvegicus]

269339 Seq. No.

19090 2.R1011 Contig ID 5'-most EST ntr700072672.h1

Method BLASTX



NCBI GI g486784 573 BLAST score 3.0e-59 E value Match length 233 % identity 50 Golgi-associated particle 102K chain - human NCBI Description 269340 Seq. No. 19090 3.R1011 Contig ID LIB3067-028-Q1-K1-A3 5'-most EST BLASTX Method g3023522 NCBI GI BLAST score 334 7.0e-31 E value 175 Match length 42 % identity COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP) NCBI Description (P102) >gi 2454309 (AF002705) beta prime COP [Rattus norvegicus] 269341 Seq. No. 19099 1.R1011 Contig ID clt700046086.fl 5'-most EST Method BLASTX g3184258 NCBI GI BLAST score 173 3.0e-12E value Match length 91 % identity 37 (U82130) tumor susceptibility protein [Homo sapiens] NCBI Description 269342 Seq. No. 19106 1.R1011 Contig ID ceu700428185.h1 5'-most EST BLASTX Method q4097569 NCBI GI 273 BLAST score 1.0e-23 E value 96 Match length 59 % identity NCBI Description (U64915) GMFP4 [Glycine max] 269343 Seq. No. 19106_2.R1011 Contig ID LIB3116-017-P1-K1-C1 5'-most EST BLASTX Method g4097569 NCBI GI BLAST score 261

2.0e-22 E value 96 Match length 57 % identity

NCBI Description (U64915) GMFP4 [Glycine max]

269344 Seq. No.

19107 1.R1011 Contig ID $uC-zm\overline{f}lmo17257d11b1$ 5'-most EST

BLASTX Method



```
NCBI GI
                  g2281633
                  311
BLAST score
                  3.0e-28
E value
Match length
                  85
                  69
% identity
                  (AF003097) AP2 domain containing protein RAP2.4
NCBI Description
                   [Arabidopsis thaliana]
                  269345
Seq. No.
                  19107 2.R1011
Contig ID
                  uC-zmflmo17042b12b1
5'-most EST
Method
                  BLASTX
                  g2281633
NCBI GI
                  296
BLAST score
                  1.0e-26
E value
Match length
                  67
                  81
% identity
                  (AF003097) AP2 domain containing protein RAP2.4
NCBI Description
                   [Arabidopsis thaliana]
                  269346
Seq. No.
                  19112 1.R1011
Contig ID
                  LIB3156-007-Q1-K1-G6
5'-most EST
                  BLASTX
Method
                  g1652105
NCBI GI
                   152
BLAST score
                   1.0e-09
E value
Match length
                   45
                   60
% identity
NCBI Description (D90902) hypothetical protein [Synechocystis sp.]
                  269347
Seq. No.
                   19112_2.R1011
Contig ID
                  LIB3116-017-P1-K1-C7
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1652105
BLAST score
                   187
                   6.0e-14
E value
                   53
Match length
                   64
% identity
NCBI Description (D90902) hypothetical protein [Synechocystis sp.]
                   269348
Seq. No.
                   19112 3.R1011
Contig ID
                   LIB3150-073-P2-K1-E11
5'-most EST
                   BLASTN
Method
NCBI GI
                   q2832242
BLAST score
                   59
E value
                   2.0e-24
                   152
Match length
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
```

Seq. No. 269349 Contig ID 19124 1.R1011

5'-most EST uC-zmflmo17202c09a1



Seq. No. 269350

Contig ID 19128_1.R1011 5'-most EST uwc700150591.h1

Seq. No. 269351

Contig ID 19135_1.R1011 5'-most EST clt700043295.f1

Method BLASTX
NCBI GI g3183285
BLAST score 326
E value 7.0e-30
Match length 235
% identity 36

NCBI Description HYPOTHETICAL 54.4 KD PROTEIN IN AROH-NLPC INTERGENIC REGION

>gi_1742787_dbj_BAA15475_ (D90813) ORF_ID:o322#7; similar
to [SwissProt Accession Number Q06373] [Escherichia coli]

>gi 1787999 (AE000266) orf, hypothetical protein

[Escherichia coli]

Seq. No. 269352

Contig ID 19138_1.R1011 5'-most EST wty700169430.h1

Method BLASTX
NCBI GI g1661162
BLAST score 268
E value 3.0e-23
Match length 72
% identity 78

NCBI Description (U74296) water stress inducible protein [Oryza sativa]

Seq. No. 269353

Contig ID 19138 2.R1011

5'-most EST LIB3116-017-P1-K1-G8

Method BLASTX
NCBI GI g1661162
BLAST score 246
E value 9.0e-21
Match length 72
% identity 72

NCBI Description (U74296) water stress inducible protein [Oryza sativa]

Seq. No. 269354

Contig ID 19146 1.R1011

5'-most EST LIB3116-018-P1-K1-A5

Seq. No. 269355

Contig ID 19147_1.R1011 5'-most EST clt700041794.f1

Method BLASTX
NCBI GI g1652601
BLAST score 165
E value 5.0e-11
Match length 188
% identity 26

NCBI Description (D90906) hypothetical protein [Synechocystis sp.]

Seq. No. 269356

% identity



```
Contig ID
                  19151 1.R1011
                  LIB3150-117-P2-K1-B12
5'-most EST
                  BLASTX
Method
                  q1353709
NCBI GI
BLAST score
                  341
                  9.0e-32
E value
Match length
                  95
% identity
                  71
                  (U42385) FIN16 gene product [Mus musculus]
NCBI Description
                  269357
Seq. No.
                  19162 1.R1011
Contig ID
                  LIB3069-057-Q1-K1-D8
5'-most EST
                   269358
Seq. No.
                  19166 1.R1011
Contig ID
                   pwr700452678.h1
5'-most EST
                   269359
Seq. No.
                   19167 1.R1011
Contig ID
                   LIB3116-018-P1-K1-F3
5'-most EST
Seq. No.
                   269360
                   19168 1.R1011
Contig ID
                   clt700043827.fl
5'-most EST
                   BLASTX
Method
                   q2244709
NCBI GI
BLAST score
                   391
E value
                   1.0e-37
                   158
Match length
                   56
% identity
                  (AB005295) HY5 [Arabidopsis thaliana]
NCBI Description
                   >gi 2251085_dbj_BAA21327_ (AB005456) HY5 [Arabidopsis
                   thaliana]
                   269361
Seq. No.
                   19170 1.R1011
Contig ID
                   uC-zm\overline{f}lmo17153h02b1
5'-most EST
                   BLASTX
Method
                   q4218535
NCBI GI
                   609
BLAST score
                   5.0e-63
E value
Match length
                   270
                   50
% identity
NCBI Description (AJ010829) GRAB1 protein [Triticum sp.]
                   269362
Seq. No.
Contig ID
                   19170 2.R1011
5'-most EST
                   LIB143-033-Q1-E1-A12
Method
                   BLASTX
                   q480618
NCBI GI
                   158
BLAST score
                   2.0e-10
E value
                   90
Match length
                   43
```

37490

>gi 1345506 emb_CAA52771_ (X74755) ATAF1 [Arabidopsis

NCBI Description ATAF1 protein - Arabidopsis thaliana (fragment)



thaliana]

 Seq. No.
 269363

 Contig ID
 19171_1.R1011

 5'-most EST
 fC-zmle700432990f4

 Method
 BLASTX

NCBI GI g3980400
BLAST score 366
E value 6.0e-35
Match length 121
% identity 56

NCBI Description (AC004561) putative tropinone reductase [Arabidopsis

thaliana]

Seq. No. 269364

Contig ID 19173_1.R1011

5'-most EST LIB3116-018-P1-K1-G10

Method BLASTX
NCBI GI g3169174
BLAST score 240
E value 4.0e-20
Match length 73
% identity 56

NCBI Description (AC004401) putative serine carboxypeptidase I [Arabidopsis

thaliana]

Seq. No. 269365
Contig ID 19173_2.R1011
5'-most EST uer700579892.h1

Method BLASTX
NCBI GI g3169173
BLAST score 322
E value 9.0e-32

Match length 199 % identity 37

NCBI Description (AC004401) putative serine carboxypeptidase I [Arabidopsis

thaliana] >gi_3445215 (AC004786) putative serine

carboxypeptidase I [Arabidopsis thaliana]

Seq. No. 269366

Contig ID 19177_1.R1011

5'-most EST LIB3116-018-P1-K1-G6

Method BLASTX
NCBI GI g4097571
BLAST score 168
E value 1.0e-11
Match length 67
% identity 54

NCBI Description (U64916) GMFP5 [Glycine max]

Seq. No. 269367

Contig ID 19269 1.R1011 5'-most EST xsy700212114.h1

Method BLASTX
NCBI GI g4558568
BLAST score 360
E value 4.0e-34



Match length 171 % identity 43

NCBI Description (AC007138) hypothetical protein [Arabidopsis thaliana]

Seq. No. 269368

Contig ID 19390 1.R1011

5'-most EST LIB3116-025-P1-K2-A5

Seq. No. 269369

Contig ID 19391 1.R1011

5'-most EST LIB3116-025-P1-K2-A6

Seq. No. 269370

Contig ID 19392_1.R1011

5'-most EST LIB3116-025-P1-K2-A9

Seq. No. 269371

Contig ID 19394 1.R1011

5'-most EST LIB3067-047-Q1-K1-E1

Method BLASTN
NCBI GI g1213425
BLAST score 37

E value 4.0e-11 Match length 65 89

NCBI Description Aegilops columnaris cytochrome c oxidase subunit III (cox3)

gene, mitochondrial gene encoding mitochondrial protein,

complete cds

Seq. No. 269372

Contig ID 19410_1.R1011

5'-most EST LIB3116-025-P1-K2-D3

Method BLASTX
NCBI GI g1731990
BLAST score 281
E value 6.0e-25
Match length 150

% identity 43

NCBI Description (Y09602) serine carboxypeptidase II, CP-MII [Hordeum

vulgare]

Seq. No. 269373

Contig ID 19416_1.R1011 5'-most EST uC-zmflb73003c06b1

Seq. No. 269374

Contig ID 19418_1.R1011 5'-most EST xsy700213382.h1

Method BLASTX
NCBI GI g2282586
BLAST score 306
E value 1.0e-27
Match length 148
% identity 41

NCBI Description (U82011) methyltransferase [Prunus armeniaca]

Seq. No. 269375

% identity

NCBI Description



```
Contig ID
                  19418 2.R1011
                  xjt700092519.h1
5'-most EST
Seq. No.
                  269376
Contig ID
                  19424 1.R1011
5'-most EST
                  LIB3116-025-P1-K2-F5
                  BLASTX
Method
NCBI GI
                  q4138265
BLAST score
                  183
                  2.0e-13
E value
Match length
                   41
                   66
% identity
                   (AJ006228) Avr9 elicitor response protein [Nicotiana
NCBI Description
                  tabacum]
                  269377
Seq. No.
Contig ID
                  19428 1.R1011
5'-most EST
                  LIB3116-025-P1-K2-G10
Method
                  BLASTX
NCBI GI
                   q2979496
BLAST score
                   210
                   2.0e-16
E value
Match length
                   204
% identity
                   34
                  (AB012142) mRNA capping enzyme [Homo sapiens]
NCBI Description
                   >qi 3097308 dbj BAA25894 (AB009022) capping enzyme 1 [Homo
                   sapiens]
Seq. No.
                   269378
                   19429 1.R1011
Contig ID
                   LIB3116-025-P1-K2-G12
5'-most EST
                   269379
Seq. No.
                   19438 1.R1011
Contig ID
                   LIB3116-025-P1-K2-H2
5'-most EST
                   269380
Seq. No.
Contig ID
                   19453 1.R1011
                   uC-zmflb73117c04a1
5'-most EST
                   BLASTX
Method
                   q3776013
NCBI GI
BLAST score
                   309
E value
                   5.0e-28
                   70
Match length
                   86
% identity
NCBI Description (AJ010470) RNA helicase [Arabidopsis thaliana]
                   269381
Seq. No.
                   19470_1.R1011
Contig ID
                   LIB3116-026-P1-K2-D8
5'-most EST
Method
                   BLASTX
                   g2224911
NCBI GI
BLAST score
                   1678
                   0.0e+00
E value
                   430
Match length
```

(U93048) somatic embryogenesis receptor-like kinase [Daucus



carota]

269382 Seq. No. 19476 1.R1011 Contig ID uC-zmflmo17059d04b1 5'-most EST BLASTX Method g1781299 NCBI GI BLAST score 269 7.0e-23 E value

82

62 % identity (Y09506) transformer-SR ribonucleoprotein [Nicotiana NCBI Description

tabacum]

269383 Seq. No.

Match length

19476 3.R1011 Contig ID

LIB143-020-Q1-E1-H4 5'-most EST

Method BLASTX g1781299 NCBI GI BLAST score 165 3.0e-11E value

Match length 46 65 % identity

(Y09506) transformer-SR ribonucleoprotein [Nicotiana NCBI Description

tabacum]

269384 Seq. No.

19476 4.R1011 Contig ID $uC-zm\overline{f}1b73070e05b1$ 5'-most EST

BLASTX Method g1781299 NCBI GI BLAST score 269 2.0e-23 E value Match length 82

62 % identity

NCBI Description (Y09506) transformer-SR ribonucleoprotein [Nicotiana

tabacum]

269385 Seq. No.

19476 6.R1011 Contig ID

 $uC-zm\overline{f}lmo17068h04b2$ 5'-most EST

Method BLASTX NCBI GI g1781299 BLAST score 166 E value 2.0e-11 Match length 52 % identity 62

(Y09506) transformer-SR ribonucleoprotein [Nicotiana NCBI Description

tabacum]

269386 Seq. No.

Contig ID 19476 7.R1011

LIB3059-003-Q1-K1-B11 5'-most EST

Seq. No. 269387

19488 1.R1011 Contig ID $ntr70\overline{0}076571.h1$ 5'-most EST



```
BLASTX
Method
                  q282994
NCBI GI
                  981
BLAST score
                  1.0e-107
E value
                   248
Match length
                   71
% identity
                  Sip1 protein - barley >gi_167100 (M77475) seed imbibition
NCBI Description
                  protein [Hordeum vulgare]
                   269388
Seq. No.
                   19488 2.R1011
Contig ID
                   LIB3116-026-P1-K2-H12
5'-most EST
                   BLASTX
Method
                   g629602
NCBI GI
                   369
BLAST score
                   1.0e-55
E value
                   154
Match length
                   67
% identity
                   probable imbibition protein - wild cabbage
NCBI Description
                   >gi_488787_emb_CAA55893_ (X79330) putative imbibition
                   protein [Brassica oleracea]
                   269389
Seq. No.
                   19506 1.R1011
Contig ID
5'-most EST
                   LIB3116-027-P1-K1-B6
Method
                   BLASTX
                   q4512685
NCBI GI
                   603
BLAST score
                   2.0e-62
E value
                   245
Match length
                   52
% identity
                   (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087)
                   hypothetical protein [Arabidopsis thaliana]
                   269390
Seq. No.
Contig ID
                   19524 1.R1011
                   LIB3179-002-P2-K1-F7
5'-most EST
                   BLASTX
Method
NCBI GI
                   a2440160
BLAST score
                   181
E value
                   3.0e-13
Match length
                   110
% identity
                   (Y14836) beta-galactosidase [Phagemid cloning vector
NCBI Description
                   pTZ19U]
Seq. No.
                   269391
Contig ID
                   19627 1.R1011
                   LIB3137-027-Q1-K1-F6
5'-most EST
Seq. No.
                   269392
                   19627 2.R1011
Contig ID
                   uC-zm\overline{f}1b73031g04b1
5'-most EST
                   BLASTX
Method
```

g2135333

197

NCBI GI

BLAST score



```
4.0e-15
E value
Match length
                  116
                  40
% identity
                  Hep27 protein - human >gi 1079566 (U31875) Hep27 protein
NCBI Description
                  [Homo sapiens]
                  269393
Seq. No.
Contig ID
                  19634 1.R1011
                  LIB3116-031-P1-K1-D12
5'-most EST
                  269394
Seq. No.
                  19636 1.R1011
Contig ID
5'-most EST
                  wty700164355.hl
                  BLASTX
Method
                   q3024570
NCBI GI
                   150
BLAST score
E value
                   1.0e-09
                   104
Match length
% identity
                   31
                   DNA-DIRECTED RNA POLYMERASE SUBUNIT M
NCBI Description
                   >gi 2129313_pir__C64443 transcription-associated protein
                   'TFIIS' homolog - Methanococcus jannaschii >gi_1591780
                   (U67557) transcription-associated protein ('TFIIS')
                   [Methanococcus jannaschii]
                   269395
Seq. No.
                   19639 1.R1011
Contig ID
5'-most EST
                   LIB3116-031-P1-K1-F12
Seq. No.
                   269396
                   19650 1.R1011
Contig ID
                   wty700172289.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3618214
                   179
BLAST score
                   1.0e-12
E value
                   119
Match length
                   35
% identity
                  (AL031579) dihydrofolate reductase [Schizosaccharomyces
NCBI Description
                   pombe]
                   269397
Seq. No.
                   19650 3.R1011
Contig ID
                   uC-zmflb73273h04a1
5'-most EST
                   269398
Seq. No.
                   19672 1.R1011
Contig ID
                   LIB3068-036-Q1-K1-F6
5'-most EST
Method
                   BLASTX
                   q400077
NCBI GI
                   430
BLAST score
                   3.0e-42
E value
                   102
Match length
                 -- 82
% identity
```

PRECURSOR >gi_486850_pir__S36236 wound-induced protein WIP1 precursor - maize >gi_296180_emb_CAA50519_ (X71396) wound

NCBI Description BOWMAN-BIRK TYPE WOUND INDUCED PROTEINASE INHIBITOR WIP1

Method

NCBI GI

BLASTX

g2464880



induced protein [Zea mays]

269399 Seq. No. 19673 1.R1011 Contig ID 5'-most EST LIB3060-012-Q1-K1-F5 BLASTX Method q3668091 NCBI GI 236 BLAST score 1.0e-19 E value Match length 177 7 % identity NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana] Seq. No. 269400 19678 1.R1011 Contig ID 5'-most EST uC-zmroteosinte062e08b1 BLASTX Method g4455240 NCBI GI 403 BLAST score E value 7.0e-39 Match length 181 % identity 51 NCBI Description (AL035523) putative protein [Arabidopsis thaliana] 269401 Seq. No. 19686 1.R1011 Contig ID 5'-most EST LIB83-002-Q1-E1-H9 269402 Seq. No. 19688 1.R1011 Contig ID 5'-most EST uC-zmflmo17013c03b1 269403 Seq. No. 19691_1.R1011 Contig ID LIB3062-040-Q1-K1-F8 5'-most EST Method BLASTX NCBI GI q1352663 BLAST score 693 5.0e-73E value Match length 127 95 % identity NCBI Description SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-3 CATALYTIC SUBUNIT >gi_1076388_pir__ S52659 phosphoprotein phosphatase (EC 3.1.3.16) 2A isoform 3 - Arabidopsis thaliana >gi 466441 (M96841) Ser/Thr protein phosphatase [Arabidopsis thaliana] >gi 4559341 gb AAD23003.1 AC007087 22 (AC007087) serine/threonine protein phosphatase PP2A-3 catalytic subunit [Arabidopsis thaliana] >qi 4567320 qb AAD23731.1 AC005956 20 (AC005956) serine/threonine protein phosphatase [Arabidopsis thaliana] Seq. No. 269404 19694 1.R1011 Contig ID uC-zmroteosinte058h11b2 5'-most EST



```
BLAST score
                  220
                  4.0e-38
E value
Match length
                  186
% identity
                  51
                  (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
                  269405
Seq. No.
                  19696 1.R1011
Contia ID
                  uC-zmflmo17273d07b1
5'-most EST
Seq. No.
                  269406
                  19699 1.R1011
Contig ID
                  wyr700239381.h1
5'-most EST
Seq. No.
                   269407
Contig ID
                  19714 1.R1011
                   rvt700549324.h1
5'-most EST
                   269408
Seq. No.
                   19719 1.R1011
Contig ID
                   gct701180522.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1653488
BLAST score
                   202
                   1.0e-15
E value
                   108
Match length
                   46
% identity
NCBI Description (D90914) hypothetical protein [Synechocystis sp.]
                   269409
Seq. No.
                   19722 1.R1011
Contig ID
                   LIB3116-034-P1-K1-B7
5'-most EST
                   269410
Seq. No.
                   19722 2.R1011
Contig ID
                   LIB83-002-Q1-E1-A9
5'-most EST
                   269411
Seq. No.
                   19736 1.R1011
Contig ID
                   nwy700445657.hl
5'-most EST
                   BLASTX
Method
                   g3786011
NCBI GI
BLAST score
                   482
                   9.0e-55
E value
                   147
Match length
                   80
% identity
                   (AC005499) putative elongation factor [Arabidopsis
NCBI Description
                   thaliana]
                   269412
Seq. No.
                   19736 2.R1011
Contig ID
                   uC-zmflmo17117d09b1
5'-most EST
Method
                   BLASTX
                   q3786011
NCBI GI
```

147

45

5.0e-09

BLAST score

E value Match length



% identity (AC005499) putative elongation factor [Arabidopsis NCBI Description thaliana] Seq. No. 269413 19744 1.R1011 Contig ID LIB3069-037-Q1-K1-G9 5'-most EST BLASTX Method g2245125 NCBI GI 204 BLAST score 6.0e-16 E value 51 Match length 69 % identity (Z97343) hypothetical protein [Arabidopsis thaliana] NCBI Description 269414 Seq. No. Contig ID 19745 1.R1011 5'-most EST LIB83-002-Q1-E1-H4 Method BLASTX q4467098 NCBI GI 471 BLAST score 7.0e-47E value 147 Match length % identity 65 (AL035538) putative protein [Arabidopsis thaliana] NCBI Description 269415 Seq. No. 19746 1.R1011 Contig ID 5'-most EST LIB3136-005-Q1-K1-H11 Method BLASTX NCBI GI q4249413 BLAST score 207 3.0e-16 E value Match length 46 78 % identity (AC006072) unknown protein [Arabidopsis thaliana] NCBI Description 269416 Seq. No. 19746 2.R1011 Contig ID fC-zmro700576185a2 5'-most EST Method BLASTN g22430 NCBI GI BLAST score 67 3.0e-29E value 139 Match length 87 % identity Maize pseudo-Gpa2 pseudogene for glyceraldehyde-3-phosphate NCBI Description dehydrogenase subunit A 269417 Seq. No. 19748 1.R1011 Contig ID uC-zmflb73062c11b1 5'-most EST BLASTX

Method q541825 NCBI GI BLAST score 641

1.0e-66 E value Match length 245



% identity 65
NCBI Description protein kinase - spinach >gi_457711_emb_CAA82993_ (Z30332)

protein kinase [Spinacia oleracea]

Seq. No. 269418

Contig ID 19753_1.R1011 5'-most EST gct701169186.h1

Method BLASTX
NCBI GI g1663722
BLAST score 1067
E value 1.0e-116
Match length 255
% identity 76

NCBI Description (U50845) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]

Seq. No. 269419

Contig ID 19754_1.R1011 5'-most EST uC-zmflb73232f05b1

Method BLASTN
NCBI GI g2062705
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 269420 Contig ID 19755_1.R1011

5'-most EST LIB1 $4\overline{3}$ -047-Q1-E1-G11

Method BLASTX
NCBI GI g4204294
BLAST score 360
E value 4.0e-34
Match length 111
% identity 69

NCBI Description (AC003027) lcl_prt_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 269422

Contig ID 19764_1.R1011

5'-most EST LIB3150-001-Q1-N1-C1

Seq. No. 269423

Contig ID 19764_2.R1011

5'-most EST LIB3069-044-Q1-K1-A6

Seq. No. 269424

Contig ID 19767_1.R1011

5'-most EST uC-zmflmo17097g09b1

Method BLASTX
NCBI GI g4584548
BLAST score 914
E value 8.0e-99



```
219
Match length
                   75
% identity
                  (AL049608) putative protein [Arabidopsis thaliana]
NCBI Description
                   269425
Seq. No.
                   19767 4.R1011
Contig ID
                   LIB3180-022-P2-M1-G6
5'-most EST
                   BLASTX
Method
                   q4584548
NCBI GI
                   210
BLAST score
                   1.0e-16
E value
Match length
                   48
                   79
% identity
NCBI Description (AL049608) putative protein [Arabidopsis thaliana]
Seq. No.
                   269426
                   19768 1.R1011
Contig ID
                   LIB3150-001-Q1-N1-C3
5'-most EST
Method
                   BLASTX
                   q2583133
NCBI GI
                   494
BLAST score
                   1.0e-49
E value
Match length
                   125
% identity
                   74
NCBI Description (AC002387) unknown protein [Arabidopsis thaliana]
                   269427
Seq. No.
Contig ID
                   19768 2.R1011
5'-most EST
                   uC-zmrob73050g04b1
                   BLASTX
Method
NCBI GI
                   g2583133
BLAST score
                   230
E value
                   6.0e-19
Match length
                   56
                   75
% identity
NCBI Description (AC002387) unknown protein [Arabidopsis thaliana]
                   269428
Seq. No.
                   19769 1.R1011
Contig ID
                   uC-zmflMo17006h06b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2499945
BLAST score
                   422
                   3.0e-41
E value
                   156
Match length
% identity
NCBI Description
                   URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
                   PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                   DECARBOXYLASE >gi_1076363_pir_S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) /
```

orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842)

pyrE-F [Arabidopsis thaliana]

Seq. No. 269429 Contig ID 19773 1.R1011

5'-most EST uC-zmflmo17408a09a1



Method BLASTX NCBI GI g3892048 BLAST score 925 E value 1.0e-100 Match length 261 % identity 67

(AC002330) putative tryptophan synthase alpha 1-like NCBI Description

protein [Arabidopsis thaliana]

269430 Seq. No.

19775 1.R1011 Contig ID

5'-most EST LIB3150-001-Q1-N1-D1

64

Method BLASTX g4522004 NCBI GI BLAST score 433 1.0e-42 E value Match length 140

% identity NCBI Description (AC007069) putative histidine kinase, sensory transduction

[Arabidopsis thaliana]

269431 Seq. No.

19784 1.R1011 Contig ID

5'-most EST LIB3279-049-P1-K1-A10

269432 Seq. No.

Contig ID 19784 2.R1011

5'-most EST uC-zmflb73004c05a1

Seq. No. 269433

19784 3.R1011 Contig ID 5'-most EST rvt700549327.h1

Seq. No. 269434

19791 1.R1011 Contig ID 5'-most EST xsy700211822.h1

Method BLASTX NCBI GI g3790102 BLAST score 1270 E value 1.0e-140 Match length 350 % identity 68

(AF095521) pyrophosphate-dependent phosphofructokinase NCBI Description

alpha subunit [Citrus X paradisi]

269435 Seq. No.

19793 1.R1011 Contig ID

5'-most EST LIB3137-008-Q1-K1-E5

269436 Seq. No.

19794 1.R1011 Contig ID

5'-most EST uC-zmflmo17295g02b1

Method BLASTX g4062934 NCBI GI BLAST score 1779 E value 0.0e + 00Match length 375



% identity (D88272) formate dehydrogenase [Hordeum vulgare] NCBI Description 269437 Seq. No. 19799 1.R1011 Contig ID LIB3150-001-Q1-N1-F8 5'-most EST Method BLASTX NCBI GI g116229 587 BLAST score 1.0e-60 E value 186 Match length 66 % identity MITOCHONDRIAL CHAPERONIN HSP60 PRECURSOR NCBI Description >gi_99676_pir__S20876 chaperonin hsp60 precursor -Arabidopsis thaliana >gi_16221_emb_CAA77646_ (Z11547) chaperonin hsp60 [Arabidopsis thaliana] 269438 Seq. No. 19813 1.R1011 Contig ID uC-zmflb73158f11a1 5'-most EST 269439 Seq. No. 19817 1.R1011 Contig ID LIB3150-001-Q1-N1-H6 5'-most EST BLASTX Method q3851005 NCBI GI BLAST score 1897 0.0e + 00E value 365 Match length 100 % identity (AF069911) pyruvate dehydrogenase E1 alpha subunit [Zea NCBI Description mays] 269440 Seq. No. 19817_2.R1011 Contig ID 5'-most EST uC-zmrob73049q11a1 Method BLASTN NCBI GI q1185553 BLAST score 62 3.0e-26 E value 114 Match length 45 % identity Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2) NCBI Description gene, complete cds 269441 Seq. No. Contig ID 19817 3.R1011 5'-most EST uC-zmflmo17130c03b1 Method BLASTN NCBI GI q1185553 BLAST score 61

BLAST score 61 E value 1.0e-25 Match length 124

45

% identity

NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)

gene, complete cds



Seq. No. 269442

Contig ID 19832_1.R1011

5'-most EST LIB3150-002-Q1-N1-B12

Method BLASTX
NCBI GI g1136434
BLAST score 210
E value 3.0e-16
Match length 75
% identity 53

NCBI Description (D80009) KIAA0187 [Homo sapiens]

Seq. No. 269443

Contig ID 19845 1.R1011

5'-most EST uC-zmflMo17007d03b1

Seq. No. 269444

Contig ID 19846_1.R1011

5'-most EST uC-zmflmo17308g12b1

Method BLASTX
NCBI GI g3779024
BLAST score 1070
E value 1.0e-117
Match length 288
% identity 67

NCBI Description (AC005171) unknown protein [Arabidopsis thaliana]

Seq. No. 269445

Contig ID 19861 1.R1011

5'-most EST LIB3150-105-P2-K1-F9

Method BLASTX
NCBI GI g4220523
BLAST score 557
E value 8.0e-57
Match length 251
% identity 47

NCBI Description (AL035356) putative alliin lyase [Arabidopsis thaliana]

Seq. No. 269446

Contig ID 19861 2.R1011

5'-most EST LIB3059-036-Q1-K1-H11

Method BLASTX
NCBI GI 94220523
BLAST score 529
E value 1.0e-53
Match length 186
% identity 52

NCBI Description (AL035356) putative alliin lyase [Arabidopsis thaliana]

Seq. No. 269447

Contig ID 19868 1.R1011

5'-most EST LIB3150-002-Q1-N1-E8

Method BLASTX
NCBI GI g3928543
BLAST score 159
E value 1.0e-10
Match length 134
% identity 36



NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No. 269448

Contig ID 19881_1.R1011 5'-most EST tzu700205181.h1

Method BLASTX
NCBI GI g3874440
BLAST score 149
E value 3.0e-09
Match length 107
% identity 31

NCBI Description (Z81038) Similarity to Bovine NADH-ubiquinone

oxidoreducatse B8 subunit (SW:Q02370) [Caenorhabditis

elegans]

Seq. No. 269449

Contig ID 19881_3.R1011 5'-most EST hbs701185375.h1

Seq. No. 269450

Contig ID 19888_1.R1011

5'-most EST LIB3150-002-Q1-N1-G8

Seq. No. 269451

Contig ID 19894 1.R1011

5'-most EST LIB3136-009-Q1-K1-A1

Method BLASTX
NCBI GI g4006864
BLAST score 405
E value 3.0e-39
Match length 155
% identity 54

NCBI Description (Z99707) nucleoporin-like protein [Arabidopsis thaliana]

Seq. No. 269452

Contig ID 19897_1.R1011 5'-most EST ymt700220790.h1

Method BLASTX
NCBI GI g2244826
BLAST score 1380
E value 1.0e-153
Match length 442
% identity 60

NCBI Description (Z97336) replication control protein homolog [Arabidopsis

thaliana]

Seq. No. 269453

Contig ID 19901_1.R1011

5'-most EST LIB3069-020-Q1-K1-A4

Seq. No. 269454

Contig ID 19907_1.R1011 5'-most EST xsy700208065.h1

Method BLASTX NCBI GI g2739168 BLAST score 360



3.0e - 34E value 143 Match length % identity 50 (AF032386) aldose-1-epimerase-like protein [Nicotiana NCBI Description tabacum] 269455 Seq. No. 19916 1.R1011 Contig ID uC-zmflmo17238f05b1 5'-most EST BLASTX Method g1055161 NCBI GI 207 BLAST score 3.0e-16 E value Match length 115 % identity 45 (U40029) similar to human 100 kDa coactivator (U22055) NCBI Description [Caenorhabditis elegans] 269456 Seq. No. 19916 2.R1011 Contig ID $xmt70\overline{0}265053.h1$ 5'-most EST Seq. No. 269457 19919 2.R1011 Contig ID LIB3150-004-Q1-N1-A4 5'-most EST Method BLASTX g2244965 NCBI GI BLAST score 430 2.0e-42 E value 122 Match length 67 % identity (Z97340) unnamed protein product [Arabidopsis thaliana] NCBI Description 269458 Seq. No. 19939 1.R1011 Contig ID $wyr70\overline{0}235809.h1$ 5'-most EST BLASTX Method NCBI GI g3075399 160 BLAST score 2.0e-10 E value 94 Match length 39 % identity NCBI Description (AC004484) SF16-like protein [Arabidopsis thaliana] 269459 Seq. No. 19943_1.R1011 Contig ID ntr700075668.h1 5'-most EST BLASTX Method q3643608 NCBI GI 890 BLAST score E value 1.0e-95

347 Match length 53 % identity

(AC005395) hypothetical protein [Arabidopsis thaliana] NCBI Description

269460 Seq. No. 19944_1.R1011 Contig ID



5'-most EST LIB3150-004-Q1-N1-D2

Method BLASTX NCBI GI g1723929 BLAST score 533 E value 3.0e-54Match length 169 60 % identity

HYPOTHETICAL 171.5 KD HELICASE IN NUT1-ARO2 INTERGENIC NCBI Description

REGION >qi 2131231 pir S60416 DNA helicase YGL150c - yeast

(Saccharomyces cerevisiae) >gi 1322734 emb_CAA96861_

(Z72672) ORF YGL150c [Saccharomyces cerevisiae]

Seq. No. 269461

Contig ID 19949 1.R1011

LIB3150-004-Q1-N1-E4 5'-most EST

BLASTX Method NCBI GI g3047084 BLAST score 588 E value 2.0e-68 Match length 194 % identity

(AF058914) similar to aminoacyl-tRNA synthetases NCBI Description

[Arabidopsis thaliana]

Seq. No. 269462

Contig ID 19955 1.R1011

5'-most EST LIB3150-004-Q1-N1-H1

Seq. No. 269463

Contig ID 19959 1.R1011

uC-zmflmo17303g09b1 5'-most EST

Method BLASTX g2190419 NCBI GI BLAST score 157 2.0e-10 E value 105 Match length 36

% identity

NCBI Description (Y13632) dem [Lycopersicon esculentum]

Seq. No. 269464

19963 1.R1011 Contig ID

5'-most EST uC-zmflmo17100g05b1

Seq. No. 269465

19964 1.R1011 Contig ID

5'-most EST LIB3150-040-Q1-N1-F3

Method BLASTX NCBI GI g2494223 319 BLAST score E value 4.0e-29 85 Match length % identity 67

NCBI Description

DYNEIN LIGHT CHAIN 1, CYTOPLASMIC >gi_1209059 (U32855) cytoplasmic dynein light chain 1 [Drosophila melanogaster] >gi 4097197 (U48846) 8kd dynein light chain [Drosophila melanogaster] >gi_4097201 (U48848) 8kd dynein light chain

[Drosophila melanogaster]



Seq. No. 269466

Contig ID 19967 1.R1011

5'-most EST LIB3150-005-Q1-N1-A9

Method BLASTX
NCBI GI g4510348
BLAST score 185
E value 7.0e-14
Match length 102
% identity 43

NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 269467

Contig ID 19969_1.R1011 5'-most EST fwa700097277.h1

Method BLASTX
NCBI GI g4309698
BLAST score 337
E value 1.0e-31
Match length 117
% identity 58

NCBI Description (AC006266) putative glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 269468

Contig ID 19970_1.R1011 5'-most EST pmx700090673.h1

Method BLASTX
NCBI GI g2281093
BLAST score 1469
E value 1.0e-163
Match length 337
% identity 78

NCBI Description (AC002333) beta transducin isolog [Arabidopsis thaliana]

Seq. No. 269469

Contig ID 19976_1.R1011

5'-most EST LIB3150-005-Q1-N1-B7

Seq. No. 269470

Contig ID 19981_1.R1011 5'-most EST uC-zmflb73202e08b1

Method BLASTX
NCBI GI g4490739
BLAST score 350
E value 5.0e-33
Match length 100
% identity 65

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 269471

Contig ID 19988_1.R1011 5'-most EST wyr700239576.h1

Seq. No. 269472

Contig ID 19995_1.R1011 5'-most EST uC-zmflB73021c04b1



Method BLASTX
NCBI GI g4056494
BLAST score 599
E value 1.0e-61
Match length 220
% identity 58

NCBI Description (AC005896) putative protein translocase [Arabidopsis

thaliana]

Seq. No. 269473

Contig ID 19996_1.R1011

5'-most EST LIB3150-005-Q1-N1-E12

Method BLASTX
NCBI GI g2392895
BLAST score 307
E value 4.0e-28
Match length 107
% identity 61

NCBI Description (AF017056) brassinosteroid insensitive 1 [Arabidopsis

thaliana]

Seq. No. 269474

Contig ID 19999_1.R1011 5'-most EST uC-zmflb73069g05b1

Seq. No. 269475

Contig ID 20003_1.R1011 5'-most EST wyr700236269.h1

Method BLASTX
NCBI GI g1361311
BLAST score 457
E value 2.0e-45
Match length 227
% identity 46

NCBI Description CMP-2-keto-3-deoxyoctulosonic acid synthetase homolog -

Chlamydia trachomatis >gi_557478 (U15192)

CMP-2-keto-3-deoxyoctulosonic acid synthetase [Chlamydia

trachomatis]

Seq. No. 269476

Contig ID 20004 1.R1011

5'-most EST LIB3150-005-Q1-N1-F11

Seq. No. 269477

Contig ID 20005 1.R1011

5'-most EST uC-zmflmo17286b09b1

Method BLASTX
NCBI GI g3668074
BLAST score 693
E value 8.0e-73
Match length 230
% identity 57

NCBI Description (AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No. 269478

Contig ID 20011_1.R1011 5'-most EST fwa700097731.h1

Match length

% identity

95

75

```
269479
Seq. No.
Contig ID
                  20012 1.R1011
5'-most EST
                  fwa700099839.h1
                  BLASTX
Method
                  g1350548
NCBI GI
BLAST score
                  252
                  2.0e-21
E value
                  114
Match length
% identity
                  43
NCBI Description (L47609) heat shock-like protein [Picea glauca]
                  269480
Seq. No.
                  20012 3.R1011
Contig ID
5'-most EST
                  LIB84-015-Q1-E1-C8
Method
                  BLASTX
NCBI GI
                  g1350548
BLAST score
                  256
                  1.0e-21
E value
Match length
                  108
% identity
                  46
NCBI Description (L47609) heat shock-like protein [Picea glauca]
                  269481
Seq. No.
                  20013 1.R1011
Contig ID
5'-most EST
                  ntr700075818.hl
                  BLASTX
Method
NCBI GI
                  g2102679
BLAST score
                  229
                  1.0e-18
E value
                  190
Match length
                  33
% identity
NCBI Description
                  (U07424) putative tRNA synthetase-like protein [Homo
                  sapiens] >gi 4104935 gb AAD02221 (AF042347) putative
                  phenylalanyl-tRNA synthetase alpha-subunit; PheHA [Homo
                  sapiens]
Seq. No.
                  269482
Contig ID
                  20015 1.R1011
5'-most EST
                  LIB3150-032-Q1-N1-E4
Method
                  BLASTX
                  g100484
NCBI GI
BLAST score
                  181
E value
                  6.0e-13
Match length
                  66
% identity
                  47
NCBI Description hypothetical protein - garden snapdragon
Seq. No.
                  269483
Contig ID
                  20016 1.R1011
5'-most EST
                  cat700016093.rl
Method
                  BLASTX
NCBI GI
                  q4567227
BLAST score
                  360
E value
                  3.0e - 34
```



NCBI Description (AC007119) putative transport protein [Arabidopsis thaliana]

Seq. No. 269484

Contig ID 20037_1.R1011

5'-most EST LIB3153-006-Q1-K1-C12

Seq. No. 269485

Contig ID 20038 1.R1011

5'-most EST LIB3136-008-Q1-K1-H7

Method BLASTX
NCBI GI g2829902
BLAST score 858
E value 2.0e-92
Match length 255

% identity 67

NCBI Description (AC002311) Putative sulphate transporter protein#protein

[Arabidopsis thaliana]

Seq. No. 269486

Contig ID 20042_1.R1011 5'-most EST uC-zmflb73014a09b1

Method BLASTX
NCBI GI g999542
BLAST score 592
E value 4.0e-61
Match length 170
% identity 65

NCBI Description Spinacia oleracea >gi_999543_pdb_1GYL_B Spinacia oleracea

Seq. No. 269487

Contig ID 20049_1.R1011 5'-most EST qmh700029507.f1

Method BLASTX
NCBI GI g1658193
BLAST score 515
E value 2.0e-52
Match length 128
% identity 84

NCBI Description (U74319) obtusifoliol 14-alpha demethylase CYP51 [Sorghum

bicolor]

Seq. No. 269488

Contig ID 20066_1.R1011 5'-most EST tfd700571645.h1

Seq. No. 269489

Contig ID 20078 1.R1011

5'-most EST uC-zmroteosinte032g11b1

Method BLASTX
NCBI GI g2129622
BLAST score 546
E value 9.0e-56
Match length 124
% identity 80

NCBI Description immunophilin FKBP15-1 - Arabidopsis thaliana >gi_1272406

(U52046) immunophilin [Arabidopsis thaliana]



269490 Seq. No.

20078 2.R1011 Contig ID 5'-most EST pmx700087221.h1

BLASTX Method g2129622 NCBI GI BLAST score 403 2.0e-39 E value 89 Match length 83 % identity

immunophilin FKBP15-1 - Arabidopsis thaliana >gi 1272406 NCBI Description

(U52046) immunophilin [Arabidopsis thaliana]

269491 Seq. No.

Contig ID 20084 1.R1011

5'-most EST uC-zmflmo17263d08b1

Method BLASTX NCBI GI g1079069 BLAST score 167 E value 6.0e-11 Match length 120 % identity 33

NCBI Description Drosophila translocation protein 1 - fruit fly (Drosophila

melanogaster) >gi 558181 emb CAA86222 (Z38100) Drosophila

translocation protein 1 [Drosophila melanogaster]

269492 Seq. No.

Contig ID 20084 2.R1011 5'-most EST nbm700475640.h1

269493 Seq. No.

20085 1.R1011 Contig ID

5'-most EST LIB3150-007-Q1-N1-A10

269494 Seq. No.

20086 1.R1011 Contig ID 5'-most EST $uC-zm\overline{f}lb73014a01b1$

Method BLASTX NCBI GI q3228517 BLAST score 533 E value 2.0e-54 Match length 168 62 % identity

NCBI Description (AF007788) ETTIN [Arabidopsis thaliana]

269495 Seq. No.

20087 1.R1011 Contig ID

5'-most EST LIB143-017-Q1-E1-F1

Seq. No. 269496

Contig ID 20089 1.R1011 5'-most EST $xmt70\overline{0}265015.h1$

Seq. No. 269497

20091 1.R1011 Contig ID 5'-most EST wty700171255.hl

Method BLASTX



```
NCBI GI g4530585
BLAST score 331
E value 1.0e-30
Match length 86
% identity 69
```

NCBI Description (AF130978) B12D protein [Ipomoea batatas]

Seq. No. 269498

Contig ID 20091_4.R1011 5'-most EST wyr700240267.h1

Seq. No. 269499

Contig ID 20100 1.R1011

5'-most EST LIB3150-007-Q1-N1-B5

Seq. No. 269500

Contig ID 20104 1.R1011

5'-most EST LIB3150-085-P1-N1-A8

Method BLASTX
NCBI GI g465975
BLAST score 299
E value 4.0e-27
Match length 98
% identity 61

NCBI Description PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME

III >gi_482102_pir__S40731 ATP-dependent RNA helicase

homolog T26G10.1 - Caenorhabditis elegans

>gi_3880293_emb_CAA82362_ (Z29115) similar to RNA

helicases, deleted exon 1397-1495 which introduced stop codon at 3' splice; 5' splice looks v. good; ?possible alternate final exon.; cDNA EST yk368a4.3 comes from this

gene; cDNA EST yk368a4.5 comes fr

Seq. No. 269501

Contig ID 20106_1.R1011

5'-most EST LIB3156-002-Q1-K1-F2 Method BLASTX

Method BLASTX
NCBI GI g2462749
BLAST score 543
E value 3.0e-55
Match length 307
% identity 40

NCBI Description (AC002292) Putative Serine/Threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 269502

Contig ID 20110_1.R1011 5'-most EST nbm700467986.h1

Method BLASTX
NCBI GI g4406775
BLAST score 188
E value 2.0e-13
Match length 157
% identity 32

NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]

Seq. No. 269503



```
Contig ID
                   20113 1.R1011
                   ntr700072930.hl
5'-most EST
Method
                   BLASTX
                   g4220529
NCBI GI
BLAST score
                   1357
                   1.0e-150
E value
Match length
                   379
% identity
                   67
                   (AL035356) putative protein [Arabidopsis thaliana]
NCBI Description
                   269504
Seq. No.
Contig ID
                   20121 1.R1011
                   pmx700087673.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3861188
BLAST score
                   250
                   3.0e-21
E value
Match length
                   94
% identity
                   49
                   (AJ235272) 50S RIBOSOMAL PROTEIN L24 (rplX) [Rickettsia
NCBI Description
                   prowazekii]
Seq. No.
                   269505
Contig ID
                   20122 1.R1011
5'-most EST
                   dyk70\overline{0}103291.h1
Method
                   BLASTX
NCBI GI
                   g2583081
BLAST score
                   259
E value
                   6.0e-22
Match length
                   109
% identity
                   50
                   (AF026977) microsomal glutathione S-transferase 3 [Homo
NCBI Description
                   sapiens]
                   269506
Seq. No.
                   20129 1.R1011
Contig ID
                   uC-zmflmo17236f01b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2252472
BLAST score
                   1234
                   1.0e-136
E value
Match length
                   318
                   73
% identity
                  (Z97558) argininosuccinate lyase [Arabidopsis thaliana]
NCBI Description
                   269507
Seq. No.
                   20129 2.R1011
Contig ID
5'-most EST
                   uC-zmroteosinte033a08b1
Method
                   BLASTX
NCBI GI
                   g2252472
                   522
BLAST score
E value
                   4.0e-53
```

155 Match length % identity

(Z97558) argininosuccinate lyase [Arabidopsis thaliana] NCBI Description

Seq. No. 269508

Seq. No.

Contig ID



```
20129 3.R1011
Contig ID
                  uC-zmflb73356a01a2
5'-most EST
Method
                  BLASTX
                  g2252472
NCBI GI
                   \bar{7}49
BLAST score
                  2.0e-79
E value
Match length
                  193
                   75
% identity
                  (Z97558) argininosuccinate lyase [Arabidopsis thaliana]
NCBI Description
                  269509
Seq. No.
Contig ID
                   20131 1.R1011
5'-most EST
                  uC-zmflmo17001c07b1
Method
                  BLASTX
NCBI GI
                  q3068771
BLAST score
                   499
E value
                   2.0e-50
Match length
                  176
                   57
% identity
NCBI Description (AF058987) xanthine dehydrogenase [Ceratitis capitata]
Seq. No.
                  269510
                   20134 1.R1011
Contig ID
5'-most EST
                   fdz701158974.h2
Method
                  BLASTX
NCBI GI
                  g1001629
BLAST score
                  180
E value
                   3.0e-13
Match length
                   72
                   49
% identity
NCBI Description (D64002) hypothetical protein [Synechocystis sp.]
                   269511
Seq. No.
                   20138 1.R1011
Contig ID
                   uwc700154158.hl
5'-most EST
Seq. No.
                   269512
Contig ID
                   20138 2.R1011
5'-most EST
                   gct701169549.h1
Method
                   BLASTX
NCBI GI
                   q4454465
BLAST score
                   262
E value
                   3.0e-22
Match length
                   112
% identity
                   41
NCBI Description
                  (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                   269513
                   20138 3.R1011
Contig ID
5'-most EST
                   LIB143-057-Q1-E1-H11
Seq. No.
                   269514
                   20147 1.R1011
Contig ID
                  LIB3150-007-Q1-N1-H6
5'-most EST
```

20157 1.R1011

269515



```
5'-most EST
                  LIB3150-008-Q1-N1-A8
Seq. No.
                  269516
Contig ID
                  20162 1.R1011
                  LIB3150-019-Q1-N1-H4
5'-most EST
Seq. No.
                  269517
                  20177 1.R1011
Contig ID
                  uC-zmflb73119a06b1
5'-most EST
Method
                  BLASTX
                  g3874228
NCBI GI
BLAST score
                  290
                  3.0e-29
E value
                  215
Match length
% identity
                  42
                  (Z49909) cDNA EST CEMSF21F comes from this gene; cDNA EST
NCBI Description
                  EMBL:D73546 comes from this gene; cDNA EST EMBL:D73669
                  comes from this gene; cDNA EST EMBL:D70979 comes from this
                  gene; cDNA EST EMBL:D71075 comes from this gene; cDNA E
                  269518
Seq. No.
                  20179 1.R1011
Contig ID
5'-most EST
                  LIB3060-048-Q1-K1-H12
Method
                  BLASTX
                  g3201541
NCBI GI
                  857
BLAST score
                  4.0e-92
E value
Match length
                  204
% identity
                  78
NCBI Description (AJ005077) TCTR2 protein [Lycopersicon esculentum]
                  269519
Seq. No.
Contig ID
                  20183 1.R1011
5'-most EST
                  ypc700804314.hl
Method
                  BLASTX
NCBI GI
                  g4469020
BLAST score
                  468
                  9.0e-47
E value
                  137
Match length
% identity
                  (AL035602) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                   269520
Seq. No.
                   20185 1.R1011
Contig ID
                  uC-zmrob73050a05a1
5'-most EST
Method
                  BLASTX
NCBI GI
                   g2653879
BLAST score
                  897
E value
                   1.0e-96
Match length
                   316
```

% identity

(AF026389) adenyl cyclase [Nicotiana tabacum] NCBI Description

269521 Seq. No.

20192 1.R1011 Contig ID

LIB3150-052-Q1-N1-C8 5'-most EST



Method BLASTX
NCBI GI g3608495
BLAST score 1058
E value 1.0e-115
Match length 287
% identity 77

NCBI Description (AF089738) plastid division protein FtsZ [Arabidopsis thaliana] >qi 4510351 qb AAD21440.1 (AC006921) plastid

division protein FtsZ [Arabidopsis thaliana]

Seq. No. 269522

Contig ID 20199_1.R1011 5'-most EST uC-zmflb73356a09a2

Method BLASTX
NCBI GI g1321627
BLAST score 304
E value 1.0e-27
Match length 67
% identity 82

NCBI Description (D83656) thylakoid-bound ascorbate peroxidase [Cucurbita

sp.]

Seq. No. 269523

Contig ID 20203_1.R1011

5'-most EST LIB3150-008-Q1-N1-G7

Method BLASTX
NCBI GI g4469015
BLAST score 390
E value 6.0e-38
Match length 103
% identity 72

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 269524

Contig ID 20205_1.R1011 5'-most EST ceu700428362.h1

Method BLASTX
NCBI GI g3414809
BLAST score 186
E value 7.0e-14
Match length 139
% identity 9

NCBI Description (AF061529) rjs [Mus musculus]

Seq. No. 269525

Contig ID 20206 1.R1011

5'-most EST LIB3150-008-Q1-N1-H12

Seq. No. 269526

Contig ID 20224_1.R1011 5'-most EST xmt700268112.h1

Seq. No. 269527

Contig ID 20226_1.R1011

5'-most EST uC-zmflmo17179f03b1

Method BLASTX NCBI GI g4455316



BLAST score 225 E value 5.0e-18 Match length 218 % identity 28

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 269528

Contig ID 20228_1.R1011 5'-most EST pmx700084480.h1

Method BLASTX
NCBI GI g118304
BLAST score 724
E value 3.0e-76
Match length 368
% identity 43

NCBI Description DIAMINOPIMELATE DECARBOXYLASE (DAP DECARBOXYLASE)

>gi_77626_pir__A31133 diaminopimelate decarboxylase (EC

4.1.1.20) - Pseudomonas aeruginosa

Seq. No. 269529

Contig ID 20228_2.R1011

5'-most EST uC-zmflmo17340b02a1

Seq. No. 269530

Contig ID 20244_1.R1011 5'-most EST uC-zmflb73193f08b1

Seq. No. 269531

Contig ID 20250 1.R1011

5'-most EST LIB3150-009-Q1-N1-D9

Method BLASTX
NCBI GI g4544436
BLAST score 205
E value 3.0e-16
Match length 95

% identity 48

NCBI Description (AC006592) anthocyanidin-3-glucoside rhamnosyltransferase,

3' partial [Arabidopsis thaliana]

Seq. No. 269532

Contig ID 20255_1.R1011 5'-most EST xyt700344744.h1

Seq. No. 269533

Contig ID 20259_1.R1011

5'-most EST LIB3150-009-Q1-N1-E6

Seq. No. 269534

Contig ID 20272_1.R1011 5'-most EST ntr700076177.h1

Seq. No. 269535

Contig ID 20292 1.R1011

5'-most EST LIB3150-010-Q1-N1-A7

Method BLASTX NCBI GI g112947 BLAST score 244



E value 1.0e-20 Match length 122 % identity 42

NCBI Description AAC-RICH MRNA CLONE AAC3 PROTEIN >gi 84121 pir S05357

hypothetical protein (clone AAC3) - slime mold

(Dictyostelium discoideum) (fragment)

>gi 7176 emb CAA34531 (X16524) coding region (AA 1 - 437)

[Dictyostelium discoideum]

Seq. No. 269536

Contig ID 20293_1.R1011

5'-most EST LIB3150-010-Q1-N1-A8

Seq. No. 269537

Contig ID 20294_1.R1011 5'-most EST uC-zmflb73220b08b2

Method BLASTX
NCBI GI g120941
BLAST score 203
E value 9.0e-16
Match length 62
% identity 58

NCBI Description GAR1 PROTEIN >gi_83030_pir__S19634 nucleolar protein GAR1 -

yeast (Saccharomyces cerevisiae) >gi_3728_emb_CAA45162_ (X63617) GAR1 [Saccharomyces cerevisiae] >gi_487935 (U00060) Garlp: Small nucleolar RNA protein required for

pre-rRNA splicing [Saccharomyces cerevisiae]

Seq. No. 269538

Contig ID 20309 1.R1011

5'-most EST LIB3150-010-Q1-N1-C7

Seq. No. 269539

Contig ID 20311_1.R1011 5'-most EST clt700041912.f1

Method BLASTX
NCBI GI g3256770
BLAST score 301
E value 1.0e-26
Match length 314
% identity 31

NCBI Description (AP000002) 318aa long hypothetical UDP-glucose 4-epimerase

[Pyrococcus horikoshii]

Seq. No. 269540

Contig ID 20311_2.R1011 5'-most EST uC-zmflb73075d03a1

Seq. No. 269541

Contig ID 20320 1.R1011

5'-most EST LIB31 $\overline{5}$ 0-010-Q1-N1-D9

Method BLASTX
NCBI GI g2370497
BLAST score 151
E value 1.0e-09
Match length 59
% identity 46



NCBI Description (Z98944) beta transducin [Schizosaccharomyces pombe]

Seq. No. 269542

Contig ID 20322 1.R1011

5'-most EST LIB31\overline{5}0-075-P2-N2-G3

Method BLASTX
NCBI GI g1184774
BLAST score 612
E value 8.0e-64
Match length 119
% identity 98

NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]

Seq. No. 269543

Contig ID 20325_1.R1011 5'-most EST nbm700464934.h1

Method BLASTX
NCBI GI g4454026
BLAST score 1051
E value 1.0e-114
Match length 358
% identity 59

NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No. 269544

Contig ID 20325 2.R1011

5'-most EST uC-zmflmo17264d01a2

Method BLASTX
NCBI GI g4454026
BLAST score 288
E value 9.0e-26
Match length 63
% identity 83

NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No. 269545

Contig ID 20329_1.R1011 5'-most EST xjt700096901.h1

Seq. No. 269546

Contig ID 20331_1.R1011 5'-most EST uC-zmroB73020g12b1

Seq. No. 269547

Contig ID 20340_1.R1011 5'-most EST uC-zmflb73304b04b1

Seq. No. 269548

Contig ID 20367 1.R1011

5'-most EST LIB3150-108-P1-N1-A6

Method BLASTX
NCBI GI g2245089
BLAST score 261
E value 7.0e-27
Match length 167
% identity 48



NCBI Description (Z97343) asparagine--tRNA ligase homolog [Arabidopsis thaliana]

Seq. No. 269549

Contig ID 20368_1.R1011

5'-most EST uC-zmroteosinte104f01b2

Seq. No. 269550

Contig ID 20368_2.R1011 5'-most EST tzu700206706.h1

Seq. No. 269551

Contig ID 20373_1.R1011

5'-most EST uC-zmflmo17001a10b1

Method BLASTX
NCBI GI g3327196
BLAST score 226
E value 6.0e-31
Match length 126
% identity 62

NCBI Description (AB014591) KIAA0691 protein [Homo sapiens]

Seq. No. 269552

Contig ID 20388_1.R1011

5'-most EST LIB3150-012-Q1-N1-A7

Method BLASTX
NCBI GI g82798
BLAST score 220
E value 1.0e-17
Match length 94
% identity 48

NCBI Description DNA-directed RNA polymerase (EC 2.7.7.6) I 189K chain -

fission yeast (Schizosaccharomyces pombe)

>gi_4995_emb_CAA32887_ (X14783) nucl product, RNA

polymerase I largest subunit (AA 1-1689)

[Schizosaccharomyces pombe]

Seq. No. 269553

Contig ID 20390_1.R1011

5'-most EST LIB3150-059-Q1-N1-F7

Method BLASTX
NCBI GI g231654
BLAST score 567
E value 3.0e-58
Match length 168
% identity 71

NCBI Description BRITTLE-1 PROTEIN PRECURSOR >gi_82676 pir JQ1459 Bt1

protein precursor - maize >gi_168426 (M79333) brittle-1

protein [Zea mays]

Seq. No. 269554

Contig ID 20390 2.R1011

5'-most EST LIB3061-008-Q1-K1-D10

Method BLASTX
NCBI GI g231654
BLAST score 912
E value 2.0e-98



Match length 192 % identity 46

NCBI Description BRITTLE-1 PROTEIN PRECURSOR >gi_82676_pir__JQ1459 Bt1 protein precursor - maize >gi_168426 (M79333) brittle-1

protein [Zea mays]

Seq. No. 269555

Contig ID 20390 3.R1011

5'-most EST LIB3151-034-Q1-K1-D12

Method BLASTX
NCBI GI g231654
BLAST score 875
E value 2.0e-95
Match length 183
% identity 51

NCBI Description BRITTLE-1 PROTEIN PRECURSOR >gi 82676 pir JQ1459 Bt1

protein precursor - maize >gi_168426 (M79333) brittle-1

protein [Zea mays]

Seq. No. 269556

Contig ID 20390 5.R1011

5'-most EST LIB3061-046-Q1-K1-E1

Method BLASTN
NCBI GI g168425
BLAST score 93
E value 7.0e-45
Match length 185
% identity 89

NCBI Description Zea mays brittle-1 protein (bt1) mRNA, complete cds

Seq. No. 269557

Contig ID 20390_7.R1011

5'-most EST LIB3059-047-Q1-K1-F5

Method BLASTX
NCBI GI g231654
BLAST score 330
E value 1.0e-30
Match length 66
% identity 95

NCBI Description BRITTLE-1 PROTEIN PRECURSOR >gi 82676 pir JQ1459 Bt1

protein precursor - maize >gi 168426 (M79333) brittle-1

protein [Zea mays]

Seq. No. 269558

Contig ID 20405_1.R1011 5'-most EST uC-zmflb73276f11b1

Method BLASTX
NCBI GI g4588619
BLAST score 334
E value 2.0e-30
Match length 426
% identity 27

NCBI Description (AF114160) adherin Nipped-B [Drosophila melanogaster]

Seq. No. 269559

Contig ID 20407 1.R1011

5'-most EST LIB3180-042-P2-M2-F5



Seq. No. 269560

Contig ID 20412_1.R1011

5'-most EST LIB3150-052-Q1-N1-D1

Method BLASTX
NCBI GI g393707
BLAST score 480
E value 4.0e-48
Match length 146
% identity 64

NCBI Description (X67696) acetyl-CoA acyltransferase [Cucumis sativus]

Seq. No. 269561

Contig ID 20429 1.R1011

5'-most EST LIB3150-012-Q1-N1-E7

Seq. No. 269562

Contig ID 20434_1.R1011 5'-most EST wty700171021.h1

Method BLASTX
NCBI GI 94587578
BLAST score 716
E value 2.0e-75
Match length 204
% identity 69

NCBI Description (AC006550) Belongs to PF_00004 ATPases associated with various cellular activities. [Arabidopsis thaliana]

Seq. No. 269563

Contig ID 20434_2.R1011 5'-most EST uC-zmflB73010c03b1

Seq. No. 269564

Contig ID 20434_3.R1011 5'-most EST nbm700467055.h1

Seq. No. 269565

Contig ID 20453_1.R1011 5'-most EST uC-zmflB73108f12b2

Method BLASTX
NCBI GI g1872521
BLAST score 472
E value 8.0e-47
Match length 161
% identity 58

NCBI Description (U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi 1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis

thaliana]

Seq. No. 269566

Contig ID 20467_1.R1011 5'-most EST fwa700098936.h1

Seq. No. 269567

Contig ID 20478_1.R1011

5'-most EST LIB3062-039-Q1-K1-B2



Seq. No. 269568

Contig ID 20481_1.R1011 5'-most EST LIB143-059-Q1-E1-B1

Seq. No. 269569

Contig ID 20482_1.R1011 5'-most EST wty700162664.h1

Method BLASTX
NCBI GI g1723565
BLAST score 147
E value 4.0e-09
Match length 181
% identity 29

NCBI Description HYPOTHETICAL 51.8 KD PROTEIN C17C9.06 IN CHROMOSOME I

>gi_1314158_emb_CAA97352_ (Z73099) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 269570

Contig ID 20483_1.R1011

5'-most EST LIB3279-007-P1-K1-F8

Seq. No. 269571

Contig ID 20484_1.R1011 5'-most EST wty700171935.h1

Seq. No. 269572

Contig ID 20487 1.R1011

5'-most EST uC-zmflMo17010g10b1

Method BLASTX

NCBI GI g2739433

BLAST score 161

E value 1.0e-10

Match length 58

% identity 47

NCBI Description (U70369) hematopoietic-specific IL-2 deubiquitinating

enzyme [Mus musculus]

Seq. No. 269573

Contig ID 20489_1.R1011 5'-most EST yyf700349035.h1

Method BLASTX
NCBI GI g2811026
BLAST score 310
E value 4.0e-28
Match length 80
% identity 75

NCBI Description TCP1-CHAPERONIN COFACTOR A HOMOLOG >gi_1946375 (U93215)

TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana] >gi 2347204 (AC002338) TCP1-chaperonin cofactor A isolog

[Arabidopsis thaliana]

Seq. No. 269574

Contig ID 20490_1.R1011

5'-most EST LIB3150-047-Q1-N1-D5

Seq. No. 269575

Contig ID 20491 1.R1011



5'-most EST LIB3150-013-Q1-N1-C5 Method BLASTX NCBI GI g3913437 BLAST score 734

E value 6.0e-78 Match length 147 % identity 94

NCBI Description PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA

HELICASE >gi_1402875_emb_CAA66825_ (X98130) RNA helicase
[Arabidopsis thaliana] >gi_1495271_emb_CAA66613_ (X97970)

RNA helicase [Arabidopsis thaliana]

Seq. No. 269576

Contig ID 20491_2.R1011

5'-most EST LIB3061-013-Q1-K1-D4

Method BLASTX
NCBI GI g3023637
BLAST score 172
E value 3.0e-12

Match length 67 % identity 52

NCBI Description PROBABLE ATP-DEPENDENT RNA HELICASE HRH1 (DEAH BOX PROTEIN

8) >gi_1362899_pir__A56236 probable RNA helicase 1 - human >gi 807817 dbj BAA09078 (D50487) RNA helicase (HRH1) [Homo

sapiens]

Seq. No. 269577

Contig ID 20493_1.R1011 5'-most EST pmx700091825.h1

Method BLASTN
NCBI GI g949979
BLAST score 157
E value 1.0e-82
Match length 244
% identity 91

NCBI Description Z.mays Glossy2 locus DNA

Seq. No. 269578

Contig ID 20493 2.R1011

5'-most EST uC-zmroteosinte096a06b2

Method BLASTN
NCBI GI g949979
BLAST score 71
E value 2.0e-31
Match length 135
% identity 88

NCBI Description Z.mays Glossy2 locus DNA

Seq. No. 269579

Contig ID 20494_1.R1011

5'-most EST LIB31 $\overline{5}$ 0-013-Q1-N1-C9

Method BLASTX
NCBI GI g3023511
BLAST score 443
E value 2.0e-43
Match length 196
% identity 45



NCBI Description PROBABLE ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 3 (ENDOPEPTIDASE CLP 3) >qi 1653656 dbj BAA18568 (D90915)

ATP-dependent Clp protease proteolytic subunit

[Synechocystis sp.]

269580 Seq. No.

Contig ID 20497 1.R1011

LIB3153-009-Q1-K1-B4 5'-most EST

269581 Seq. No.

Contig ID 20501 1.R1011 5'-most EST xsy700217417.h1

Method BLASTX NCBI GI q2623295 BLAST score 224 E value 3.0e-18Match length 84

% identity 52

NCBI Description (AC002409) hypothetical protein [Arabidopsis thaliana]

269582 Seq. No.

Contig ID 20508 1.R1011 5'-most EST uC-zmflb73210f05b1

Method BLASTX NCBI GI q461753 BLAST score 186 1.0e-13 E value Match length 42 90 % identity

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

PRECURSOR >gi 419773 pir S31164 ATP-dependent ClpB

proteinase regulatory chain homolog precursor, chloroplast - garden pea >gi 169128 (L09547) nuclear encoded precursor

to chloroplast protein [Pisum sativum]

269583 Seq. No.

Contig ID 20508 2.R1011 5'-most EST uC-zmflb73195a04b1

BLASTX Method q399213 NCBI GI BLAST score 625 E value 5.0e-65 Match length 128 % identity 93

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

CD4B PRECURSOR >gi_100190 pir B35905 CD4B protein - tomato

>gi_170435 (M32604) ATP-dependent protease (CD4B)

[Lycopersicon esculentum]

269584 Seq. No.

20508 5.R1011 Contig ID 5'-most EST $xmt70\overline{0}260023.h1$

Method BLASTX NCBI GI q399213 BLAST score 1015 E value 1.0e-111 Match length 228



% identity 87

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG CD4B PRECURSOR >gi_100190_pir_B35905 CD4B protein - tomato >gi_170435 (M32604) ATP-dependent protease (CD4B) [Lycopersicon esculentum]

Contig ID 20512_1.R1011 5'-most EST LIB3150-013-Q1-N1-E4 Seq. No. 269586

269585

Contig ID 20532_1.R1011
5'-most EST uC-zmflb73001g09b1
Method BLASTX
NCBI GI g4204265
BLAST score 890
E value 1.0e-95

E value 1.0e-9
Match length 396
% identity 49

Seq. No.

NCBI Description (AC005223) 45643 [Arabidopsis thaliana]

Seq. No. 269587

Contig ID 20537_1.R1011

5'-most EST LIB3150-013-Q1-N1-H1

Method BLASTN
NCBI GI g3170600
BLAST score 50
E value 4.0e-19
Match length 74
% identity 92

NCBI Description Zea mays zinc finger protein ID1 (id1) mRNA, complete cds

Seq. No. 269588

Contig ID 20537 2.R1011

5'-most EST LIB3151-005-Q1-K1-H12

Seq. No. 269589

Contig ID 20542 1.R1011

5'-most EST uC-zmroteosinte021c10b1

Method BLASTX
NCBI GI g129960
BLAST score 353
E value 3.0e-33
Match length 184
% identity 44

NCBI Description 4-NITROPHENYLPHOSPHATASE (PNPPASE)

Seq. No. 269590

Contig ID 20543_1.R1011

5'-most EST LIB3150-053-Q1-N1-A5

Method BLASTX
NCBI GI g3036805
BLAST score 238
E value 5.0e-20
Match length 103
% identity 46

NCBI Description (AL022373) thaumatin-like protein [Arabidopsis thaliana]



Seq. No. 269591 Contig ID 20545_1.R1011

5'-most EST ymt700223456.h1

Method BLASTX
NCBI GI g3176710
BLAST score 381
E value 5.0e-58
Match length 289
% identity 43

NCBI Description (AC002392) unknown protein [Arabidopsis thaliana]

Seq. No. 269592

Contig ID 20545_2.R1011 5'-most EST rvt700549542.h1

Method BLASTN
NCBI GI g5091496
BLAST score 60

E value 3.0e-25 Match length 104 89

NCBI Description Oryza sativa genomic DNA, chromosome 6, clone P0680A03,

complete sequence

Seq. No. 269593

Contig ID 20550_1.R1011 5'-most EST uC-zmflb73225d09b1

Method BLASTX
NCBI GI g3004547
BLAST score 176
E value 1.0e-12
Match length 105
% identity 43

NCBI Description (AC003673) unknown protein [Arabidopsis thaliana]

>gi_4185150 (AC005724) unknown protein [Arabidopsis

thaliana]

Seq. No. 269594

Contig ID 20567_1.R1011 5'-most EST gwl700614231.h1

Method BLASTX
NCBI GI g4191778
BLAST score 1027
E value 1.0e-112
Match length 349
% identity 59

NCBI Description (AC005917) putative nucleosome assembly protein I

[Arabidopsis thaliana]

Seq. No. 269595

Contig ID 20567_2.R1011

5'-most EST LIB3180-044-P2-M2-D1

Method BLASTX
NCBI GI g4191778
BLAST score 347
E value 8.0e-50
Match length 149



% identity 74

NCBI Description (AC005917) putative nucleosome assembly protein I

[Arabidopsis thaliana]

Seq. No. 269596

Contig ID 20586_1.R1011

5'-most EST LIB3279-005-P1-K1-E11

Method BLASTX
NCBI GI g3015621
BLAST score 339
E value 2.0e-31
Match length 199
% identity 42

NCBI Description (AF035460) low molecular weight heat shock protein

precursor [Zea mays]

Seq. No. 269597

Contig ID 20587 1.R1011 5'-most EST gwl700615193.h1

Seq. No. 269598

Contig ID 20587_2.R1011 5'-most EST uC-zmflb73028a06b1

Seq. No. 269599

Contig ID 20587_3.R1011 5'-most EST uC-zmflb73121c12b2

Seq. No. 269600

Contig ID 20587 4.R1011

5'-most EST uC-zmflMo17018d07b1

Method BLASTX
NCBI GI g3413716
BLAST score 593
E value 6.0e-61
Match length 365
% identity 43

NCBI Description (AC004747) unknown protein [Arabidopsis thaliana]

>gi 3643589 (AC005395) unknown protein [Arabidopsis

thalianal

Seq. No. 269601

Contig ID 20600 2.R1011

5'-most EST uC-zmflMo17093c08b1

Method BLASTX
NCBI GI g4567283
BLAST score 240
E value 5.0e-20
Match length 167
% identity 37

NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

Seq. No. 269602

Contig ID 20605_1.R1011 5'-most EST uC-zmflb73055e05b1

Method BLASTX NCBI GI g4262240



```
BLAST score
                   1069
E value
                   1.0e-117
Match length
                   265
% identity
                   73
NCBI Description (AC006200) putative stress protein [Arabidopsis thaliana]
                   269603
Seq. No.
Contig ID
                   20616 1.R1011
5'-most EST
                   LIB3180-057-P2-M1-G12
Method
                  BLASTX
NCBI GI
                   g100849
BLAST score
                   548
E value
                   4.0e-56
                   136
Match length
                   79
% identity
NCBI Description
                   acetolactate synthase (EC 4.1.3.18) (clone pSOG108) - maize
                   >gi 22139 emb CAA45116 (X63553) acetohydroxyacid synthase
                   [Zea mays]
                   269604
Seq. No.
Contig ID
                   20628 1.R1011
5'-most EST
                  LIB3180-035-P2-M2-G3
                   269605
Seq. No.
                   20631 1.R1011
Contig ID
5'-most EST
                  LIB3150-040-Q1-N1-H10
Method
                  BLASTX
NCBI GI
                   g2459429
BLAST score
                   583
E value
                   4.0e-60
Match length
                   148
% identity
                   72
NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]
                   269606
Seq. No.
Contig ID
                   20631 2.R1011
5'-most EST
                  uC-zm\overline{f}lmo17059h12a1
Method
                  BLASTX
NCBI GI
                  q2459429
BLAST score
                   216
E value
                   3.0e-17
Match length
                   57
% identity
                   67
NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]
Seq. No.
                   269607
Contig ID
                   20631_3.R1011
```

5'-most EST xyt700342632.h1

Method BLASTX q2459429 NCBI GI BLAST score 785 E value 1.0e-83 202 Match length 70 % identity

NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]

Seq. No. 269608

Contig ID 20631_4.R1011 5'-most EST uC-zmromo17023b02a1

Seq. No. 269609

Contig ID 20635_1.R1011 5'-most EST cat700019671.r1

Method BLASTX
NCBI GI g3885336
BLAST score 558
E value 5.0e-57
Match length 226
% identity 47

NCBI Description (AC005623) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No. 269610

Contig ID 20655_1.R1011 5'-most EST uC-zmflb73077h10b2

Method BLASTX
NCBI GI g3776564
BLAST score 374
E value 1.0e-35
Match length 162
% identity 50

NCBI Description (AC005388) Similar to hypothetical protein T1D16.16

gi_3075397 from A. thaliana BAC gb_AC004484. [Arabidopsis

thaliana]

Seq. No. 269611

Contig ID 20657_1.R1011 5'-most EST hvj700623309.h1

Method BLASTX
NCBI GI g3249066
BLAST score 600
E value 6.0e-62
Match length 221
% identity 58

NCBI Description (AC004473) Similar to S. cerevisiae SIK1P protein

gb_984964. ESTs gb_F15433 and gb_AA395158 come from this

gene. [Arabidopsis thaliana]

Seq. No. 269612

Contig ID 20657 2.R1011

5'-most EST uC-zmflmo17155g07b1

Method BLASTX
NCBI GI g3249066
BLAST score 667
E value 4.0e-70
Match length 193
% identity 71

NCBI Description (AC004473) Similar to S. cerevisiae SIK1P protein

gb_984964. ESTs gb_F15433 and gb_AA395158 come from this

gene. [Arabidopsis thaliana]

Seq. No. 269613

Contig ID 20657 3.R1011 5'-most EST nbm700472004.h1

E value

Match length

NCBI Description

% identity



```
269614
Seq. No.
                  20658 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17012f02b1
Method
                  BLASTX
                  g3264767
NCBI GI
BLAST score
                  426
                  3.0e-41
E value
                  260
Match length
                  42
% identity
                  (AF071893) AP2 domain containing protein [Prunus armeniaca]
NCBI Description
                  269615
Seq. No.
                  20658 2.R1011
Contig ID
5'-most EST
                  LIB3136-013-Q1-K1-B5
                  269616
Seq. No.
                  20658 4.R1011
Contig ID
                  uC-zm\overline{f}1b73290f05b1
5'-most EST
                  BLASTX
Method
                  g3264767
NCBI GI
BLAST score
                  257
                   4.0e-22
E value
                  52
Match length
                  88
% identity
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
                  269617
Seq. No.
                  20667 1.R1011
Contig ID
                  uC-zmflmo17293e10b1
5'-most EST
Seq. No.
                  269618
                   20667_2.R1011
Contig ID
5'-most EST
                  uC-zmflmo17375g09a1
Seq. No.
                  269619
Contig ID
                   20670 1.R1011
5'-most EST
                  uC-zmflmo17035c11a1
Method
                  BLASTX
NCBI GI
                  q2827002
BLAST score
                   325
E value
                   3.0e-30
Match length
                   69
% identity
NCBI Description (AF005993) HSP70 [Triticum aestivum]
Seq. No.
                   269620
Contig ID
                   20690 1.R1011
5'-most EST
                  xjt700096728.h1
Method
                  BLASTX
NCBI GI
                   q2559012
BLAST score
                  1795
```

37532

(AF026293) chaperonin containing t-complex polypeptide 1,

beta subunit; CCT-beta [Homo sapiens] >gi 4090929

0.0e + 00

518

67



(AF026166) chaperonin-containing TCP-1 beta subunit homolog [Homo sapiens]

Seq. No. 269621

Contig ID 20690 2.R1011

5'-most EST LIB31 $\overline{5}$ 0-067-P2-K1-F9

Method BLASTX
NCBI GI g549056
BLAST score 173
E value 3.0e-12
Match length 53
% identity 66

NCBI Description T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA)

>gi_631651_pir__S43059 CCT (chaperonin containing TCP-1)
beta chain - mouse >gi_468546_emb_CAA83428_ (Z31553) CCT
(chaperonin containing TCP-1) beta subunit [Mus musculus]

Seq. No. 269622

Contig ID 20692 1.R1011

5'-most EST uC-zmflmo17163d03b1

Method BLASTX
NCBI GI g1169200
BLAST score 388
E value 5.0e-37
Match length 243
% identity 58

NCBI Description DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR

>gi_421829_pir__S33706 DNA-damage resistance protein Arabidopsis thaliana >gi_166694 (M98455) [Arabidopsis
thaliana recombination and DNA-damage resistance protein
(DRT111) mRNA, complete cds.], gene product [Arabidopsis

thaliana]

Seq. No. 269623

Contig ID 20693_1.R1011 5'-most EST cat700017896.r1

Seq. No. 269624

Contig ID 20699_1.R1011

5'-most EST $uC-zm\overline{f}lMo17085d03b1$

Seq. No. 269625

Contig ID 20704 1.R1011

5'-most EST LIB3159-019-Q1-K1-H8

Method BLASTX
NCBI GI g4218014
BLAST score 1080
E value 1.0e-118
Match length 247
% identity 83

NCBI Description (AC006135) putative spliceosomal protein (RNA binding

protein) [Arabidopsis thaliana]

Seq. No. 269626

Contig ID 20705_1.R1011 5'-most EST uwc700153476.h1



Seq. No. 269627

Contig ID 20714_1.R1011

5'-most EST LIB3150-101-P1-N1-H2

Method BLASTX
NCBI GI g2947062
BLAST score 597
E value 3.0e-61
Match length 573
% identity 35

NCBI Description (AC002521) unknown protein [Arabidopsis thaliana]

Seq. No. 269628

Contig ID 20714 2.R1011

5'-most EST $uC-zm\overline{f}lm017212d10b1$

Seq. No. 269629

Contig ID 20715_1.R1011 5'-most EST uC-zmflB73009a12b1

Seq. No. 269630

Contig ID 20721_1.R1011

5'-most EST uC-zmflmo17051g08b1

Method BLASTX
NCBI GI g4128033
BLAST score 506
E value 9.0e-51
Match length 290
% identity 20

NCBI Description (AJ012376) ATP-binding cassette transporter-1 (ABC-1) [Homo

sapiens]

Seq. No. 269631

Contig ID 20722 1.R1011

5'-most EST LIB3150-016-Q1-N1-B9

Seq. No. 269632

Contig ID 20724_1.R1011

5'-most EST $uC-zm\overline{f}lmo17297f12b1$

Method BLASTX
NCBI GI g3834307
BLAST score 335
E value 4.0e-31
Match length 120
% identity 62

NCBI Description (AC005679) Strong similarity to gene T10I14.120 gi_2832679

putative protein from Arabidopsis thaliana BAC gb_AL021712.

ESTs gb_N65887 and gb_N65627 come from this gene.

[Arabidopsis thaliana]

Seq. No. 269633

Contig ID 20724_2.R1011

5'-most EST uC-zmflmo17054d12b1

Method BLASTX
NCBI GI g3834307
BLAST score 239
E value 5.0e-20
Match length 53



% identity 85

NCBI Description (AC005679) Strong similarity to gene T10I14.120 gi 2832679

putative protein from Arabidopsis thaliana BAC gb_AL021712.

ESTs gb N65887 and gb N65627 come from this gene.

[Arabidopsis thaliana]

Seq. No. 269634

Contig ID 20728_1.R1011

5'-most EST LIB3180-024-P2-M1-G2

Seq. No. 269635

Contig ID 20750_1.R1011

5'-most EST LIB3151-040-Q1-K1-G1

Seq. No. 269636

Contig ID 20750_3.R1011 5'-most EST uC-zmflb73274e05b1

Seq. No. 269637

Contig ID 20762_1.R1011 5'-most EST nbm700476112.h1

Method BLASTX
NCBI GI g4507067
BLAST score 361
E value 7.0e-44
Match length 292
% identity 41

NCBI Description SWI/SNF related, matrix associated, actin dependent

regulator of chromatin, subfamily a, member 1

>gi_134584_sp_P28370_SN21_HUMAN POSSIBLE GLOBAL

TRANSCRIPTION ACTIVATOR SNF2L1 >gi_479804_pir_S35457 SNF2 protein homolog - human >gi_292496 (M88163) transcription

activator [Homo sapiens]

Seq. No. 269638

Contig ID 20770 1.R1011

5'-most EST LIB3150-017-Q1-N1-A7

Method BLASTX
NCBI GI g477094
BLAST score 453
E value 3.0e-45
Match length 115
% identity 71

NCBI Description STE11 protein kinase homolog NPK1 - common tobacco

Seq. No. 269639

Contig ID 20775_1.R1011

5'-most EST uC-zmflb73290h10b1

Method BLASTX
NCBI GI g3242980
BLAST score 359
E value 7.0e-34
Match length 155
% identity 46

NCBI Description (AF069985) nitrilase homolog 1 [Mus musculus]

Seq. No. 269640



Contig ID 20777 1.R1011

uC-zmflm017233d04b1 5'-most EST

Method BLASTX NCBI GI q2618689 BLAST score 1904 0.0e+00E value Match length 446 % identity 81

(AC002510) unknown protein [Arabidopsis thaliana] NCBI Description

269641 Seq. No.

Contig ID 20779 1.R1011 $nbm70\overline{0}468728.h1$ 5'-most EST

Seq. No. 269642

Contig ID 20784 1.R1011

5'-most EST LIB3070-005-Q1-N1-C7

269643 Seq. No.

Contig ID 20788 1.R1011

5'-most EST LIB3062-042-Q1-K1-A8

Method BLASTX NCBI GI g4388717 BLAST score 801 E value 9.0e-86 Match length 215 69 % identity

NCBI Description (AC006413) putative nuclear phosphoprotein (contains

multiple TPR repeats prosite:QDOC50005) [Arabidopsis

thaliana]

269644 Seq. No.

20790 1.R1011 Contig ID

5'-most EST uC-zmroteosinte109d01b3

Method BLASTX NCBI GI g4580397 BLAST score 273 E value 2.0e-23 240 Match length

31 % identity

NCBI Description (AC007171) putative RNA helicase [Arabidopsis thaliana]

Seq. No. 269645

20790 2.R1011 Contig ID 5'-most EST tfd700569989.h1

269646 Seq. No.

Contig ID 20798 1.R1011

5'-most EST LIB3150-017-Q1-N1-D4

Seq. No. 269647

Contig ID 20810 1.R1011 5'-most EST nbm700475463.h1

269648 Seq. No.

Contig ID 20817 1.R1011 5'-most EST uC-zmflb73182d02b1

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269649
Seq. No.
Contig ID
                  20819 1.R1011
5'-most EST
                  uC-zmflb73033f12a1
Seq. No.
                  269650
Contig ID
                  20825 1.R1011
5'-most EST
                  LIB3059-036-Q1-K1-E3
Method
                  BLASTX
NCBI GI
                  g4056568
BLAST score
                  2606
E value
                  0.0e+00
Match length
                  556
% identity
                  57
NCBI Description (U90944) PDI-like protein [Zea mays]
Seq. No.
                  269651
Contig ID
                  20831 1.R1011
5'-most EST
                  xjt700094502.h1
Method
                  BLASTX
NCBI GI
                  q3047116
BLAST score
                  373
E value
                  3.0e-66
Match length
                  188
% identity
                  61
NCBI Description
                  (AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.
                  269652
Contig ID
                  20849 1.R1011
5'-most EST
                  uC-zmroteosinte053e11b2
Method
                  BLASTX
NCBI GI
                  q4539334
BLAST score
                  346
E value
                  2.0e-32
Match length
                  126
% identity
                  54
NCBI Description
                  (AL035539) putative protein [Arabidopsis thaliana]
                  269653
Seq. No.
Contig ID
                  20851 1.R1011
5'-most EST
                  LIB3150-022-Q1-N1-D2
Method
                  BLASTX
NCBI GI
                  q1703394
BLAST score
                  322
E value
                  1.0e-29
Match length
                  111
                  55
% identity
NCBI Description
                  ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5
                  >gi_1150556_emb_CAA55338_ (X78604) ARF-like protein 5
                  [Rattus norvegicus]
Seq. No.
                  269654
Contig ID
                  20857 1.R1011
5'-most EST
                  uC-zmflb73160g09b2
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37537

269655

20858 1.R1011

Seq. No. Contig ID



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5'-most EST
                  LIB3150-018-Q1-N1-B10
Seq. No.
                  269656
Contig ID
                   20860 1.R1011
5'-most EST
                  LIB3150-018-Q1-N1-B2
                  BLASTX
Method
NCBI GI
                  g3184074
BLAST score
                   275
                   2.0e-31
E value
                   256
Match length
                   32
% identity
NCBI Description
                   (AL023779) coatomer beta' subunit (beta' coat protein)
                   [Schizosaccharomyces pombe]
                   269657
Seq. No.
Contig ID
                   20869 1.R1011
5'-most EST
                   ntr700073061.h1
                   BLASTX
Method
NCBI GI
                   q1871196
BLAST score
                   696
E value
                   4.0e-73
Match length
                   179
                   74
% identity
                   (U90439) GMP kinase isolog [Arabidopsis thaliana]
NCBI Description
                   >gi 2335091 (AC002339) putative GMP kinase [Arabidopsis
                   thaliana]
                   269658
Seq. No.
Contiq ID
                   20872 1.R1011
                   LIB3062-020-Q1-K1-C12
5'-most EST
Method
                   BLASTX
                   q4505743
NCBI GI
                   257
BLAST score
                   7.0e-22
E value
                   137
Match length
                   37
% identity
                   prefoldin 5 >gi_2498565_sp_Q99471_MM1_HUMAN C-MYC BINDING
NCBI Description
                   PROTEIN MM-1 >gi_1731809_dbj_BAA14006_ (D89667) c-myc
                   binding protein [Homo sapiens]
                   269659
Seq. No.
                   20875_1.R1011
Contig ID
5'-most EST
                   pmx700081917.hl
                   269660
Seq. No.
                   20887_1.R1011
Contig ID
5'-most EST
                   LIB31\overline{5}0-018-Q1-N1-E6
Method
                   BLASTX
                   q285739
NCBI GI
BLAST score
                   343
E value
                   3.0e-32
                   147
Match length
                   48
% identity
```

Seq. No. 269661

NCBI Description

embryogenesis-associated protein [Daucus carota]

(D14605) AX110P [Daucus carota] >gi_740202_prf__2004427A



Contig ID 20889 1.R1011

5'-most EST LIB3150-018-Q1-N1-E8

Method BLASTX
NCBI GI g3033392
BLAST score 311
E value 5.0e-29
Match length 90
% identity 74

NCBI Description (AC004238) putative translation initiation factor EIF-2B-epsilon subunit [Arabidopsis thaliana]

Seq. No. 269662

Contig ID 20890_1.R1011 5'-most EST uC-zmflb73157g04b2

Seq. No. 269663

Contig ID 20894_1.R1011

5'-most EST LIB3069-026-Q1-K1-G12

Seq. No. 269664

Contig ID 20894_2.R1011

5'-most EST LIB3150-018-Q1-N1-F2

Seq. No. 269665

Contig ID 20898_1.R1011 5'-most EST fwa700100106.h1

Seq. No. 269666

Contig ID 20898 3.R1011

5'-most EST LIB3059-044-Q1-K1-C11

Seq. No. 269667

Contig ID 20903_1.R1011 5'-most EST uC-zmflb73242g07b2

Seq. No. 269668

Contig ID 20908_1.R1011

5'-most EST uC-zmroteosinte120c09b2

Method BLASTX
NCBI GI g2673920
BLAST score 315
E value 1.0e-28
Match length 108
% identity 58

NCBI Description (AC002561) similar to Drosophila couch potato protein

[Arabidopsis thaliana]

Seq. No. 269669

Contig ID 20908_2.R1011 5'-most EST nbm700464882.h1

Seq. No. 269670

Contig ID 20910_1.R1011

5'-most EST LIB3150-018-Q1-N1-H3

Method BLASTX NCBI GI g2245109 BLAST score 390



E value 9.0e-38 Match length 124 % identity 61

NCBI Description (Z97343) carboxyl-terminal proteinase homolog [Arabidopsis

thaliana]

Seq. No. 269671

Contig ID 20913 1.R1011

5'-most EST LIB3150-018-Q1-N1-H6

Method BLASTX
NCBI GI g2815493
BLAST score 732
E value 2.0e-77
Match length 364
% identity 40

NCBI Description SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)

(CP-MI) >gi 1731988 emb CAA70816_ (Y09603) serine

carboxypeptidase I, CP-MI [Hordeum vulgare]

Seq. No. 269672

Contig ID 20920_1.R1011 5'-most EST uC-zmflb73264a02b1

Method BLASTX
NCBI GI g3201615
BLAST score 970
E value 1.0e-105
Match length 409
% identity 51

NCBI Description (AC004669) unknown protein [Arabidopsis thaliana]

Seq. No. 269673

Contig ID 20928_1.R1011 5'-most EST ypc700804378.h1

Method BLASTX
NCBI GI g3033400
BLAST score 843
E value 1.0e-117
Match length 383
% identity 62

NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 269674

Contig ID 20932_1.R1011

5'-most EST uC-zmflmo17069c10b1

Method BLASTX
NCBI GI g4584548
BLAST score 850
E value 1.0e-119
Match length 251
% identity 81

NCBI Description (AL049608) putative protein [Arabidopsis thaliana]

Seq. No. 269675

Contig ID 20932_2.R1011

5'-most EST LIB3059-053-Q1-K1-E5

Method BLASTX



```
NCBI GI
                  g4584548
                   409
BLAST score
                   6.0e-40
E value
                  84
Match length
                   88
% identity
                  (AL049608) putative protein [Arabidopsis thaliana]
NCBI Description
                  269676
Seq. No.
Contig ID
                   20941 1.R1011
5'-most EST
                  pmx700087238.hl
                   269677
Seq. No.
```

Contig ID 20949_1.R1011 5'-most EST LIB3150-019-Q1-N1-D11 Method BLASTX NCBI GI g3249095 BLAST score 431

NCBI GI g3249095
BLAST score 431
E value 2.0e-64
Match length 229
% identity 58

NCBI Description (AC003114) Contains similarity to dihydrofolate reductase (dfr1) gb L13703 from Schizosaccharomyces pombe. ESTs

gb_N37567 and gb_T43002 come from this gene. [Arabidopsis

thaliana]

Seq. No. 269678

Contig ID 20954_1.R1011 5'-most EST uC-zmflMo17006a07b1

Method BLASTX
NCBI GI 94314388
BLAST score 397
E value 2.0e-38
Match length 138
% identity 52

NCBI Description (AC006232) hypothetical protein [Arabidopsis thaliana]

Seq. No. 269679

Contig ID 20955_1.R1011 5'-most EST LIB84-014-Q1-E1-E1

Method BLASTX
NCBI GI g1402891
BLAST score 309
E value 1.0e-27
Match length 172
% identity 45

NCBI Description (X98130) unknown [Arabidopsis thaliana]

Seq. No. 269680

Contig ID 20957 1.R1011

5'-most EST LIB3150-019-Q1-N1-E1

Method BLASTX
NCBI GI g3560533
BLAST score 955
E value 1.0e-103
Match length 195
% identity 92

NCBI Description (AF042333) 24-methylene lophenol C24(1)methyltransferase



[Oryza sativa]

Seq. No. 269681

Contig ID 20957_2.R1011 5'-most EST uC-zmflb73301c07a1

Method BLASTN
NCBI GI g2245648
BLAST score 45
E value 6.0e-16
Match length 53
% identity 96

NCBI Description Zea mays discolored-1 (mutant allele dsc1-Ref::Mu1) gene,

partial sequence

Seq. No. 269682

Contig ID 20966_1.R1011 5'-most EST pwr700453639.h1

Method BLASTX
NCBI GI g3450889
BLAST score 455
E value 4.0e-45
Match length 148
% identity 65

NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No. 269683

Contig ID 20974_1.R1011

5'-most EST LIB3060-038-Q1-K1-H5

Seq. No. 269684

Contig ID 20982_1.R1011

5'-most EST uC-zmflmo17055h05b1

Method BLASTX
NCBI GI g3360502
BLAST score 788
E value 3.0e-84
Match length 189
% identity 83

NCBI Description (AF061279) heat shock protein [Plectonema boryanum]

Seq. No. 269685

Contig ID 20983_1.R1011 5'-most EST ymt700220829.h1

Method BLASTX
NCBI GI g3687250
BLAST score 316
E value 6.0e-29
Match length 122
% identity 49

NCBI Description (AC005169) putative arginine n-methyltransferase

[Arabidopsis thaliana]

Seq. No. 269686

Contig ID 20984_1.R1011 5'-most EST uC-zmflB73047c08b1

Method BLASTX NCBI GI g3135268

```
BLAST score
E value
                   2.0e-39
Match length
                   223
% identity
NCBI Description
                  (AC003058) putative RNA-binding protein [Arabidopsis
                   thaliana]
                   269687
Seq. No.
Contig ID
                   21011 1.R1011
5'-most EST
                   nbm70\overline{0}469262.h1
Method
                   BLASTX
NCBI GI
                   a4432867
BLAST score
                   251
                   6.0e-21
E value
Match length
                   218
% identity
                   34
NCBI Description
                  (AC006300) putative dnaJ-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   269688
                   21011 2.R1011
Contig ID
5'-most EST
                   uC-zmflMo17012a12b1
Method
                   BLASTX
NCBI GI
                   q4204849
BLAST score
                   1157
E value
                   1.0e-127
Match length
                   301
% identity
NCBI Description (U55875) protein kinase [Arabidopsis thaliana]
Seq. No.
                   269689
Contig ID
                   21014_1.R1011
5'-most EST
                   uC-zmf1b73222g05b1
Method
                   BLASTX
NCBI GI
                   g4105563
BLAST score
                   2425
E value
                   0.0e + 00
Match length
                   469
% identity
                   99
NCBI Description (AF047490) zeta-carotene desaturase precursor [Zea mays]
Seq. No.
                   269690
                   21015_1.R1011
Contig ID
5'-most EST
                   LIB3150-020-Q1-N1-B7
Seq. No.
                   269691
```

Contig ID 21018 1.R1011

5'-most EST LIB3136-013-Q1-K1-E9

Seq. No. 269692

21038 1.R1011 Contig ID

5'-most EST uC-zmflmo17134e08b1

Method BLASTX NCBI GI g2443473 BLAST score 638 E value 1.0e-66 Match length 171



% identity 72

NCBI Description (AF001035) ASF/SF2 homolog [Arabidopsis thaliana]

Seq. No. 269693

Contig ID 21040 1.R1011

5'-most EST LIB3150-020-Q1-N1-F10

Seq. No. 269694

Contig ID 21043 1.R1011

5'-most EST LIB3150-020-Q1-N1-F2

Seq. No. 269695

Contig ID 21050 1.R1011

5'-most EST uC-zmflmo17099b12b1

Method BLASTX
NCBI GI g1890281
BLAST score 309
E value 3.0e-28
Match length 157
% identity 24

NCBI Description (U89984) transformation-sensitive protein homolog

[Acanthamoeba castellanii]

Seq. No. 269696

Contig ID 21050 2.R1011

5'-most EST LIB3150-054-Q1-N1-G3

Method BLASTX
NCBI GI g1890281
BLAST score 264
E value 6.0e-23
Match length 94
% identity 29

NCBI Description (U89984) transformation-sensitive protein homolog

[Acanthamoeba castellanii]

Seq. No. 269697

Contig ID 21053_1.R1011 5'-most EST uC-zmflb73022c05b1

Seq. No. 269698

Contig ID 21064 1.R1011

5'-most EST LIB3181-007-P1-M1-B8

Seq. No. 269699

Contig ID 21069 1.R1011

5'-most EST LIB3136-022-Q1-K1-H6

Method BLASTX
NCBI GI g2731377
BLAST score 328
E value 5.0e-30
Match length 236
% identity 35

NCBI Description (U28739) similar to alcohol dehydrogenase/ribitol

dehydrogenase [Caenorhabditis elegans]

Seq. No. 269700

Contig ID 21074 1.R1011

Seq. No.

Contig ID

5'-most EST

269706

21115 1.R1011

LIB3150-021-Q1-N1-G11



```
5'-most EST
                  uC-zmflmo17299h10b1
                  269701
Seq. No.
                  21074 2.R1011
Contig ID
                  nwy700447227.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g2462758
BLAST score
                  330
E value
                  2.0e-30
Match length
                  128
% identity
                  49
                  (AC002292) putative RNA-binding protein [Arabidopsis
NCBI Description
                  thalianal
Seq. No.
                  269702
Contig ID
                  21094 1.R1011
5'-most EST
                  xyt700342214.h1
Method
                  BLASTX
NCBI GI
                  g1362103
BLAST score
                  371
E value
                  2.0e-35
Match length
                  118
% identity
                  60
NCBI Description
                  ubiquitin conjugating enzyme - tomato
                  >gi_886679_emb_CAA58111_ (X82938) ubiquitin conjugating
                  enzyme [Lycopersicon esculentum]
Seq. No.
                  269703
Contig ID
                  21110_1.R1011
5'-most EST
                  LIB3067-002-Q1-K1-B1
Seq. No.
                  269704
Contig ID
                  21111 1.R1011
5'-most EST
                  uC-zmflm017211a12b1
                  BLASTX
Method
NCBI GI
                  g2414681
BLAST score
                  1577
E value
                  1.0e-176
Match length
                  432
% identity
                  68
NCBI Description (Z99174) cysteine proteinase precursor [Vicia narbonensis]
Seq. No.
                  269705
Contig ID
                  21111 2.R1011
5'-most EST
                  LIB30\overline{5}9-002-Q1-K2-G4
Method
                  BLASTX
NCBI GI
                  g4154279
BLAST score
                  418
E value
                  7.0e-41
Match length
                  105
% identity
NCBI Description
                  (AF082346) C13 endopeptidase NP1 precursor [Hordeum
                  vulgare]
```

37545



Method BLASTN
NCBI GI g1816587
BLAST score 194
E value 1.0e-105
Match length 290
% identity 92

NCBI Description Zea mays LON2 protease (LON2) mRNA, complete cds

Seq. No. 269707

Contig ID 21118_1.R1011

5'-most EST LIB3066-008-Q1-K1-G12

Seq. No. 269708

Contig ID 21126 1.R1011

5'-most EST LIB3150-021-Q1-N1-H4

Method BLASTN
NCBI GI g485376
BLAST score 98
E value 3.0e-48
Match length 150
% identity 92

NCBI Description Zea mays alpha-3-tubulin gene, complete cds

Seq. No. 269709

Contig ID 21129_1.R1011 5'-most EST uC-zmflmo17289h04b1

Seq. No. 269710

Contig ID 21138 1.R1011

5'-most EST LIB3150-022-Q1-N1-A9

Method BLASTX
NCBI GI g4309697
BLAST score 270
E value 2.0e-23
Match length 110

% identity 52

NCBI Description (AC006266) putative DNA-directed RNA polymerase subunit

[Arabidopsis thaliana]

Seq. No. 269711

Contig ID 21142 1.R1011

5'-most EST uC-zmflmo17187f01b1

Method BLASTX
NCBI GI g3763932
BLAST score 805
E value 5.0e-86
Match length 227
% identity 70

NCBI Description (AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No. 269712

Contig ID 21152_1.R1011 5'-most EST pmx700091579.h1

Seq. No. 269713

Contig ID 21171_1.R1011 5'-most EST xmt700259325.h1

37546



Method BLASTX
NCBI GI g2499606
BLAST score 1176
E value 1.0e-129
Match length 263
% identity 82

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 2 (MAP KINASE 2)

(ATMPK2) >gi_533281_dbj_BAA03536_ (D14714) ATMPK2

[Arabidopsis thaliana]

Seq. No. 269714

Contig ID 21171 2.R1011 5'-most EST gwl700618378.h1

Method BLASTX
NCBI GI g2499611
BLAST score 427
E value 4.0e-42
Match length 112
% identity 72

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7)

(ATMPK7) >gi_629548_pir__S40473 mitogen-activated protein

kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana

>gi_457406_dbj_BAA04870_ (D21843) MAP kinase [Arabidopsis

thaliana]

Seq. No. 269715

Contig ID 21173_1.R1011 5'-most EST fwa700097336.h1

Seq. No. 269716

Contig ID 21175_1.R1011 5'-most EST yyf700350828.h1

Seq. No. 269717

Contig ID 21176 1.R1011

5'-most EST uC-zmflmo17267e03b1

Method BLASTX
NCBI GI g2914700
BLAST score 1307
E value 1.0e-145
Match length 326
% identity 79

NCBI Description (AC003974) tRNA-processing protein SEN3-like [Arabidopsis

thaliana]

Seq. No. 269718

Contig ID 21187_1.R1011 5'-most EST pmx700084234.h1

Method BLASTX
NCBI GI g2462744
BLAST score 521
E value 3.0e-53
Match length 132
% identity 73

NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 269719



Contig ID 21188_1.R1011 5'-most EST LIB3152-045-P1-K1-A3

Seq. No. 269720

Contig ID 21188_2.R1011

5'-most EST uC-zmflmo17132c03a1

Seq. No. 269721

Contig ID 21195_1.R1011 5'-most EST xmt700265480.h1

Seq. No. 269722

Contig ID 21213_1.R1011

5'-most EST LIB3150-023-Q1-N1-B10

Method BLASTX
NCBI GI g3522937
BLAST score 489
E value 3.0e-49
Match length 146
% identity 56

NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

Seq. No. 269723

Contig ID 21215 1.R1011

5'-most EST uC-zmflmo17021a10b1

Seq. No. 269724

Contig ID 21215_2.R1011 5'-most EST zuv700352669.h1

Seq. No. 269725

Contig ID 21215_3.R1011 5'-most EST xjt700094379.h1

Seq. No. 269726

Contig ID 21216_1.R1011 5'-most EST wen700334022.h1

Method BLASTX
NCBI GI g133867
BLAST score 768
E value 9.0e-82
Match length 160
% identity 92

NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal

protein S11 - maize >gi_22470_emb_CAA39438_ (X55967)

ribosomal protein S11 [Zea mays]

Seq. No. 269727

Contig ID 21222 1.R1011

5'-most EST LIB3060-054-Q1-K1-B1

Seq. No. 269728

Contig ID 21226_1.R1011 5'-most EST uC-zmflb73069e01b1

Method BLASTX NCBI GI g4646217 BLAST score 1692



E value 0.0e+00
Match length 332
% identity 94

NCBI Description (AC007290) putative phosphoprotein phosphatase [Arabidopsis

thaliana]

Seq. No. 269729

Contig ID 21226_2.R1011

5'-most EST uC-zmflmo17156e05a1

Method BLASTX
NCBI GI g4646217
BLAST score 223
E value 3.0e-18
Match length 45
% identity 89

NCBI Description (AC007290) putative phosphoprotein phosphatase [Arabidopsis

thaliana]

Seq. No. 269730

Contig ID 21231 1.R1011

5'-most EST LIB3150-023-Q1-N1-D10

Method BLASTX
NCBI GI g1151244
BLAST score 968
E value 1.0e-105

Match length 305 % identity 60

NCBI Description (U43377) GTP-binding protein [Arabidopsis thaliana]

Seq. No. 269731

Contig ID 21231_2.R1011 5'-most EST mwy700439385.h1

Method BLASTX
NCBI GI g1151244
BLAST score 384
E value 6.0e-37
Match length 108
% identity 69

NCBI Description (U43377) GTP-binding protein [Arabidopsis thaliana]

Seq. No. 269732

Contig ID 21237 1.R1011

5'-most EST LIB3067-039-Q1-K1-H2

Seq. No. 269733

Contig ID 21244_1.R1011

5'-most EST LIB31 $\overline{5}$ 0-050-Q1-N1-C1

Method BLASTX
NCBI GI g2708532
BLAST score 941
E value 1.0e-102
Match length 308
% identity 58

NCBI Description (AF029351) putative RNA binding protein [Nicotiana tabacum]

Seq. No. 269734

Contig ID 21245_1.R1011



```
LIB3150-023-Q1-N1-E7
5'-most EST
                  269735
Seq. No.
Contig ID
                  21246 1.R1011
5'-most EST
                  LIB3180-055-P2-M1-G9
                  BLASTX
Method
NCBI GI
                  q4512591
                   426
BLAST score
                   2.0e-41
E value
Match length
                  291
% identity
                   34
NCBI Description
                 (AB023789) flavanone 3-hydroxyrase [Ipomoea batatas]
                  269736
Seq. No.
                  21257 2.R1011
Contig ID
5'-most EST
                  LIB148-016-Q1-E1-F7
Method
                  BLASTX
NCBI GI
                  g3540193
BLAST score
                   415
                   2.0e-40
E value
Match length
                   106
                   74
% identity
                  (AC004122) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   269737
Seq. No.
Contig ID
                   21262 1.R1011
5'-most EST
                  LIB3150-023-Q1-N1-H10
                   269738
Seq. No.
                   21262 2.R1011
Contig ID
5'-most EST
                   uC-zmflb73029c05b1
                   269739
Seq. No.
                   21269_1.R1011
Contig ID
                   LIB3151-012-Q1-K1-E9
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2828012
BLAST score
                   1202
E value
                   1.0e-144
Match length
                   281
% identity
NCBI Description (AF036891) starch synthase I precursor [Zea mays]
                   269740
Seq. No.
                   21291 1.R1011
Contig ID
5'-most EST
                   LIB3180-045-P2-M2-H2
Method
                   BLASTX
NCBI GI
                   g3540204
BLAST score
                   477
E value
                   1.0e-47
Match length
                   143
% identity
                   62
NCBI Description (AC004260) Hypothetical protein [Arabidopsis thaliana]
```

Seq. No. 269741

Contig ID 21293_1.R1011 5'-most EST uC-zmrob73078a12b1



Method BLASTX
NCBI GI g2213585
BLAST score 516
E value 4.0e-52
Match length 187
% identity 55

NCBI Description (AC000348) T7N9.5 [Arabidopsis thaliana]

Seq. No. 269742

Contig ID 21296_1.R1011 5'-most EST ymt700219507.h1

Method BLASTX
NCBI GI g3367591
BLAST score 390
E value 9.0e-38
Match length 135
% identity 53

NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

Seq. No. 269743

Contig ID 21317 1.R1011

5'-most EST LIB3150-026-Q1-N1-E2

Method BLASTX
NCBI GI g4510396
BLAST score 535
E value 6.0e-55
Match length 116
% identity 84

NCBI Description (AC006587) hypothetical protein [Arabidopsis thaliana]

Seq. No. 269744

Contig ID 21323 1.R1011

5'-most EST LIB3136-017-Q1-K1-H10

Method BLASTX
NCBI GI g4314378
BLAST score 280
E value 8.0e-25
Match length 95
% identity 61

NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 269745

Contig ID 21328_1.R1011

5'-most EST LIB3067-004-Q1-K1-H9

Method BLASTX
NCBI GI g2749943
BLAST score 261
E value 2.0e-22
Match length 121
% identity 44

NCBI Description (U71244) pathogenesis-related group 5 protein [Brassica

rapa]

Seq. No. 269746

Contig ID 21331_1.R1011

5'-most EST LIB3150-026-Q1-N1-F4



```
269747
Seq. No.
Contig ID
                   21334 1.R1011
5'-most EST
                   uC-zmflb73125g11b2
Method
                   BLASTX
NCBI GI
                   g2129753
BLAST score
                   509
E value
                   2.0e-51
Match length
                   144
% identity
                   71
NCBI Description
                   threonine synthase (EC 4.2.99.2) precursor - Arabidopsis
                   thaliana (fragment) >gi_1448917 (L41666) threonine synthase
                   [Arabidopsis thaliana]
                   269748
Seq. No.
Contig ID
                   21347 1.R1011
5'-most EST
                   LIB3150-026-Q1-N1-H10
                   269749
Seq. No.
Contig ID
                   21356 1.R1011
5'-most EST
                   LIB3150-027-Q1-N1-A1
                   269750
Seq. No.
Contig ID
                   21357 1.R1011
5'-most EST
                   tzu700206777.h1
Method
                   BLASTX
NCBI GI
                   q4510373
BLAST score
                   384
E value
                   1.0e-36
Match length
                   193
% identity
                   40
NCBI Description
                  (AC007017) putative harpin-induced protein [Arabidopsis
                   thaliana]
                   269751
Seq. No.
Contig ID
                   21357 3.R1011
5'-most EST
                   ntr700076640.h1
Seq. No.
                   269752
Contig ID
                   21357 4.R1011
5'-most EST
                  ntr700076623.h1
Seq. No.
                   269753
Contig ID
                   21358 1.R1011
5'-most EST
                  LIB3150-027-Q1-N1-A11
Method
                  BLASTX
NCBI GI
                  g118619
BLAST score
                   298
E value
                   4.0e-27
Match length
                   65
% identity
                   80
NCBI Description
```

SUCCINATE DEHYDROGENASE (UBIQUINONE) IRON-SULFUR PROTEIN

PRECURSOR (IP) >gi_66072_pir__RDBYIS succinate

dehydrogenase (ubiquinone) (EC 1.3.5.1) iron-sulfur protein precursor - yeast (Saccharomyces cerevisiae) >gi 172549 (J05487) succinate dehydrogenase iron-protein subunit (SDH) (EC 1.3.99.1) [Saccharomyces cerevisiae]

>gi_1360235_emb CAA97492_ (Z73146) ORF YLL041c

37552



[Saccharomyces cerevisiae]

```
269754
Seq. No.
                   21358 2.R1011
Contig ID
5'-most EST
                   ntr700073017.hl
                   BLASTX
Method
NCBI GI
                   g118619
BLAST score
                   211
E value
                   7.0e-17
                   49
Match length
% identity
                   76
                   SUCCINATE DEHYDROGENASE (UBIQUINONE) IRON-SULFUR PROTEIN
NCBI Description
                   PRECURSOR (IP) >gi_66072_pir__RDBYIS succinate dehydrogenase (ubiquinone) (EC 1.3.5.1) iron-sulfur protein
                   precursor - yeast (Saccharomyces cerevisiae) >gi_172549
                   (J05487) succinate dehydrogenase iron-protein subunit (SDH)
                   (EC 1.3.99.1) [Saccharomyces cerevisiae]
                   >gi 1360235 emb CAA97492 (Z73146) ORF YLL041c
                   [Saccharomyces cerevisiae]
                   269755
Seq. No.
                   21370 1.R1011
Contig ID
5'-most EST
                   LIB3159-007-Q1-K1-A6
Method
                   BLASTX
                   q3925763
NCBI GI
BLAST score
                   282
                   1.0e-24
E value
Match length
                   168
                   38
% identity
NCBI Description (AL034352) hypothetical protein [Schizosaccharomyces pombe]
                   269756
Seq. No.
Contig ID
                   21375 1.R1011
5'-most EST
                   uC-zmflb73126e12b1
Method
                   BLASTX
NCBI GI
                   g3415117
BLAST score
                   784
E value
                   1.0e-83
Match length
                   176
% identity
                   41
NCBI Description (AF081203) villin 3 [Arabidopsis thaliana]
                   269757
Seq. No.
                   21379 1.R1011
Contig ID
5'-most EST
                   uwc700154910.h1
Method
                   BLASTX
NCBI GI
                   g2982293
BLAST score
                   245
E value
                   3.0e-20
Match length
                   54
% identity
NCBI Description (AF051231) ISP42-like protein [Picea mariana]
```

37553

269758

21379 2.R1011

uC-zmflb73058e05b1

Seq. No.

Contig ID 5'-most EST

% identity



```
Seq. No.
                   269759
                  21394 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73283g09b2
Method
                  BLASTN
                  q3885879
NCBI GI
                  72
BLAST score
E value
                   3.0e-32
                  96
Match length
                  94
% identity
                  Oryza sativa protochlorophyllide reductase homolog mRNA,
NCBI Description
                  partial cds
                   269760
Seq. No.
                   21397 1.R1011
Contig ID
5'-most EST
                  LIB3150-027-Q1-N1-D8
Method
                  BLASTX
                  q3894193
NCBI GI
BLAST score
                  596
E value
                   2.0e-61
Match length
                   263
% identity
                   44
                  (AC005662) putative strictosidine synthase [Arabidopsis
NCBI Description
                   thaliana]
                   269761
Seq. No.
                   21399 1.R1011
Contig ID
5'-most EST
                  LIB3150-027-Q1-N1-E7
Method
                  BLASTX
                  g3021409
NCBI GI
BLAST score
                   372
                   3.0e - 35
E value
                  104
Match length
% identity
                   59
NCBI Description (Y12781) transducin (beta) like 1 protein [Homo sapiens]
                   269762
Seq. No.
Contig ID
                   21399 2.R1011
5'-most EST
                  LIB3150-027-Q1-N1-E1
Method
                   BLASTX
NCBI GI
                   g3021409
BLAST score
                   479
E value
                   2.0e-48
Match length
                  124
% identity
NCBI Description (Y12781) transducin (beta) like 1 protein [Homo sapiens]
Seq. No.
                   269763
Contig ID
                   21402 1.R1011
5'-most EST
                  LIB3118-010-Q1-K1-F7
Method
                   BLASTX
NCBI GI
                   q4510423
BLAST score
                   355
E value
                   3.0e - 33
Match length
                   111
```

NCBI Description (AC006929) unknown protein [Arabidopsis thaliana]



Seq. No. 269764

Contig ID 21413_1.R1011 5'-most EST kem700611111.h1

Method BLASTX
NCBI GI g1304599
BLAST score 159
E value 1.0e-10
Match length 54
% identity 48

NCBI Description (U41315) ZNF127-Xp [Homo sapiens]

Seq. No. 269765

Contig ID 21423_1.R1011 5'-most EST fwa700097383.h1

Method BLASTX
NCBI GI g2529342
BLAST score 926
E value 1.0e-100
Match length 178
% identity 95

NCBI Description (L76554) transketolase [Spinacia oleracea]

Seq. No. 269766

Contig ID 21425_1.R1011 5'-most EST uC-zmflb73156c08b1

Seq. No. 269767

Contig ID 21425_3.R1011

5'-most EST LIB3279-015-P1-K1-E2

Seq. No. 269768

Contig ID 21430_1.R1011 5'-most EST afb700381777.h1

Method BLASTX
NCBI GI g1717975
BLAST score 359
E value 1.0e-33
Match length 126
% identity 50

NCBI Description 14.5 KD TRANSLATIONAL INHIBITOR PROTEIN (P14.5) (UK114 ANTIGEN HOMOLOG) >gi_1177435_emb_CAA64670_ (X95384) 14.5

kDa translational inhibitor protein, p14.5 [Homo sapiens]

Seq. No. 269769

Contig ID 21438_1.R1011

5'-most EST LIB3066-010-Q1-K1-E5

Method BLASTX
NCBI GI g2244797
BLAST score 241
E value 9.0e-20
Match length 207
% identity 34

NCBI Description (297336) hypothetical protein [Arabidopsis thaliana]

Seq. No. 269770

Contig ID 21438 2.R1011

5'-most EST LIB3067-038-Q1-K1-E11

37555



Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 2.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 269771

Contig ID 21438_3.R1011

5'-most EST LIB3069-004-Q1-K1-D11

Seq. No. 269772

Contig ID 21439_1.R1011 5'-most EST gct701172714.h2

Seq. No. 269773

Contig ID 21439 2.R1011

5'-most EST LIB3150-028-Q1-N1-A3

Seq. No. 269774

Contig ID 21449_1.R1011 5'-most EST ntr700072924.h1

Seq. No. 269775

Contig ID 21453 1.R1011

5'-most EST uC-zmroteosinte053f01b2

Method BLASTX
NCBI GI g2500036
BLAST score 474
E value 1.0e-47
Match length 133

Match length 133 % identity 71

NCBI Description DIHYDROOROTASE PRECURSOR (DHOASE) >gi_2121273 (AF000146)

dihydroorotase [Arabidopsis thaliana]

>gi_3292818_emb_CAA19808_ (AL031018) dihydroorotase

[Arabidopsis thaliana]

Seq. No. 269776

Contig ID 21456 1.R1011

5'-most EST LIB3150-028-Q1-N1-C1

Method BLASTX
NCBI GI g4262229
BLAST score 470
E value 6.0e-47
Match length 148
% identity 66

NCBI Description (AC006200) unknown protein [Arabidopsis thaliana]

Seq. No. 269777

Contig ID 21460_1.R1011 5'-most EST fC-zmf1700349202j1

Method BLASTX
NCBI GI g4263695
BLAST score 202
E value 6.0e-15
Match length 450



```
% identity
                   (AC006223) putative myosin II heavy chain [Arabidopsis
NCBI Description
                   thaliana]
                   269778
Seq. No.
Contig ID
                   21470 1.R1011
5'-most EST
                  LIB3150-028-Q1-N1-E3
                   269779
Seq. No.
                   21486 1.R1011
Contig ID
5'-most EST
                  LIB3150-028-Q1-N1-F6
                  {\tt BLASTX}
Method
NCBI GI
                   g4586061
BLAST score
                   194
                   1.0e-14
E value
Match length
                   97
                   44
% identity
NCBI Description (AC007020) putative BOP1 protein [Arabidopsis thaliana]
                   269780
Seq. No.
Contig ID
                   21488 1.R1011
5'-most EST
                   LIB3069-020-Q1-K1-B1
                   269781
Seq. No.
Contig ID
                   21489 1.R1011
5'-most EST
                  LIB3150-049-Q1-N1-B4
Method
                   BLASTX
NCBI GI
                   q2257756
BLAST score
                   536
E value
                   1.0e-54
Match length
                   138
% identity
                   75
                  (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays]
NCBI Description
                   >gi_3650466 (AF026917) histone deacetylase HD2-p39 [Zea
                   mays]
Seq. No.
                   269782
                   21489 2.R1011
Contig ID
5'-most EST
                   uC-zmflb73196c12b1
Method
                   BLASTN
NCBI GI
                   g2257755
BLAST score
                   87
E value
                   6.0e-41
Match length
                   360
% identity
                   81
NCBI Description
                   Zea mays nucleolar histone deacetylase HD2-p39 mRNA,
                   complete cds
                   269783
Seq. No.
                   21489 5.R1011
Contig ID
5'-most EST
                   uC-zmflb73100c06a1
Method
                   BLASTN
```

NCBI GI g2257755

BLAST score 53 E value 6.0e-21 Match length 131 85 % identity



NCBI Description Zea mays nucleolar histone deacetylase HD2-p39 mRNA, complete cds

Seq. No. 269784

Contig ID 21492 1.R1011

5'-most EST uC-zmflmo17055g04b1

Method BLASTX
NCBI GI g4263791
BLAST score 1446
E value 1.0e-161
Match length 351
% identity 78

NCBI Description (AC006068) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 269785

Contig ID 21492 2.R1011

5'-most EST uC-zmflmo17403a09a1

Method BLASTX
NCBI GI 94263791
BLAST score 207
E value 2.0e-16
Match length 50
% identity 76

NCBI Description (AC006068) putative receptor protein kinase [Arabidopsis

thaliana]

Seq. No. 269786

Contig ID 21504 1.R1011

5'-most EST LIB31 $\overline{5}$ 0-029-Q1-N1-A1

Seq. No. 269787

Contig ID 21509_1.R1011 5'-most EST xyt700347280.h1

Method BLASTX
NCBI GI g1076758
BLAST score 779
E value 6.0e-83
Match length 216
% identity 75

NCBI Description heat-shock protein precursor - rye >gi_2130093_pir__\$65776

heat-shock protein, 82K, precursor - rye

>gi 556673 emb CAA82945 (Z30243) heat-shock protein

[Secale cereale]

Seq. No. 269788

Contig ID 21509_2.R1011 5'-most EST xmt700267778.h1

Method BLASTX
NCBI GI g1076758
BLAST score 155
E value 3.0e-10
Match length 66
% identity 56

NCBI Description heat-shock protein precursor - rye >gi_2130093_pir__\$65776

heat-shock protein, 82K, precursor - rye

>gi 556673_emb_CAA82945_ (Z30243) heat-shock protein



[Secale cereale]

Seq. No. 269789

Contig ID 21511_1.R1011

5'-most EST LIB3150-029-Q1-N1-A5

Method BLASTX
NCBI GI g4587599
BLAST score 243
E value 8.0e-21
Match length 60
% identity 65

NCBI Description (AC006951) hypothetical protein [Arabidopsis thaliana]

Seq. No. 269790

Contig ID 21516 1.R1011

5'-most EST LIB3150-029-Q1-N1-B11

Seq. No. 269791

Contig ID 21519_1.R1011

5'-most EST LIB3067-025-Q1-K1-A10

Seq. No. 269792

Contig ID 21566_1.R1011

5'-most EST LIB3150-058-Q1-N1-H7

Method BLASTX
NCBI GI g3953471
BLAST score 166
E value 3.0e-11
Match length 138
% identity 33

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No. 269793

Contig ID 21575_1.R1011

5'-most EST LIB3060-041-Q1-K1-D3

Seq. No. 269794

Contig ID 21580 1.R1011

5'-most EST LIB3059-003-Q1-K1-E5

Seq. No. 269795

Contig ID 21580 2.R1011

5'-most EST LIB3150-071-P1-N1-B6

Seq. No. 269796

Contig ID 21585 1.R1011

5'-most EST LIB3150-030-Q1-N1-C4

Seq. No. 269797

Contig ID 21586 1.R1011

5'-most EST LIB3137-038-Q1-K1-H10

Method BLASTX
NCBI GI g1173286
BLAST score 645
E value 2.0e-67
Match length 170

Match length 170 % identity 73



NCBI Description 40S RIBOSOMAL PROTEIN S9 >gi_112274_pir__S21497 ribosomal protein S9 - rat >gi_57143_emb_CAA47013_ (X66370) ribosomal protein S9 [Rattus norvegicus]

Seq. No. 269798

Contig ID 21592_1.R1011 5'-most EST nwy700444904.h1

Method BLASTX
NCBI GI g3912953
BLAST score 260
E value 7.0e-37
Match length 302
% identity 38

NCBI Description PUTATIVE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE DEAMINASE (ACC

DEAMINASE) >gi_3256439_dbj_BAA29122.1_ (AP000001) 328aa long hypothetical 1-aminocyclopropane-1-carboxylate

deaminase [Pyrococcus horikoshii]

Seq. No. 269799

Contig ID 21601_1.R1011 5'-most EST uC-zmflb73296a08b2

Method BLASTX
NCBI GI g2388580
BLAST score 977
E value 1.0e-106
Match length 290

% identity 63 NCBI Description (AC000098) Similar to Sequence 10 from patent 5477002

(gb 1253956). [Arabidopsis thaliana]

Seq. No. 269800

Contig ID 21602_1.R1011 5'-most EST xmt700264425.h1

Seq. No. 269801

Contig ID 21608_1.R1011 5'-most EST uC-zmrob73022b12a1 Method BLASTX

NCBI GI g2653285
BLAST score 231
E value 3.0e-19
Match length 57
% identity 84

NCBI Description (AJ003025) enoyl-ACP reductase [Oryza sativa]

Seq. No. 269802

Contig ID 21609 1.R1011

5'-most EST LIB3136-014-Q1-K2-G8

Method BLASTX
NCBI GI g2058282
BLAST score 584
E value 5.0e-60
Match length 162
% identity 68

NCBI Description (X97377) atranbpla [Arabidopsis thaliana]

Seq. No. 269803



Contig ID 21609 2.R1011 LIB3180-061-P2-M1-H11 5'-most EST BLASTX Method NCBI GI q1732511 459 BLAST score E value 4.0e-47121 Match length 72 % identity (U62742) Ran binding protein 1 homolog [Arabidopsis NCBI Description thaliana] 269804 Seq. No. 21609 5.R1011 Contig ID 5'-most EST ntr700073466.h1 BLASTX Method NCBI GI g1732511 BLAST score 178 9.0e-16 E value Match length 48 76 % identity NCBI Description (U62742) Ran binding protein 1 homolog [Arabidopsis thaliana] 269805 Seq. No. 21613 1.R1011 Contig ID LIB3150-030-Q1-N1-D3 5'-most EST 269806 Seq. No. 21615 1.R1011 Contig ID 5'-most EST LIB3136-001-P1-K1-C2 Seq. No. 269807 21616_1.R1011 Contig ID 5'-most EST LIB143-005-Q1-E1-F7 269808 Seq. No. 21624_1.R1011 Contig ID LIB3062-004-Q1-K1-F2 5'-most EST Method BLASTX g1169782 NCBI GI BLAST score 862 E value 1.0e-125 Match length 303

% identity

NCBI Description FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis

thaliana]

Seq. No. 269809 Contig ID

21642 1.R1011 5'-most EST uC-zmflm017209d06b1

Method BLASTX NCBI GI q4503527 BLAST score 379

E value 3.0e-36 Match length 177 % identity 42

NCBI Description UNKNOWN >gi 1778051 (U62583) Prt1 homolog [Homo sapiens]



```
269810
Seq. No.
                   21645 1.R1011
Contig ID
                   ntr700076642.h1
5'-most EST
                   269811
Seq. No.
                   21645 2.R1011
Contig ID
                   LIB3059-018-Q1-K1-G8
5'-most EST
                   269812
Seq. No.
Contig ID
                   21649 1.R1011
                   xsy70\overline{0}214537.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4467128
BLAST score
                   1188
                   1.0e-131
E value
Match length
                   367
% identity
                   64
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                   269813
Seq. No.
Contig ID
                   21649 2.R1011
                   LIB14\overline{3}-049-Q1-E1-D1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4467128
BLAST score
                   295
                   2.0e-26
E value
Match length
                   70
                   76
% identity
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
                   269814
Seq. No.
Contig ID
                   21676_1.R1011
5'-most EST
                   LIB3279-059-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   q70772
BLAST score
                   410
                   7.0e-40
E value
                   82
Match length
                   100
% identity
NCBI Description histone H4 - wheat >gi_70773_pir__HSPM4 histone H4 - garden
                   pea
                   269815
Seq. No.
Contig ID
                   21684 1.R1011
5'-most EST
                   LIB3150-031-Q1-N1-D2
Seq. No.
                   269816
Contig ID
                   21694 1.R1011
5'-most EST
                   uC-zmflmo17072f02b1
Method
                   BLASTX
NCBI GI
                   q1082798
BLAST score
                   1069
E value
                   1.0e-116
```

% identity 44
NCBI Description spliceosome-associated protein SAP 61 - human >gi_508723

501

Match length



(U08815) SAP 61 [Homo sapiens]

 Seq. No.
 269817

 Contig ID
 21694_2.R1011

 5'-most EST
 uC-zmflmo17341d07b1

 Method
 BLASTX

Method BLASTX
NCBI GI g1082801
BLAST score 160
E value 1.0e-10
Match length 98
% identity 35

NCBI Description splicing factor SF3a60 - human >gi_551450_emb_CAA57388_

(X81789) splicing factor SF3a60 [Homo sapiens]

Seq. No. 269818

Contig ID 21700_1.R1011

5'-most EST LIB3136-034-Q1-K1-H12

Method BLASTX
NCBI GI g1076626
BLAST score 450
E value 2.0e-44
Match length 88
% identity 94

NCBI Description glycine rich protein - common tobacco

>gi_790473_emb_CAA58702_ (X83731) soluble, glycine rich

protein [Nicotiana tabacum]

Seq. No. 269819

Contig ID 21700 4.R1011 5'-most EST xjt700096788.h1

Seq. No. 269820

Contig ID 21708_1.R1011

5'-most EST LIB3069-006-Q1-K1-B3

Method BLASTX
NCBI GI g1707642
BLAST score 1046
E value 1.0e-114
Match length 282
% identity 74

NCBI Description (Y07748) TMK [Oryza sativa]

Seq. No. 269821

Contig ID 21720_1.R1011 5'-most EST mwy700439061.h1

Seq. No. 269822

Contig ID 21720_2.R1011

5'-most EST LIB143-063-Q1-E1-B5

Seq. No. 269823

Contig ID 21724_1.R1011 5'-most EST uC-zmflb73052d07b1

Method BLASTX
NCBI GI g4538903
BLAST score 423
E value 1.0e-43



Match length 362 % identity 35

NCBI Description (AL049482) putative protein [Arabidopsis thaliana]

Seq. No. 269824

Contig ID 21727_1.R1011

5'-most EST LIB3159-003-Q1-K1-C4

Seq. No. 269825

Contig ID 21728 1.R1011

5'-most EST LIB189-018-Q1-E1-B3

Method BLASTX
NCBI GI g3912917
BLAST score 414
E value 1.0e-40
Match length 108
% identity 74

NCBI Description (AF001308) putative NAK-like ser/thr protein kinase

[Arabidopsis thaliana]

Seq. No. 269826

Contig ID 21736_1.R1011 5'-most EST fwa700098931.h1

Method BLASTX
NCBI GI g2160182
BLAST score 551
E value 3.0e-56
Match length 163
% identity 69

NCBI Description (AC000132) ESTs gb_ATTS1236,gb_T43334,gb_N97019,gb_AA395203

come from this gene. [Arabidopsis thaliana]

Seq. No. 269827

Contig ID 21737_1.R1011 5'-most EST ntr700076647.h1

Method BLASTX
NCBI GI g3033391
BLAST score 404
E value 3.0e-39
Match length 172
% identity 48

NCBI Description (AC004238) putative amino acid transporter [Arabidopsis

thaliana]

Seq. No. 269828

Contig ID 21738_1.R1011

5'-most EST LIB3150-073-P1-N1-A4

Seq. No. 269829

Contig ID 21738 2.R1011

5'-most EST LIB3158-008-Q1-K1-D1

Seq. No. 269830

Contig ID 21740_1.R1011 5'-most EST uC-zmrob73077h09b1

Method BLASTX NCBI GI g2723471



BLAST score 171 E value 4.0e-13 Match length 111 % identity 40

NCBI Description (D87819) sucrose transporter [Oryza sativa]

Seq. No. 269831

Contig ID 21749_1.R1011 5'-most EST rv1700457127.h1

Seq. No. 269832

Contig ID 21755_1.R1011

5'-most EST LIB30 $\overline{6}$ 7-019-Q1-K1-D5

Method BLASTX
NCBI GI g136632
BLAST score 2758
E value 0.0e+00
Match length 626
% identity 84

NCBI Description UBIQUITIN-ACTIVATING ENZYME E1 1 >gi 100841 pir A38373

ubiquitin--protein ligase (EC 6.3.2.19) E1 - wheat

>gi_285451_pir__A42873 ubiquitin-activating enzyme E1, UBA1
- Wheat >gi_170780 (M55604) ubiquitin-activating enzyme E1

[Triticum aestivum]

Seq. No. 269833

Contig ID 21755_2.R1011 5'-most EST cyk700050354.f1

Method BLASTX
NCBI GI g401237
BLAST score 866
E value 2.0e-93
Match length 189
% identity 87

NCBI Description UBIQUITIN-ACTIVATING ENZYME E1 2 >gi 170684 (M90663)

ubiquitin activating enyme [Triticum aestivum]

Seq. No. 269834

Contig ID 21755 4.R1011 5'-most EST ymt700219757.h1

Method BLASTX
NCBI GI g136632
BLAST score 209
E value 9.0e-17
Match length 63
% identity 68

NCBI Description UBIQUITIN-ACTIVATING ENZYME E1 1 >gi 100841 pir A38373

ubiquitin--protein ligase (EC 6.3.2.19) E1 - wheat

>gi_285451_pir__A42873 ubiquitin-activating enzyme E1, UBA1
- Wheat >gi_170780 (M55604) ubiquitin-activating enzyme E1

[Triticum aestivum]

Seq. No. 269835

Contig ID 21766_1.R1011

5'-most EST uC-zmflb73295a10b2

Method BLASTX NCBI GI g2795803



BLAST score 184 2.0e-13 E value Match length 91 19 % identity

(AC003674) putative beta-1,3-endoglucanase [Arabidopsis NCBI Description

thaliana] >gi 3355491 (AC004218) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

269836 Seq. No.

21769 1.R1011 Contig ID 5'-most EST xsy700213785.h1

269837 Seq. No.

21774 1.R1011 Contig ID cat700019657.rl 5'-most EST

Method BLASTX q4263711 NCBI GI BLAST score 371 2.0e-35 E value 167 Match length 48 % identity

(AC006223) putative CCR4-associated transcription factor NCBI Description

[Arabidopsis thaliana]

269838 Seq. No.

21777 1.R1011 Contig ID $nbm70\overline{0}471562.h1$ 5'-most EST

Method BLASTX g2982942 NCBI GI 846 BLAST score 8.0e-91 E value 287 Match length 58 % identity

NCBI Description (AE000679) GMP synthase [Aquifex aeolicus]

269839 Seq. No.

21780_1.R1011 Contig ID 5'-most EST hvj700622619.h1

Method BLASTX NCBI GI q4503729 293 BLAST score 5.0e-26 E value Match length 135 50 % identity

FK506-binding protein 4 (59kD) NCBI Description

>gi_399866_sp_Q02790_FKB4_HUMAN P59 PROTEIN (HSP BINDING IMMUNOPHILIN) (HBI) (POSSIBLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (ROTAMASE) (FKBP52 PROTEIN) (52 KD

FK506 BINDING PROTEIN) (P52) (FKBP59)
>gi 422824 pir A46372 immunophilin FKBP52 - human
>gi 186390 (M88279) 'FKBP52; 52 kD FK506 binding protein'

[Homo sapiens]

269840 Seq. No.

21783 1.R1011 Contig ID

LIB3062-042-Q1-K1-A1 5'-most EST

Method BLASTX



NCBI GI g1174583 BLAST score 427 E value 2.0e-41 Match length 264 % identity 35

NCBI Description TRANSALDOLASE >gi_1074653_pir__D64167 hypothetical protein

HI1125 - Haemophilus influenzae (strain Rd KW20)

>gi 1574680 (U32792) transaldolase B (talB) [Haemophilus

influenzae Rd]

Seq. No. 269841

Contig ID 21783_3.R1011

5'-most EST uC-zmromo17030b05a1

Seq. No. 269842

Contig ID 21786_1.R1011

5'-most EST LIB189-018-Q1-E1-B5

Method BLASTX
NCBI GI g3319774
BLAST score 201

E value 2.0e-15
Match length 46
% identity 78

NCBI Description (Y16228) TOM7 protein [Solanum tuberosum]

Seq. No. 269843

Contig ID 21802 1.R1011

5'-most EST LIB3059-011-Q1-K1-A12

Seq. No. 269844

Contig ID 21809_1.R1011 5'-most EST xyt700344936.h1

Method BLASTX
NCBI GI g4455293
BLAST score 256
E value 6.0e-22
Match length 84

% identity 67

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 269845

Contig ID 21819_1.R1011 5'-most EST dyk700103125.h1

Seq. No. 269846

Contig ID 21830_1.R1011

5'-most EST uC-zmflmo17288f09b1

Method BLASTX
NCBI GI g1063684
BLAST score 317
E value 6.0e-29
Match length 187
% identity 38

NCBI Description (U39072) AtGRP2b [Arabidopsis thaliana]

Seq. No. 269847

Contig ID 21831 1.R1011



```
uC-zmrob73055d05b1
5'-most EST
                  BLASTX
Method
                  g2827709
NCBI GI
                  1253
BLAST score
                   1.0e-138
E value
                  304
Match length
                  80
% identity
                  (ALO21684) predicted protein [Arabidopsis thaliana]
NCBI Description
                  269848
Seq. No.
                   21842 1.R1011
Contig ID
                  yyf700350220.h1
5'-most EST
                   269849
Seq. No.
                   21848 1.R1011
Contig ID
                   nbm700468775.h1
5'-most EST
                   BLASTX
Method
                   g1076389
NCBI GI
                   648
BLAST score
                   8.0e-68
E value
                   149
Match length
                   84
% identity
                   protein phosphatase 2A pDF1 - Arabidopsis thaliana
NCBI Description
                   >gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65
                   kDa regulatory subunit [Arabidopsis thaliana]
                   269850
Seq. No.
                   21853 1.R1011
Contig ID
                   xyt700346680.hl
5'-most EST
                   BLASTX
Method
                   q2827084
NCBI GI
                   1198
BLAST score
                   1.0e-132
E value
                   323
Match length
                   78
% identity
NCBI Description (AF020273) malate dehydrogenase precursor [Medicago sativa]
Seq. No.
                   269851
                   21853 2.R1011
Contig ID
                   pwr700448836.hl
5'-most EST
                   269852
Seq. No.
                   21853 3.R1011
Contig ID
5'-most EST
                   LIB3180-039-P2-M2-F10
                   269853
Seq. No.
Contig ID
                   21857 1.R1011
                   LIB3150-033-Q1-N1-F7
5'-most EST
                   269854
Seq. No.
                   21877 1.R1011
Contiq ID
```

5'-most EST pmx700086042.h1

269855 Seq. No.

21878 1.R1011 Contig ID uC-zmflb73238f11b2 5'-most EST

Method BLASTX



```
g2213594
NCBI GI
                  358
BLAST score
                  1.0e-33
E value
                  234
Match length
                  41
% identity
                  (AC000348) T7N9.14 [Arabidopsis thaliana]
NCBI Description
                  269856
Seq. No.
                  21884 1.R1011
Contig ID
                  xjt700092530.h1
5'-most EST
                  BLASTX
Method
                  g4235430
NCBI GI
                   926
BLAST score
                   1.0e-100
E value
                   330
Match length
                   58
% identity
                  (AF098458) latex-abundant protein [Hevea brasiliensis]
NCBI Description
                   269857
Seq. No.
                   21884 2.R1011
Contig ID
                   qmh700029716.f1
5'-most EST
                   BLASTX
Method
                   g3152600
NCBI GI
                   197
BLAST score
                   3.0e-15
E value
                   64
Match length
                   61
% identity
                   (AC002986) Contains similarity to S. cerevisiae
NCBI Description
                   hypothetical protein YOR197w, gb Z75105. ESTs gb H37409,
                   gb_AA395290, and gb_T43907 come from this gene.
                   [Arabidopsis thaliana]
                   269858
Seq. No.
                   21887 1.R1011
Contig ID
                   LIB3060-014-Q1-K1-C1
 5'-most EST
                   269859
Seq. No.
                   21888_1.R1011
 Contig ID
                   xsy700212768.hl
 5'-most EST
                   269860
 Seq. No.
                   21892 1.R1011
 Contig ID
                   LIB3180-023-P2-M1-E6
 5'-most EST
                   BLASTX
 Method
                   g1706330
 NCBI GI
                   150
 BLAST score
                   1.0e-09
 E value
                   35
 Match length
                   80
 % identity
 NCBI Description PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC)
                   >gi_1362116_pir__S57821 pyruvate decarboxylase (EC 4.1.1.1)
                    2 - common tobacco >gi_551263_emb_CAA57448_ (X81855)
                    pyruvate decarboxylase [Nicotiana tabacum]
                    269861
 Seq. No.
```

37569

21898 1.R1011

uC-zmflmo17011b08b1

Contig ID

5'-most EST



Method BLASTX
NCBI GI g119958
BLAST score 785
E value 1.0e-83
Match length 152
% identity 100

NCBI Description FERREDOXIN III PRECURSOR (FD III) >gi_168473 (M73831) ferredoxin [Zea mays] >gi 1864001 dbj_BAA19251_ (AB001387)

Fd III [Zea mays] >gi 444686 prf 1907324C

ferredoxin: ISOTYPE=III [Zea mays]

Seq. No. 269862

Contig ID 21898_2.R1011

5'-most EST LIB3059-008-Q1-K1-G10

Method BLASTN
NCBI GI g1864000
BLAST score 176
E value 2.0e-94
Match length 336
% identity 97

NCBI Description Maize DNA for Fd III, complete cds

Seq. No. 269863

Contig ID 21898_3.R1011

5'-most EST LIB3061-013-Q1-K1-E3

Method BLASTN
NCBI GI g1864000
BLAST score 275
E value 1.0e-153

E value 1.0e-Match length 310 % identity 97

NCBI Description Maize DNA for Fd III, complete cds

Seq. No. 269864

Contig ID 21899_1.R1011

5'-most EST uC-zmroteosinte026h02b1

Method BLASTX
NCBI GI g3882149
BLAST score 480
E value 8.0e-48
Match length 204
% identity 44

NCBI Description (AB018257) KIAA0714 protein [Homo sapiens]

Seq. No. 269865

Contig ID 21913_1.R1011

5'-most EST uC-zmroteosinte047f05b1

Seq. No. 269866

Contig ID 21914_1.R1011

5'-most EST LIB3150-034-Q1-N1-D9

Seq. No. 269867

Contig ID 21916_1.R1011 5'-most EST dyk700106185.h1

Method BLASTX NCBI GI g4467147



BLAST score 439 E value 7.0e-43 Match length 429 % identity 38

NCBI Description (AL035540) putative protein [Arabidopsis thaliana]

Seq. No. 269868

Contig ID 21918_1.R1011

5'-most EST LIB3067-051-Q1-K1-B8

Seq. No. 269869

Contig ID 21918_2.R1011

5'-most EST LIB3279-057-P1-K1-F2

Seq. No. 269870

Contig ID 21920_1.R1011

5'-most EST uC-zmroteosinte018h01b1

Method BLASTX
NCBI GI g3043712
BLAST score 214
E value 8.0e-17
Match length 239
% identity 26

NCBI Description (AB011166) KIAA0594 protein [Homo sapiens]

Seq. No. 269871

Contig ID 21926_1.R1011

5'-most EST LIB3150-034-Q1-N1-F11

Method BLASTX
NCBI GI g107350
BLAST score 208
E value 4.0e-16
Match length 208
% identity 28

NCBI Description Pm5 protein - human >gi_1335273_emb_CAA40655_ (X57398) pm5

protein [Homo sapiens]

Seq. No. 269872

Contig ID 21927_1.R1011 5'-most EST rvt700549746.h1

Method BLASTX
NCBI GI g3880215
BLAST score 161
E value 1.0e-10
Match length 164
% identity 30

NCBI Description (Z82053) cDNA EST yk302b12.3 comes from this gene

[Caenorhabditis elegans]

Seq. No. 269873

Contig ID 21927_2.R1011

5'-most EST LIB3158-008-Q1-K1-G3

Seq. No. 269874

Contig ID 21929 1.R1011

5'-most EST uC-zmflmo17066e12b1



269875

```
Seq. No.
                   21932 1.R1011
Contig ID
                  LIB31\overline{5}0-034-Q1-N1-F6
5'-most EST
                   BLASTX
Method
                   q4454452
NCBI GI
                   254
BLAST score
                   8.0e-22
E value
                   72
Match length
                   62
% identity
                   (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
                   269876
Seq. No.
                   21933 1.R1011
Contig ID
                   uC-zmflmo17181h08b1
5'-most EST
                   269877
Seq. No.
                   21934 1.R1011
Contig ID
                   LIB189-030-Q1-E1-G11
5'-most EST
                   269878
Seq. No.
                   21934 2.R1011
Contig ID
                   LIB143-022-Q1-E1-B2
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2088650
                   340
BLAST score
                   2.0e-31
E value
                   207
Match length
                   52
% identity
                   (AF002109) peroxisomal ATP/ADP carrier protein isolog
NCBI Description
                   [Arabidopsis thaliana]
                   269879
Seq. No.
                   21934 4.R1011
Contiq ID
                   LIB3136-001-P1-K1-G11
5'-most EST
                   BLASTX
Method
                   g2088650
NCBI GI
                   213
BLAST score
                   7.0e-17
E value
                   82
Match length
                   52
 % identity
                   (AF002109) peroxisomal ATP/ADP carrier protein isolog
NCBI Description
                    [Arabidopsis thaliana]
                    269880
 Seq. No.
                    21947 1.R1011
 Contig ID
                    LIB3060-052-Q1-K1-D10
 5'-most EST
                    BLASTX
 Method
                    g2760832
 NCBI GI
                    455
 BLAST score
                    7.0e-45
 E value
                    238
 Match length
                    45
 % identity
                    (AC003105) similar to barley ids-4 gene product
 NCBI Description
                    [Arabidopsis thaliana]
                    269881
 Seq. No.
                    21959_1.R1011
 Contig ID
```



uC-zmflmo17341b03b1 5'-most EST

BLASTX Method q3915503 NCBI GI 183 BLAST score E value 6.0e-13 111 Match length 36 % identity

HYPOTHETICAL OXIDOREDUCTASE IN CHEV-MOBA INTERGENIC REGION NCBI Description

 $\label{eq:capprox} $$ \geq_2632227_emb_CAA10869_ (AJ222587) $$ YkuF protein [Bacillus subtilis] $$ \geq_2633777_emb_CAB13279_ (Z99111) $$ similar to$

glucose 1-dehydrogenase [Bacillus subtilis]

269882 Seq. No.

21959 2.R1011 Contig ID

uC-zmflmo17103d03b1 5'-most EST

Method BLASTX NCBI GI q3915503 378 BLAST score 7.0e-36 E value 236 Match length % identity 38

HYPOTHETICAL OXIDOREDUCTASE IN CHEV-MOBA INTERGENIC REGION NCBI Description

>gi_2632227_emb_CAA10869_ (AJ222587) YkuF protein [Bacillus
subtilis] >gi_2633777_emb_CAB13279_ (Z99111) similar to

glucose 1-dehydrogenase [Bacillus subtilis]

Seq. No. 269883

21960 1.R1011 Contig ID

 $uC-zm\overline{f}lmo17242b02b1$ 5'-most EST

BLASTX Method NCBI GI g4337025 BLAST score 192 2.0e-14 E value 78 Match length

47 % identity

(AF123253) AIM1 protein [Arabidopsis thaliana] NCBI Description

269884 Seq. No.

21960 2.R1011 Contig ID

LIB143-012-Q1-E1-H3 5'-most EST

BLASTX Method NCBI GI g4337025 BLAST score 342 5.0e-32 E value 101 Match length % identity

(AF123253) AIM1 protein [Arabidopsis thaliana] NCBI Description

269885 Seq. No.

21964 1.R1011 Contig ID 5'-most EST wty700169581.hl

269886 Seq. No.

21978 1.R1011 Contig ID nwy700445414.h1 5'-most EST

BLASTX Method NCBI GI g3367521



BLAST score 642 E value 5.0e-67 Match length 242 % identity 50

NCBI Description (AC004392) Similar to gb_U08285 membrane-associated salt-inducible protein from Nicotiana tabacum. ESTs

qb T44131 and qb T04378 come from this gene. [Arabidopsis

thaliana]

Seq. No. 269887

Contig ID 21981_1.R1011

5'-most EST LIB3137-045-Q1-K1-D6

Seq. No. 269888

Contig ID 21982_1.R1011

5'-most EST uC-zmflmo17297f11b1

Seq. No. 269889

Contig ID 21983 1.R1011

5'-most EST LIB3150-035-Q1-N1-D12

Method BLASTX
NCBI GI g4220523
BLAST score 515
E value 4.0e-52
Match length 237

% identity 47

NCBI Description (AL035356) putative alliin lyase [Arabidopsis thaliana]

Seq. No. 269890

Contig ID 21988_1.R1011

5'-most EST LIB3066-005-Q1-K1-G5

Method BLASTX
NCBI GI g4510346
BLAST score 1008
E value 1.0e-109
Match length 267
% identity 74

NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No. 269891

Contig ID 21988_2.R1011

5'-most EST LIB3158-010-Q1-K1-A2

Method BLASTX
NCBI GI g4510346
BLAST score 390
E value 2.0e-37
Match length 114
% identity 67

NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No. 269892

Contig ID 21990_1.R1011 5'-most EST xmt700266852.h1

Seq. No. 269893

Contig ID 22003 1.R1011

5'-most EST LIB3150-035-Q1-N1-F4



BLASTX Method g3885340 NCBI GI 903 BLAST score 2.0e-97 E value Match length 281 62 % identity

(AC005623) unknown protein [Arabidopsis thaliana] NCBI Description

269894 Seq. No.

22003 2.R1011 Contig ID nbm700469953.h1 5'-most EST

BLASTX Method g3885340 NCBI GI 247 BLAST score 3.0e-21E value Match length 106 54 % identity

(AC005623) unknown protein [Arabidopsis thaliana] NCBI Description

269895 Seq. No.

22004 1.R1011 Contig ID

LIB3150-035-Q1-N1-F5 5'-most EST

269896 Seq. No.

22012 1.R1011 Contig ID

LIB3150-035-Q1-N1-G4 5'-most EST

BLASTX Method g4454032 NCBI GI 750 BLAST score 2.0e-79 E value 253 Match length

57 % identity

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

269897 Seq. No.

22016 1.R1011 Contig ID 5'-most EST nbm700466755.hl

Method BLASTX a2494312 NCBI GI 437 BLAST score 2.0e-42E value 428 Match length 29 % identity

TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B NCBI Description

GDP-GTP EXCHANGE FACTOR) >gi_1537015 (U38253) initiation

factor eIF-2B gamma subunit [Rattus norvegicus]

Seq. No. 269898

22027_1.R1011 Contig ID uC-zmrob73012e11b1 5'-most EST

269899 Seq. No.

Contig ID 22028 1.R1011

 $uC-zm\overline{f}lMo17064b11b1$ 5'-most EST

BLASTX Method g3953471 NCBI GI BLAST score 882



E value 7.0e-95 Match length 305 57 % identity

(AC002328) F2202.16 [Arabidopsis thaliana] NCBI Description

Seq. No.

269900

Contig ID 5'-most EST

22036 1.R1011 LIB3150-036-Q1-N1-A9

Seq. No.

269901

Contig ID 5'-most EST 22053 1.R1011 uC-zmflb73272g05b1

Method NCBI GI

BLASTX g2270994

BLAST score E value

325 9.0e-30

Match length % identity

173 39

NCBI Description

(AF004809) Ca+2-binding EF hand protein [Glycine max]

Seq. No.

269902

Contig ID

22053 2.R1011

5'-most EST

LIB3150-036-Q1-N1-C6

Method NCBI GI BLASTN g3821780

BLAST score

36

E value Match length % identity

1.0e-10 36 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No.

269903

Contig ID

22053 3.R1011

uC-zmflmo17376f11a1 5'-most EST

Seq. No.

269904

Contig ID

22053 5.R1011

5'-most EST uC-zmflmo17259g10b1

Seq. No.

269905

Contig ID 5'-most EST 22053 6.R1011 xsy700214642.hl

Seq. No.

269906

Contig ID

22056 1.R1011

5'-most EST

LIB3150-036-Q1-N1-D10

Seq. No.

269907

Contig ID

22061 2.R1011

5'-most EST

LIB3150-056-Q1-N1-A2

Seq. No.

269908

Contig ID 5'-most EST

22064 1.R1011 bdu700382684.h1

Seq. No.

269909

Contig ID

22068_1.R1011



LIB3060-051-Q1-K1-G8 5'-most EST 269910 Seq. No. 22069 1.R1011 Contig ID LIB3067-028-Q1-K1-F7 5'-most EST 269911 Seq. No. 22076 1.R1011 Contig ID ypc700805384.h1 5'-most EST BLASTX Method g4514655 NCBI GI 1203 BLAST score 1.0e-132 E value Match length 326 68 % identity (AB024058) IDS3 [Hordeum vulgare] NCBI Description 269912 Seq. No. 22105 1.R1011 Contig ID xyt700343957.h1 5'-most EST 269913 Seq. No. 22128 1.R1011 Contig ID LIB3150-037-Q1-N1-F12 5'-most EST BLASTN Method g22176 NCBI GI 55 BLAST score 4.0e-22 E value 83 Match length 46 % identity NCBI Description Z.mays P gene 269914 Seq. No. 22167_1.R1011 Contig ID $uC-zm\overline{f}lmo17001b01b1$ 5'-most EST BLASTX Method g140496 NCBI GI 154 BLAST score 9.0e-10 E value 92 Match length 37 % identity NCBI Description HYPOTHETICAL 42.5 KD PROTEIN IN TSM1-ARE1 INTERGENIC REGION >gi_83226_pir__S19457 probable membrane protein YCR044c yeast (Saccharomyces cerevisiae) >gi_1907186_emb_CAA42292_ (X59720) YCR044c, len:357 [Saccharomyces cerevisiae] 269915 Seq. No. Contig ID 22167 2.R1011

5'-most EST rv1700456610.h1

269916 Seq. No.

22168 1.R1011 Contig ID

LIB3150-038-Q1-N1-C7 5'-most EST

BLASTX Method NCBI GI g4510352 BLAST score 155 E value 3.0e-10



Match length 80 36 % identity (AC006921) putative salt-inducible protein [Arabidopsis NCBI Description thaliana] 269917 Seq. No. 22177 1.R1011 Contig ID tzu700206174.h1 5'-most EST BLASTX Method g3075398 NCBI GI 311 BLAST score 5.0e-28 E value 205 Match length 37 % identity (AC004484) unknown protein [Arabidopsis thaliana] NCBI Description 269918 Seq. No. 22178 1.R1011 Contig ID uC-zmflb73164c03b2 5'-most EST 269919 Seq. No. Contig ID 22189 1.R1011 wyr700236446.hl 5'-most EST BLASTX Method q3122386 NCBI GI 1917 BLAST score 0.0e+00E value Match length 407 85 % identity NCBI Description WD-40 REPEAT PROTEIN MSI1 >gi 2394227 (AF016845) WD-40 repeat protein [Lycopersicon esculentum] 269920 Seq. No. 22189_3.R1011 Contig ID wty700168113.hl 5'-most EST BLASTX Method NCBI GI g3122386 BLAST score 193 6.0e-15 E value 35 Match length 97 % identity NCBI Description WD-40 REPEAT PROTEIN MSI1 >gi_2394227 (AF016845) WD-40 repeat protein [Lycopersicon esculentum] 269921 Seq. No. 22190 1.R1011 Contig ID 5'-most EST LIB3150-044-Q1-N1-H6

Method BLASTX NCBI GI q417820 BLAST score 906 6.0e-98 E value Match length 208 % identity 80

NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_167536 (M59858)

stearoyl-acyl-carrier protein desaturase [Cucumis sativus]



Seq. No. 269922 22198 1.R1011 Contig ID xmt700262872.h1 5'-most EST BLASTX Method q2135893 NCBI GI 264 BLAST score 5.0e-23E value Match length 100 51 % identity peptidylprolyl isomerase (EC 5.2.1.8) A - human NCBI Description >qi 4406227 gb AAD19906_ (AF104012) peptidyl-prolyl cis-trans isomerase E [Homo sapiens] 269923 Seq. No. 22201 1.R1011 Contig ID LIB3136-025-Q1-K1-B1 5'-most EST Method BLASTX q2244935 NCBI GI BLAST score 175 2.0e-12 E value Match length 82 51 % identity (Z97339) hypothetical protein [Arabidopsis thaliana] NCBI Description 269924 Seq. No. 22207 1.R1011 Contig ID LIB84-021-Q1-E1-G12 5'-most EST Method BLASTN NCBI GI q2062705 39 BLAST score 3.0e-12 E value 39 Match length 100 % identity NCBI Description Human butyrophilin (BTF5) mRNA, complete cds 269925 Seq. No. 22207 2.R1011 Contig ID 5'-most EST pmx700091614.h1 269926 Seq. No. 22207 4.R1011 Contig ID wty700166366.h1 5'-most EST BLASTX Method g1181615 NCBI GI 527 BLAST score 1.0e-53 E value 152 Match length % identity NCBI Description (D83078) nitrilase [Nicotiana tabacum]

269927 Seq. No.

22207 8.R1011 Contig ID ypc700804707.h1 5'-most EST

269928 Seq. No.

22214 1.R1011 Contig ID uC-zmflmo17118h10b1 5'-most EST



```
BLASTX
Method
                  g3309086
NCBI GI
                  932
BLAST score
                  1.0e-101
E value
Match length
                  221
                  81
% identity
                  (AF076253) calcineurin B-like protein 3 [Arabidopsis
NCBI Description
                  thaliana]
                  269929
Seq. No.
                   22214 4.R1011
Contig ID
                  kem700611145.h1
5'-most EST
                   269930
Seq. No.
                   22218 1.R1011
Contig ID
```

E value 2.0eMatch length 246
% identity 58

NCBI Description (AC006127) SN24_HUMAN; nuclear protein GRB1; homeotic gene

regulator; SNF2-BETA [Homo sapiens]

Seq. No. 269931

Contig ID 22222_1.R1011 5'-most EST gct701178059.h1

Seq. No. 269932

Contig ID 22226_1.R1011 5'-most EST uC-zmflb73267g08b2

Method BLASTX
NCBI GI g3202026
BLAST score 905
E value 9.0e-98

Match length 199 % identity 83

NCBI Description (AF069316) stromal L-ascorbate peroxidase precursor

[Mesembryanthemum crystallinum]

Seq. No. 269933

Contig ID 22237_1.R1011 5'-most EST cyk700050905.f1

Method BLASTX
NCBI GI g1817526
BLAST score 227
E value 2.0e-18
Match length 113
% identity 15

NCBI Description (D63884) intermediate chain 1 [Anthocidaris crassispina]

Seq. No. 269934

Contig ID 22248 1.R1011

5'-most EST LIB3067-059-Q1-K1-F6

Method BLASTX NCBI GI g2459445



BLAST score 405 E value 8.0e-39 Match length 227 % identity 42

NCBI Description (AC002332) putative ribonucleoprotein [Arabidopsis

thaliana]

Seq. No. 269935

Contig ID 22248 2.R1011

5'-most EST uC-zmflmo17300a09a1

Seq. No. 269936

Contig ID 22259_1.R1011

5'-most EST LIB3137-040-Q1-K1-B11

Seq. No. 269937

Contig ID 22273 1.R1011

5'-most EST LIB3069-012-Q1-K1-F9

Method BLASTX
NCBI GI g2853076
BLAST score 269
E value 6.0e-23

Match length 106 % identity 56

NCBI Description (AL021768) putative protein [Arabidopsis thaliana]

Seq. No. 269938

Contig ID 22276_1.R1011

5'-most EST uC-zmflmo17292b03b1

Method BLASTX
NCBI GI 94504787
BLAST score 303
E value 2.0e-27
Match length 82
% identity 62

NCBI Description integral transmembrane protein 1

>gi_1174469_sp_P46977_STT3_HUMAN OLIGOSACCHARYL TRANSFERASE STT3_SUBUNIT_HOMOLOG_(B5) (INTEGRAL MEMBRANE PROTEIN_1)

>gi 624704 (L38961) putative transmembrane protein

precursor [Homo sapiens] >gi_1588286_prf__2208301B integral

membrane protein [Homo sapiens]

Seq. No. 269939

Contig ID 22276_2.R1011

5'-most EST LIB189-017-Q1-E1-A10

Method BLASTX
NCBI GI 94504787
BLAST score 307
E value 5.0e-28
Match length 83
% identity 63

NCBI Description integral transmembrane protein 1

>gi_1174469_sp_P46977_STT3_HUMAN_OLIGOSACCHARYL_TRANSFERASE

STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1)

>qi 624704 (L38961) putative transmembrane protein

precursor [Homo sapiens] >gi_1588286_prf__2208301B integral

membrane protein [Homo sapiens]



Seq. No. 269940

Contig ID 22280 1.R1011

5'-most EST uC-zmflmo17342d06b1

Method BLASTX
NCBI GI g4584540
BLAST score 412
E value 5.0e-40
Match length 189
% identity 48

NCBI Description (AL049608) putative protein [Arabidopsis thaliana]

Seq. No. 269941

Contig ID 22283_1.R1011 5'-most EST uC-zmflb73083g10b2

Method BLASTX
NCBI GI g2739168
BLAST score 371
E value 1.0e-60
Match length 202
% identity 56

NCBI Description (AF032386) aldose-1-epimerase-like protein [Nicotiana

tabacum]

Seq. No. 269942

Contig ID 22284 1.R1011

5'-most EST LIB3159-021-Q1-K1-C8

Seq. No. 269943

Contig ID 22284 3.R1011

5'-most EST uC-zmflmo17300f09b1

Seq. No. 269944

Contig ID 22289 1.R1011 5'-most EST xsy700209501.h1

Seq. No. 269945

Contig ID 22290_2.R1011 5'-most EST uC-zmflb73178e09b1

Seq. No. 269946

Contig ID 22290 3.R1011

5'-most EST LIB3180-031-P2-M2-E10

Seq. No. 269947

Contig ID 22293_1.R1011

5'-most EST LIB3150-040-Q1-N1-A8

Method BLASTX
NCBI GI g3395584
BLAST score 358
E value 5.0e-34
Match length 148
% identity 48

NCBI Description (AL031179) importin beta subunit [Schizosaccharomyces

pombe]

Seq. No. 269948



```
22303 1.R1011
Contig ID
                  rvt700551001.hl
5'-most EST
                  BLASTX
Method
                  q2330794
NCBI GI
                   172
BLAST score
                   5.0e-22
E value
                   242
Match length
                   39
% identity
                  (Z98601) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                   269949
Seq. No.
                   22322 1.R1011
Contig ID
                   LIB3150-040-Q1-N1-E3
5'-most EST
                   269950
Seq. No.
                   22332 1.R1011
Contig ID
                   LIB3279-004-P1-K1-E12
5'-most EST
                   BLASTX
Method
                   g1397292
NCBI GI
                   408
BLAST score
                   2.0e-39
E value
                   238
Match length
% identity
                   37
                  (U61949) C. elegans DIF-1 protein (PIR:S55056)
NCBI Description
                   [Caenorhabditis elegans]
                   269951
Seq. No.
                   22339_1.R1011
Contig ID
                   LIB3066-006-Q1-K1-D9
5'-most EST
                   BLASTX
Method
                   g3805760
NCBI GI
BLAST score
                   189
                   7.0e-14
E value
                   92
Match length
                   52
% identity
NCBI Description (AC005693) unknown protein [Arabidopsis thaliana]
                   269952
Seq. No.
                   22350 1.R1011
Contig ID
                   uC-zm\overline{f}lb73096a07b1
5'-most EST
                   269953
Seq. No.
                   22352 1.R1011
Contig ID
                   LIB3180-055-P2-M1-G5
5'-most EST
                   269954
Seq. No.
 Contig ID
                   22367 1.R1011
                   uC-zmflmo17321e06b1
 5'-most EST
                    269955
 Seq. No.
                    22367 2.R1011
 Contig ID
```

Contig ID 22367_2.R1011 5'-most EST uC-zmflb73220g02b2

Seq. No. 269956

Contig ID 22367_3.R1011 5'-most EST nbm700472059.h1

Method BLASTX



NCBI GI g1297190
BLAST score 302
E value 9.0e-28
Match length 70
% identity 80

NCBI Description (U53501) Theoretical protein with similarity to GenBank

Accession Number L22302 serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 269957

Contig ID 22367_4.R1011

5'-most EST LIB3070-006-Q1-N1-H7

Method BLASTX
NCBI GI g3858939
BLAST score 291
E value 4.0e-26
Match length 70
% identity 84

NCBI Description (AL021636) serine/threonine protein kinase like protein

[Arabidopsis thaliana]

Seq. No. 269958

Contig ID 22372_1.R1011 5'-most EST uC-zmflb73192d05b1

Seq. No. 269959

Contig ID 22374 1.R1011

5'-most EST LIB3150-041-Q1-N1-C3

Seq. No. 269960

Contig ID 22379_1.R1011 5'-most EST LIB189-030-Q1-E1-G4

Method BLASTX
NCBI GI 94539006
BLAST score 415
E value 2.0e-40
Match length 120

% identity 68

NCBI Description (AL049481) putative protein [Arabidopsis thaliana]

Seq. No. 269961

Contig ID 22383 1.R1011 5'-most EST uC-zmflb73051e04b1

Method BLASTX
NCBI GI g3757523
BLAST score 1211
E value 1.0e-133
Match length 393
% identity 61

NCBI Description (AC005167) putative transportin [Arabidopsis thaliana]

Seq. No. 269962

Contig ID 22384_1.R1011

5'-most EST LIB3150-041-Q1-N1-D3

Seq. No. 269963

Contig ID 22388 1.R1011



LIB3150-041-Q1-N1-D8 5'-most EST BLASTX Method q3004550 NCBI GI BLAST score 485 2.0e-48 E value Match length 129 74 % identity (AC003673) hypothetical protein [Arabidopsis thaliana] NCBI Description 269964 Seq. No. 22392 1.R1011 Contig ID $nbm70\overline{0}467502.h1$ 5'-most EST 269965 Seq. No. 22397 1.R1011 Contig ID uC-zmflMo17003e05b1 5'-most EST BLASTX Method g1076386 NCBI GI BLAST score 617 5.0e-64 E value 136 Match length 85 % identity protein kinase ADK1 - Arabidopsis thaliana >gi 1216484 NCBI Description (U48779) dual specificity kinase 1 [Arabidopsis thaliana] 269966 Seq. No. 22397 2.R1011 Contig ID LIB3150-041-Q1-N1-E7 5'-most EST Method BLASTX g4204297 NCBI GI 162 BLAST score 9.0e-21 E value 62 Match length 87 % identity NCBI Description (AC003027) ADK1 [Arabidopsis thaliana] 269967 Seq. No. 22400 1.R1011 Contig ID LIB3150-041-Q1-N1-F1 5'-most EST 269968 Seq. No. 22404 1.R1011 Contig ID dyk700103717.h15'-most EST BLASTX Method g2460200 NCBI GI 382 BLAST score 3.0e-36 E value Match length 263 % identity NCBI Description (AF020833) eukaryotic translation initiation factor 3 subunit [Homo sapiens]

Seq. No. 269969

Contig ID 22415_1.R1011

5'-most EST LIB3066-027-Q1-K1-C12

Seq. No. 269970



```
22419 1.R1011
Contig ID
                  uC-zmrob73077c05b1
5'-most EST
                  BLASTX
Method
                  g1944000
NCBI GI
BLAST score
                  823
                  1.0e-125
E value
                  299
Match length
                  73
% identity
                  (AB002109) protein kinase [Oryza sativa]
NCBI Description
                  269971
Seq. No.
                  22422 1.R1011
Contig ID
                  LIB3150-041-Q1-N1-H3
5'-most EST
                   269972
Seq. No.
                   22438 1.R1011
Contig ID
                   uC-zmflb73226c12b1
5'-most EST
                   BLASTX
Method
                   q2257756
NCBI GI
                   189
BLAST score
                   8.0e-14
E value
                   95
Match length
                   59
% identity
                   (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays]
NCBI Description
                   >gi 3650466 (AF026917) histone deacetylase HD2-p39 [Zea
                   mays]
                   269973
Seq. No.
                   22438 2.R1011
Contig ID
                   LIB3181-002-P1-M1-C12
5'-most EST
                   269974
Seq. No.
                   22439 1.R1011
Contig ID
                   uC-zmflmo17307b08b1
5'-most EST
                   BLASTX
Method
                   q1076316
NCBI GI
                   245
BLAST score
                   2.0e-20
E value
                   107
Match length
                   44
 % identity
                   drought-induced protein Di19 - Arabidopsis thaliana
 NCBI Description
                   >gi 469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis
                   thaliana]
                   269975
 Seq. No.
                   22444 1.R1011
 Contig ID
 5'-most EST
                   LIB189-011-Q1-E1-F9
                   BLASTX
 Method
                   q2651302
 NCBI GI
                   275
 BLAST score
                   3.0e-24
 E value
                   117
 Match length
                    45
 % identity
 NCBI Description (AC002336) hypothetical protein [Arabidopsis thaliana]
```

Seq. No. 269976

Contig ID 22473_1.R1011



LIB3067-054-Q1-K1-E3 5'-most EST BLASTX Method g1076486 NCBI GI 760 BLAST score 1.0e-80 E value Match length 255 57 % identity cim1 protein - soybean >gi_555616 (U03860) cytokinin NCBI Description induced message [Glycine max] 269977 Seq. No. 22474 1.R1011 Contig ID uC-zmflMo17010c09b1 5'-most EST BLASTN Method g3821780 NCBI GI 36 BLAST score 2.0e-10 E value Match length 36 100 % identity NCBI Description Xenopus laevis cDNA clone 27A6-1 269978 Seq. No. 22474 2.R1011 Contig ID uC-zmflb73071b02b3 5'-most EST BLASTX Method g1345773 NCBI GI BLAST score 408 3.0e-39 E value 527 Match length 30 % identity NCBI Description CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1) >gi 455015 (L10410) DNA-binding protein [Mus musculus] 269979 Seq. No. 22489 1.R1011 Contig ID 5'-most EST LIB3279-013-P1-K1-C9 269980 Seq. No. 22502 1.R1011 Contig ID 5'-most EST LIB3150-043-Q1-N1-A2 Seq. No. 269981 22504 1.R1011 Contig ID LIB3150-043-Q1-N1-A4 5'-most EST BLASTX Method NCBI GI q4559380 BLAST score 555 E value 7.0e-57

Match length 228 % identity 52

NCBI Description (AC006526) putative auxin-responsive GH3 protein

[Arabidopsis thaliana]

269982 Seq. No.

22508 1.R1011 Contig ID

5'-most EST LIB3156-001-Q1-K1-A6

BLASTX Method



NCBI GI g3668118 BLAST score 792 1.0e-84 E value Match length 213 % identity 68 (AJ224078) hypothetical protein [Brassica napus] NCBI Description 269983 Seq. No. 22531 1.R1011 Contig ID pmx700091692.hl 5'-most EST Seq. No. 269984 Contig ID 22532 1.R1011 rv1700454881.h1 5'-most EST BLASTX Method

g1449179 NCBI GI BLAST score 530 6.0e-54 E value Match length 149 70 % identity

(D86506) N-ethylmaleimide sensitive fusion protein NCBI Description

[Nicotiana tabacum]

269985 Seq. No. 22532 2.R1011 Contig ID uC-zmflb73407f09a2 5'-most EST BLASTX Method g1449179 NCBI GI

BLAST score 220 9.0e-18 E value Match length 80 59 % identity

(D86506) N-ethylmaleimide sensitive fusion protein NCBI Description

[Nicotiana tabacum]

269986 Seq. No.

22545 1.R1011 Contig ID $pmx70\overline{0}091044.h1$ 5'-most EST

Method BLASTX g4337206 NCBI GI 157 BLAST score 2.0e-12 E value 109 Match length 43 % identity

(AC006403) putative replication factor-A protein NCBI Description

[Arabidopsis thaliana]

269987 Seq. No.

22548 1.R1011 Contig ID

5'-most EST uC-zmflmo17192b10b1

269988 Seq. No.

22558 1.R1011 Contig ID uC-zmrob73012f06b1 5'-most EST

Method BLASTX q3776559 NCBI GI 902 BLAST score



E value 3.0e-97 Match length 283 % identity 64

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi_3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 269989

Contig ID 22558_2.R1011 5'-most EST LIB84-025-Q1-E1-G9

Seq. No. 269990

Contig ID 22558_3.R1011

5'-most EST LIB3150-043-Q1-N1-G12

Method BLASTX
NCBI GI g3482933
BLAST score 343
E value 4.0e-32
Match length 75
% identity 84

% identity 84 NCBI Description (AC003970) Similar to cdc2 protein kinases [Arabidopsis

thaliana]

Seq. No. 269991

Contig ID 22571_1.R1011

5'-most EST LIB3150-043-Q1-N1-H3

Method BLASTX
NCBI GI g4454477
BLAST score 262
E value 1.0e-22
Match length 183

Match length 183 % identity 32

NCBI Description (AC006234) hypothetical protein [Arabidopsis thaliana]

Seq. No. 269992

Contig ID 22576_1.R1011 5'-most EST nbm700472248.h1

Method BLASTX
NCBI GI g3875304
BLAST score 597
E value 8.0e-62
Match length 183
% identity 60

NCBI Description (Z74030) predicted using Genefinder; cDNA EST EMBL:C07609

comes from this gene; cDNA EST EMBL: C09023 comes from this gene; cDNA EST yk505e9.3 comes from this gene; cDNA EST yk489h9.3 comes from this gene; cDNA EST yk489h9.5 com

Seq. No. 269993

Contig ID 22581_1.R1011

5'-most EST LIB148-045-Q1-E1-F9

Method BLASTX
NCBI GI g3668069
BLAST score 1285
E value 1.0e-142
Match length 352



% identity NCBI Description (U28007) Pto kinase interactor 1 [Lycopersicon esculentum] 269994 Seq. No. 22581 2.R1011 Contig ID 5'-most EST LIB148-011-Q1-E1-C12 Method BLASTX q3668069 NCBI GI BLAST score 263 E value 4.0e-23 95 Match length % identity 65 NCBI Description (U28007) Pto kinase interactor 1 [Lycopersicon esculentum] Seq. No. 269995 Contig ID 22584 1.R1011 5'-most EST hbs701181623.h1 Method BLASTX NCBI GI q2642158 BLAST score 271 1.0e-23 E value Match length 135 44 % identity NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana] 269996 Seq. No. Contig ID 22598 1.R1011 ypc700803492.h1 5'-most EST Method BLASTX NCBI GI g3435196 BLAST score 221 8.0e-18 E value 107 Match length % identity 42 NCBI Description (AF067773) glutamyl-tRNA synthetase [Arabidopsis thaliana] 269997 Seq. No. 22601 1.R1011 Contig ID LIB3151-018-Q1-K1-C2 5'-most EST Seq. No. 269998 Contig ID 22603 1.R1011 5'-most EST uC-zmflb73303e11b1 BLASTX Method q3600048 NCBI GI BLAST score 847 E value 6.0e-91 Match length 249

% identity 65

NCBI Description (AF080120) similar to hypothetical proteins in

Schizosaccharomyces pombe (GB:Z98533) and C. elegans

(GB:Z48334 and Z78419) [Arabidopsis thaliana]

Seq. No. 269999

Contig ID 22605 1.R1011

uC-zmflmo17045d12b1 5'-most EST



Seq. No. 270000

Contig ID 22624_1.R1011 5'-most EST wen700334006.h1

Method BLASTX
NCBI GI g203115
BLAST score 530
E value 1.0e-53
Match length 338
% identity 35

NCBI Description (M77246) beta-chain clathrin associated protein complex

AP-2 [Rattus norvegicus]

Seq. No. 270001

Contig ID 22633_1.R1011 5'-most EST uC-zmflb73032h04b1

Seq. No. 270002

Contig ID 22648 1.R1011

5'-most EST LIB31\overline{5}0-045-Q1-N1-B2

Method BLASTX
NCBI GI g2623307
BLAST score 636
E value 1.0e-66
Match length 147
% identity 84

NCBI Description (AC002409) putative ubiquitin protease [Arabidopsis

thaliana]

Seq. No. 270003

Contig ID 22649_1.R1011 5'-most EST uC-zmflb73237g04b2

Seq. No. 270004

Contig ID 22649_2.R1011 5'-most EST xsy700211902.h1

Seq. No. 270005

Contig ID 22650 1.R1011

5'-most EST uC-zmflmo17128b06b1

Method BLASTX
NCBI GI g4006854
BLAST score 393
E value 1.0e-43
Match length 177
% identity 56

NCBI Description (299707) putative protein [Arabidopsis thaliana]

Seq. No. 270006

Contig ID 22656_1.R1011 5'-most EST hvj700620480.h1

Seq. No. 270007

Contig ID 22659_1.R1011

5'-most EST LIB3150-068-P1-N1-C4

Method BLASTX NCBI GI g3122671 BLAST score 489



E value 2.0e-49
Match length 112
% identity 79
NCBI Description HYPOTHETICAL RA

HYPOTHETICAL RAE1-LIKE PROTEIN >gi_2129676_pir__S71241 probable export protein - Arabidopsis thaliana >gi_1297188 (U53501) Theoretical protein with similarity to Swiss-Prot

Accession Number P41838 poly A+ RNA export protein

[Arabidopsis thaliana]

Seq. No. 270008

Contig ID 22668 1.R1011

5'-most EST LIB3180-004-P2-M1-D4

Method BLASTX
NCBI GI g116923
BLAST score 1101
E value 1.0e-120
Match length 494
% identity 50

NCBI Description COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)

>gi_111414_pir__S13520 beta-COP protein - rat
>gi_55819 emb CAA40505_ (X57228) beta COP [Rattus

norvegicus]

Seq. No. 270009

Contig ID 22685_1.R1011 5'-most EST tfd700571617.h1

Seq. No. 270010

Contig ID 22692 1.R1011

5'-most EST LIB3150-045-Q1-N1-F9

Method BLASTX
NCBI GI g4512651
BLAST score 368
E value 6.0e-35
Match length 187
% identity 41

NCBI Description (AC007048) putative tyrosine transaminase [Arabidopsis

thaliana]

Seq. No. 270011

Contig ID 22704_1.R1011

5'-most EST uC-zmflmo17339g03b1

Method BLASTX
NCBI GI g3402703
BLAST score 568
E value 1.0e-58
Match length 156
% identity 73

NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No. 270012

Contig ID 22705 1.R1011

5'-most EST LIB3150-045-Q1-N1-H4

Seq. No. 270013

Contig ID 22710_1.R1011

5'-most EST LIB3150-046-Q1-N1-A12



BLASTX Method q3913653 NCBI GI 1079 BLAST score 1.0e-118 E value Match length 267 76 % identity

FERREDOXIN--NADP REDUCTASE, EMBRYO ISOZYME PRECURSOR (FNR) NCBI Description

>gi 1778686_dbj_BAA13417_ (D87547) precursor ferredoxin-NADP+ oxidoreductase [Oryza sativa]

270014 Seq. No.

22710 2.R1011 Contig ID

LIB143-036-Q1-E1-C8 5'-most EST

BLASTX Method g729480 NCBI GI 278 BLAST score 1.0e-24 E value Match length 101 54 % identity

FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR (FNR) NCBI Description

>gi_435647_dbj_BAA04232_ (D17410) ferredoxin-NADP+
reductase [Oryza sativa] >gi_902936_dbj_BAA07479_ (D38445)

root ferredoxin-NADP+ reductase [Oryza sativa]

>gi 1096932 prf__2113196A ferredoxin-NADP oxidoreductase

[Oryza sativa]

270015 Seq. No.

22719 1.R1011 Contig ID

LIB3067-033-Q1-K1-C11 5'-most EST

BLASTX Method q1806144 NCBI GI BLAST score 1135 1.0e-124 E value 341 Match length 64 % identity

NCBI Description (X97316) cdc2MsE [Medicago sativa]

Seq. No. 270016

22737 1.R1011 Contig ID

uC-zmflb73267e02b2 5'-most EST

BLASTX Method NCBI GI g3600047 1050 BLAST score 1.0e-114 E value 382 Match length

% identity

(AF080120) similar to elongation factor EF-Ts [Arabidopsis NCBI Description

thaliana]

270017 Seq. No.

22763 1.R1011 Contig ID

LIB3059-016-Q1-K1-A8 5'-most EST

270018 Seq. No.

22767 1.R1011 Contig ID

LIB3150-046-Q1-N1-H5 5'-most EST



```
270019
Seq. No.
Contig ID
                   22783 1.R1011
5'-most EST
                   fC-zmro700449636a1
Method
                   BLASTX
NCBI GI
                   g584892
BLAST score
                   1372
                   1.0e-152
E value
Match length
                   394
% identity
                   62
                  SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)
NCBI Description
                   >gi_629805_pir__S43516 serine carboxypeptidase I - rice
                   >gi_409580_dbj_BAA04510_ (D17586) serine carboxypeptidase I
                   [Oryza sativa]
Seq. No.
                   270020
                   22832 1.R1011
Contig ID
                  LIB3059-021-Q1-K1-E6
5'-most EST
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                   36
                   1.0e-10
E value
Match length
                   36
% identity
                   100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                   270021
                  22868 1.R1011
Contig ID
5'-most EST
                  LIB3150-048-Q1-N1-D6
                   270022
Seq. No.
Contig ID
                  22870 1.R1011
5'-most EST
                   xmt700262724.h1
Method
                  BLASTX
NCBI GI
                   q3386622
BLAST score
                  402
                   4.0e-39
E value
Match length
                  152
                   57
% identity
NCBI Description
                  (AC004665) unknown protein [Arabidopsis thaliana]
Seq. No.
                   270023
                  22873 1.R1011
Contig ID
5'-most EST
                   zuv700353547.h1
Method
                  BLASTX
NCBI GI
                  g3540195
BLAST score
                  991
E value
                   1.0e-108
Match length
                  217
% identity
NCBI Description
                 (AC004260) Unknown protein [Arabidopsis thaliana]
```

Seq. No. 270024

Contig ID 22876_1.R1011

5'-most EST LIB3150-048-Q1-N1-E3

Method BLASTX
NCBI GI g3869278
BLAST score 178



```
6.0e-13
E value
                  73
Match length
                   48
% identity
                   (AF058285) nicotinamidase/pyrazinamidase [Mycobacterium
NCBI Description
                   smegmatis]
                   270025
Seq. No.
                   22891 1.R1011
Contig ID
5'-most EST
                   LIB3279-016-P1-K1-G3
                   BLASTX
Method
                   g4263771
NCBI GI
BLAST score
                   146
                   9.0e-09
E value
Match length
                   74
                   32
% identity
                  (AC006218) putative nonspecific lipid-transfer protein
NCBI Description
                   precursor [Arabidopsis thaliana]
                   270026
Seq. No.
                   22896 1.R1011
Contig ID
                   LIB3180-028-P2-M2-A8
5'-most EST
                   270027
Seq. No.
                   22896 3.R1011
Contig ID
5'-most EST
                   uC-zmflb73015h04a2
Seq. No.
                   270028
                   22898 1.R1011
Contig ID
                   uC-zmflmo17425f11a1
5'-most EST
                   270029
Seq. No.
                   22901_1.R1011
Contig ID
                   uC-zmroteosinte041h01b1
5'-most EST
                   BLASTX
Method
                   q1669655
NCBI GI
BLAST score
                   747
E value
                   5.0e-79
                   315
Match length
                   50
% identity
NCBI Description (X95962) CER3 [Arabidopsis thaliana]
Seq. No.
                   270030
                   22906 1.R1011
Contig ID
                   nbm70\overline{0475592.h1}
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3184082
BLAST score
                   443
E value
                   1.0e-43
                   232
Match length
                   40
% identity
                   (AL023781) N-terminal acetyltransferase 1
NCBI Description
                   [Schizosaccharomyces pombe]
```

Seq. No. 270031

Contig ID 22923_1.R1011

5'-most EST LIB3150-049-Q1-N1-B6

Method BLASTX



NCBI GI g120941 BLAST score 146 E value 4.0e-09 Match length 44 % identity 59

NCBI Description GAR1 PROTEIN >gi_83030_pir__S19634 nucleolar protein GAR1 -

yeast (Saccharomyces cerevisiae) >gi_3728_emb_CAA45162_ (X63617) GAR1 [Saccharomyces cerevisiae] >gi_487935 (U00060) Garlp: Small nucleolar RNA protein required for

pre-rRNA splicing [Saccharomyces cerevisiae]

Seq. No. 270032

Contig ID 22925_1.R1011 5'-most EST nbm700477668.h1

Method BLASTX
NCBI GI g3643598
BLAST score 364
E value 2.0e-35
Match length 100
% identity 70

NCBI Description (AC005395) putative poly(A) polymerase [Arabidopsis

thaliana]

Seq. No. 270033

Contig ID 22925 2.R1011

5'-most EST LIB3151-031-Q1-K1-B10

Seq. No. 270034

Contig ID 22927_1.R1011 5'-most EST ymt700224476.h1

Seq. No. 270035

Contig ID 22933_1.R1011

5'-most EST uC-zmflmo17204e03b1

Seq. No. 270036

Contig ID 22938 1.R1011

5'-most EST LIB3150-049-Q1-N1-D12

Seq. No. 270037

Contig ID 22944_1.R1011 5'-most EST xjt700095885.h1

Seq. No. 270038

Contig ID 22944 2.R1011

5'-most EST uC-zmflmo17020d04b1

Seq. No. 270039

Contig ID 22944 3.R1011

5'-most EST uC-zmflmo17220c08a1

Seq. No. 270040

Contig ID 22947_1.R1011 5'-most EST nbm700466921.h1

Method BLASTX
NCBI GI g4038036
BLAST score 166



```
7.0e-11
E value
Match length
                  219
% identity
                  34
NCBI Description
                  (AC005936) unknown protein [Arabidopsis thaliana]
Seq. No.
                  270041
                  22962 1.R1011
Contig ID
                  uwc700152141.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3688174
BLAST score
                  510
                   2.0e-51
E value
                  165
Match length
                   61
% identity
                  (AL031804) putative protein [Arabidopsis thaliana]
NCBI Description
                   270042
Seq. No.
                  22962 2.R1011
Contig ID
                  LIB84-001-Q1-E1-B10
5'-most EST
                  BLASTX
Method
                   g3688174
NCBI GI
BLAST score
                   514
E value
                   6.0e-52
Match length
                   165
% identity
                   62
                  (AL031804) putative protein [Arabidopsis thaliana]
NCBI Description
                   270043
Seq. No.
                   22967 1.R1011
Contig ID
                   uC-zmflb73265e07b4
5'-most EST
                   270044
Seq. No.
                   22967 3.R1011
Contig ID
5'-most EST
                   LIB3061-021-Q1-K1-G3
Seq. No.
                   270045
                   22969 1.R1011
Contig ID
                   uC-zmroteosinte010h09b1
5'-most EST
Method
                   BLASTX
                   g2190544
NCBI GI
BLAST score
                   221
                   2.0e-29
E value
Match length
                   93
% identity
                   78
                   (AC001229) Similar to Saccharomyces hypothetical protein
NCBI Description
                   P9642.2 (gb U40828). [Arabidopsis thaliana]
                   270046
Seq. No.
                   22988 1.R1011
Contig ID
```

LIB3150-050-Q1-N1-A11 5'-most EST

BLASTX Method g3914006 NCBI GI 922 BLAST score E value 1.0e-100 202 Match length % identity 93

NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi_1816588

NCBI GI

BLAST score

g1655637

731



(U85495) LON2 [Zea mays]

Seq. No. 270047 Contig ID 22989 1.R1011 5'-most EST yyf700349474.h1 Method BLASTX g3367591 NCBI GI 228 BLAST score 9.0e-19 E value 99 Match length 40 % identity NCBI Description (AL031135) putative protein [Arabidopsis thaliana] Seq. No. 270048 22999 1.R1011 Contig ID 5'-most EST uC-zmflb73055e04b1 BLASTX Method g1843440 NCBI GI 234 BLAST score E value 3.0e-19 132 Match length % identity 37 NCBI Description (Z70521) unknown [Cucumis melo] Seq. No. 270049 Contig ID 22999 3.R1011 5'-most EST LIB3150-050-Q1-N1-B2 Method BLASTX NCBI GI g1843440 BLAST score 155 E value 3.0e-10 Match length 104 % identity 33 NCBI Description (Z70521) unknown [Cucumis melo] Seq. No. 270050 23009 1.R1011 Contig ID 5'-most EST dyk700104337.h1 270051 Seq. No. Contig ID 23009 2.R1011 5'-most EST LIB3060-001-Q1-K2-D5 Seq. No. 270052 23010 1.R1011 Contig ID 5'-most EST LIB3150-050-Q1-N1-C4 270053 Seq. No. Contig ID 23016 1.R1011 5'-most EST dyk700102266.h1 270054 Seq. No. Contig ID 23021 1.R1011 5'-most EST yyf700347587.h1 BLASTX Method



E value 2.0e-77 Match length 165 % identity 81

NCBI Description (Z54179) orf [Mus musculus]

Seq. No. 270055

Contig ID 23021 2.R1011

5'-most EST LIB3150-050-Q1-N1-D4

Method BLASTX
NCBI GI g1655637
BLAST score 255
E value 7.0e-22
Match length 68
% identity 75

NCBI Description (Z54179) orf [Mus musculus]

Seq. No. 270056

Contig ID 23022_1.R1011

5'-most EST LIB3150-050-Q1-N1-D5

Seq. No. 270057

Contig ID 23024_1.R1011

5'-most EST LIB3150-050-Q1-N1-D7

Seq. No. 270058

Contig ID 23035_1.R1011 5'-most EST ymt700224224.h1

Method BLASTX
NCBI GI g3947614
BLAST score 236
E value 2.0e-19
Match length 147
% identity 40

NCBI Description (AL023828) cDNA EST yk491f8.5 comes from this gene

[Caenorhabditis elegans]

Seq. No. 270059

Contig ID 23036 1.R1011

5'-most EST LIB3150-066-P2-K1-H12

Seq. No. 270060

Contig ID 23039_1.R1011 5'-most EST nbm700473795.h1

Method BLASTX
NCBI GI g2464872
BLAST score 268
E value 4.0e-23
Match length 170
% identity 41

NCBI Description (Z99707) hypothetical protein [Arabidopsis thaliana]

Seq. No. 270061

Contig ID 23039_2.R1011 5'-most EST dyk700102695.h1

Seq. No. 270062

Contig ID 23044_1.R1011



5'-most EST cat700016389.r1

Method BLASTX
NCBI GI g1171870
BLAST score 162
E value 1.0e-10
Match length 88
% identity 35

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 19 KD SUBUNIT (COMPLEX

I-19KD) (CI-19KD) (COMPLEX I-PGIV) (CI-PGIV)

>gi_89670_pir__S16208 NADH dehydrogenase (ubiquinone) (EC
1.6.5.3) 19K chain - bovine >gi_599681_emb_CAA42218_
(X59697) 19 kDa subunit of NADH:ubiquinone oxidoreductase

complex (complex I) [Bos taurus]

Seq. No. 270063

Contig ID 23044_3.R1011 5'-most EST wyr700243582.h1

Seq. No. 270064

Contig ID 23047 1.R1011

5'-most EST uC-zmroteosinte104h06b2

Seq. No. 270065

Contig ID 23053_1.R1011 5'-most EST uC-zmflm017026g12b1

Method BLASTX
NCBI GI g1336084
BLAST score 770

BLAST score 770 E value 7.0e-82 Match length 211 % identity 66

NCBI Description (U56635) Arabidopsis thaliana glutamate dehydrogenase 2

(GDH2) mRNA, complete cds. [Arabidopsis thaliana]

Seq. No. 270066

Contig ID 23053_2.R1011 5'-most EST fC-zmro700452655f1

Method BLASTX
NCBI GI g1336084
BLAST score 1091
E value 1.0e-131
Match length 280
% identity 78

NCBI Description (U56635) Arabidopsis thaliana glutamate dehydrogenase 2

(GDH2) mRNA, complete cds. [Arabidopsis thaliana]

Seq. No. 270067

Contig ID 23053_3.R1011

5'-most EST LIB3070-013-Q1-N1-F8

Seq. No. 270068

Contig ID 23064_1.R1011 5'-most EST uC-zmflb73178f08b1

Method BLASTX
NCBI GI g4406808
BLAST score 175
E value 1.0e-12



102 Match length 41 % identity

(AC006201) unknown protein [Arabidopsis thaliana] NCBI Description

270069 Seq. No.

23077 1.R1011 Contig ID uC-zmflmo17428d01a1 5'-most EST

BLASTX Method g2465923 NCBI GI 465 BLAST score 4.0e-58 E value 233 Match length 54 % identity

(AF024648) receptor-like serine/threonine kinase NCBI Description

[Arabidopsis thaliana]

270070 Seq. No.

23079 1.R1011 Contig ID

LIB143-049-Q1-E1-B4 5'-most EST

BLASTX Method g2982266 NCBI GI 1046 BLAST score 1.0e-114 E value 228 Match length 87

% identity

(AF051216) probable fibrillarin [Picea mariana] NCBI Description

Seq. No. 270071

23079 2.R1011 Contig ID uC-zmromo17009b06a1 5'-most EST

270072 Seq. No.

23079 3.R1011 Contig ID wty700171443.h1 5'-most EST

270073 Seq. No.

Contig ID 23079 5.R1011 uwc700153740.h1 5'-most EST

270074 Seq. No.

23086 1.R1011 Contig ID

5'-most EST LIB3059-059-Q1-K1-G11

Seq. No. 270075

23089 1.R1011 Contig ID

5'-most EST uC-zmroteosinte047d12b2

Method BLASTX NCBI GI g2493646 2273 BLAST score E value 0.0e + 00477 Match length % identity 97

MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR >gi_309559 NCBI Description

(L21008) chaperonin 60 [Zea mays] >gi_309561 (\overline{L} 21006)

mitochondrial chaperonin 60 [Zea mays]

270076 Seq. No.



```
Contig ID 23098_1.R1011
5'-most EST vux700158174.h1
Method BLASTX
NCBI GI g2194118
BLAST score 168
E value 1.0e-11
Match length 78
```

NCBI Description (AC002062) F20P5.4 gene product [Arabidopsis thaliana]

Seq. No. 270077

% identity

Contig ID 23098_2.R1011 5'-most EST wyr700237323.h1

Seq. No. 270078

Contig ID 23105 1.R1011

5'-most EST LIB3150-051-Q1-N1-E2

38

Seq. No. 270079

Contig ID 23107_1.R1011 5'-most EST hvj700620701.h1

Seq. No. 270080

Contig ID 23107 2.R1011

5'-most EST LIB3180-029-P2-M2-A10

Seq. No. 270081

Contig ID 23132_1.R1011

5'-most EST LIB31 $\overline{5}$ 0-051-Q1-N1-H4

Method BLASTX
NCBI GI g3451463
BLAST score 386
E value 4.0e-37
Match length 165
% identity 47

NCBI Description (AL031349) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 270082

Contig ID 23136_1.R1011 5'-most EST uC-zmflmo17103h06b1

Method BLASTX
NCBI GI g1575556
BLAST score 913
E value 6.0e-99
Match length 189
% identity 86

NCBI Description (U66299) acyl-CoA oxidase homolog [Phalaenopsis sp. 'True

Lady']

Seq. No. 270083

Contig ID 23138_1.R1011

5'-most EST uC-zmroteosinte015a07b1

Method BLASTX
NCBI GI g3913517
BLAST score 1381
E value 1.0e-153
Match length 329



% identity 3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE NCBI Description (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE) (DPNPASE) >qi 1109672 (U33283) 3'(2'),5-diphosphonucleoside 3'(2') phosphohydrolase [Oryza sativa] >gi_1586671_prf__2204308A diphosphonucleoside phosphohydrolase [Oryza sativa] 270084 Seq. No. 23140 1.R1011 Contig ID LIB3150-052-Q1-N1-A2 5'-most EST 270085 Seq. No. 23149 1.R1011 Contig ID 5'-most EST uC-zmflMo17012a05b1 Seq. No. 270086 23150 1.R1011 Contig ID uC-zmroteosinte034h11b1 5'-most EST BLASTX Method q872116 NCBI GI 781 BLAST score 4.0e-83 E value Match length 203 41 % identity (X79770) sti (stress inducible protein) [Glycine max] NCBI Description 270087 Seq. No. Contig ID 23150 2.R1011 uC-zmflb73225g02b15'-most EST BLASTX Method q872116 NCBI GI 1094 BLAST score 1.0e-119 E value 450 Match length 31 % identity NCBI Description (X79770) sti (stress inducible protein) [Glycine max] 270088 Seq. No. 23150 3.R1011 Contig ID uC-zmflmo17341d04a1 5'-most EST BLASTX Method g2129844 NCBI GI 338 BLAST score 1.0e-31 E value 93 Match length 70 % identity NCBI Description stress-induced protein stil - soybean Seq. No. 270089

Contig ID 23159_1.R1011 5'-most EST xmt700257516.h1

Seq. No. 270090

Contig ID 23165_1.R1011 5'-most EST fwa700101494.h1

Method BLASTX



NCBI GI g3482971 483 BLAST score 4.0e-48 E value Match length 107 77 % identity (AL031369) putative protein [Arabidopsis thaliana] NCBI Description 270091 Seq. No. 23165_2.R1011 Contig ID LIB3069-037-Q1-K1-G6 5'-most EST BLASTX Method g2137796 NCBI GI 171 BLAST score 5.0e-12 E value Match length 50 % identity 68 stromal cell-derived factor 2 - mouse NCBI Description >qi 1741870 dbj BAA09313 (D50646) SDF2 [Mus musculus] 270092 Seq. No. 23181_1.R1011 Contig ID 5'-most EST LIB3150-052-Q1-N1-E1 Method BLASTX g1644402 NCBI GI 196 BLAST score 1.0e-32 E value Match length 171 % identity 47 (U73524) putative ATP/GTP-binding protein [Homo sapiens] NCBI Description 270093 Seq. No. 23192 1.R1011 Contig ID 5'-most EST LIB3150-052-Q1-N1-F1 270094 Seq. No. 23201 1.R1011 Contig ID 5'-most EST LIB3150-052-Q1-N1-G1 Method BLASTX NCBI GI q2979554 BLAST score 438 2.0e-43E value Match length 133 % identity 61 (AC003680) CDC4 like protein [Arabidopsis thaliana] NCBI Description 270095 Seq. No. Contig ID 23206 1.R1011 5'-most EST LIB3150-052-Q1-N1-G5 Seq. No. 270096 23214 1.R1011 Contig ID 5'-most EST LIB3150-052-Q1-N1-H3

Method BLASTX
NCBI GI g3928083
BLAST score 366
E value 7.0e-35
Match length 72



% identity (AC005770) unknown protein [Arabidopsis thaliana] NCBI Description 270097 Seq. No. 23215 1.R1011 Contig ID LIB3150-052-Q1-N1-H4 5'-most EST 270098 Seq. No. Contig ID 23216 1.R1011 LIB3150-052-Q1-N1-H6 5'-most EST 270099 Seq. No. 23220 1.R1011 Contig ID ymt700220838.h1 5'-most EST BLASTX Method q4263790 NCBI GI 597 BLAST score 6.0e-62 E value 162 Match length 70 % identity (AC006068) putative ch-TOG protein [Arabidopsis thaliana] NCBI Description 270100 Seq. No. 23227_1.R1011 Contig ID 5'-most EST $uC-zm\overline{f}lmo17333d05b1$ BLASTX Method q4105186 NCBI GI 804 BLAST score 6.0e-86 E value 208 Match length % identity 75 (AF044128) protoporphyrinogen oxidase PX-1 [Nicotiana NCBI Description tabacum] Seq. No. 270101 Contig ID 23227 2.R1011 5'-most EST pmx700089282.h1 BLASTX Method NCBI GI q3093410 733 BLAST score E value 1.0e-127 320 Match length 74 % identity NCBI Description (AJ225107) protoporphyrinogen oxidase [Solanum tuberosum] Seq. No. 270102 Contig ID 23229 1.R1011 fwa700101128.h1 5'-most EST

Seq. No. 270103

Contig ID 23232_1.R1011 5'-most EST xmt700262832.h1

Method BLASTX
NCBI GI g2632254
BLAST score 1766
E value 0.0e+00
Match length 429



% identity (Y12465) serine/threonine kinase [Sorghum bicolor] NCBI Description Seq. No. 270104 23232 2.R1011 Contig ID $xmt70\overline{0}266754.h1$ 5'-most EST Method BLASTX g2894378 NCBI GI BLAST score 1260 0.0e + 00E value Match length 422 84 % identity (Y14573) putative ribophorin I homologue [Hordeum vulgare] NCBI Description Seq. No. 270105 Contig ID 23232 3.R1011 $uC-zm\overline{f}lmo17126b11b1$ 5'-most EST Method BLASTX NCBI GI a2894378 BLAST score 169 2.0e-11 E value Match length 54 59 % identity (Y14573) putative ribophorin I homologue [Hordeum vulgare] NCBI Description 270106 Seq. No. 23232 4.R1011 Contig ID 5'-most EST pmx700090934.h1 Method BLASTX q2894378 NCBI GI BLAST score 456 5.0e-45E value Match length 106 83 % identity (Y14573) putative ribophorin I homologue [Hordeum vulgare] NCBI Description 270107 Seq. No. Contig ID 23234 1.R1011 5'-most EST fwa700097955.h1 BLASTX Method q4531444 NCBI GI BLAST score 1456 1.0e-162 E value 447 Match length 63 % identity (AC006224) putative protein kinase [Arabidopsis thaliana] NCBI Description Seq. No. 270108 23234 2.R1011 Contig ID 5'-most EST gct701170740.hl

Seq. No. 270109

Contig ID 23238_1.R1011 5'-most EST ntr700075967.h1

Method BLASTX
NCBI GI g1653702
BLAST score 396

Match length

NCBI Description

% identity

83



```
5.0e-38
E value
                   170
Match length
                   52
% identity
                   (D90915) dihydrolipoamide acetyltransferase component (E2)
NCBI Description
                   of pyruvate dehydrogenase complex [Synechocystis sp.]
                   270110
Seq. No.
                   23243_1.R1011
Contig ID
5'-most EST
                   LIB3150-053-Q1-N1-C2
                   BLASTX
Method
                   q1703380
NCBI GI
BLAST score
                   931
                   1.0e-101
E value
Match length
                   181
                   99
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760)
                   ADP-ribosylation factor [Oryza sativa]
                   270111
Seq. No.
                   23243 2.R1011
Contig ID
                   LIB3180-009-P2-M1-A4
5'-most EST
                   BLASTX
Method
                   g1351974
NCBI GI
                    336
BLAST score
                    2.0e-31
E value
Match length
                    85
% identity
                    86
                   ADP-RIBOSYLATION FACTOR >gi 1076788 pir__S49325
NCBI Description
                   ADP-ribosylation factor - maize >gi_1076789_pir__S53486
ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_
                    (X80042) ADP-ribosylation factor [Zea mays]
                    270112
Seq. No.
                    23243 3.R1011
Contig ID
                    xyt700344091.hl
5'-most EST
Method
                    BLASTX .
NCBI GI
                    q2852443
                    246
BLAST score
                    3.0e-21
E value
                    92
Match length
                    95
% identity
NCBI Description
                   (AB003377) ADP-ribosylation factor [Salix bakko]
                    270113
Seq. No.
                    23245 1.R1011
Contig ID
5'-most EST
                    xmt70\overline{0}256919.h1
Seq. No.
                    270114
                    23250 1.R1011
Contig ID
5'-most EST
                    LIB3150-053-Q1-N1-D1
Method
                    BLASTX
NCBI GI
                    g4263519
BLAST score
                    404
E value
                    3.0e-39
```

37607

(AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis



thaliana]

Seq. No. 270115 Contig ID 23250 2.R1011 gw1700614815.h1 5'-most EST BLASTX Method NCBI GI g4263519 BLAST score 278 6.0e-25 E value Match length 57 93 % identity (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis NCBI Description thaliana] Seq. No. 270116 Contig ID 23261 1.R1011 LIB3150-053-Q1-N1-E2 5'-most EST BLASTX Method q1151134 NCBI GI 398 BLAST score 8.0e-53 E value Match length 136 85 % identity (U43034) permease 1 [Zea mays] NCBI Description 270117 Seq. No. Contig ID 23271 1.R1011 5'-most EST LIB3180-032-P2-M2-A8 Method BLASTX g3560533 NCBI GI 790 BLAST score 2.0e-84 E value 165 Match length 90 % identity (AF042333) 24-methylene lophenol C24(1)methyltransferase NCBI Description [Oryza sativa] 270118 Seq. No. 23271 2.R1011 Contig ID LIB143-005-Q1-E1-A6 5'-most EST BLASTX Method g3560533 NCBI GI BLAST score 579 6.0e-60 E value 124 Match length 86 % identity (AF042333) 24-methylene lophenol C24(1)methyltransferase NCBI Description [Oryza sativa] 270119 Seq. No. 23274 1.R1011 Contig ID LIB3150-053-Q1-N1-F6 5'-most EST

37608

270120

23277 1.R1011

uC-zmflmo17265b12b1

Seq. No.

Contig ID 5'-most EST



```
270121
Seq. No.
                  23280 1.R1011
Contig ID
                  pmx700091107.h1
5'-most EST
                  BLASTX
Method
                  g3292831
NCBI GI
                  186
BLAST score
                  2.0e-13
E value
                  90
Match length
                  40
% identity
                  (AL031018) putative serine/threonine kinase [Arabidopsis
NCBI Description
                  thaliana]
                  270122
Seq. No.
                  23282 1.R1011
Contig ID
                  uC-zmflmo17215a05b1
5'-most EST
                  BLASTX
Method
                  g2829918
NCBI GI
                  754
BLAST score
                  4.0e-80
E value
                  220
Match length
                   68
% identity
                  (AC002291) similar to "tub" protein gp_U82468_2072162
NCBI Description
                   [Arabidopsis thaliana]
                   270123
Seq. No.
                   23282 2.R1011
Contig ID
5'-most EST
                   qw1700616609.h1
                   270124
Seq. No.
                   23295 1.R1011
Contig ID
5'-most EST
                   LIB189-029-Q1-E1-B11
Method
                   BLASTX
                   q4586107
NCBI GI
                   473
BLAST score
                   2.0e-47
E value
Match length
                   124
% identity
                   18
                  (AL049638) putative disease resistance protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   270125
                   23306 1.R1011
Contig ID
                   LIB3150-054-Q1-N1-B10
5'-most EST
                   270126
Seq. No.
                   23310 1.R1011
Contig ID
5'-most EST
                   ypc700807345.h1
Method
                   BLASTX
                   q2252866
NCBI GI
                   265
BLAST score
                   7.0e-23
E value
                   88
Match length
                   74
% identity
                  (AF013294) contains region of similarity to SYT
```

270127 Seq. No.

NCBI Description

[Arabidopsis thaliana]



```
23310 2.R1011
Contig ID
                  LIB3150-054-Q1-N1-B8
5'-most EST
                  BLASTX
Method
                  g2252866
NCBI GI
                  <u>2</u>70
BLAST score
                   8.0e-24
E value
                   73
Match length
                   74
% identity
                   (AF013294) contains region of similarity to SYT
NCBI Description
                   [Arabidopsis thaliana]
                   270128
Seq. No.
                   23311 1.R1011
Contig ID
                   uC-zmflmo17052e09b1
5'-most EST
                   270129
Seq. No.
                   23320 1.R1011
Contig ID
                   uC-zmflmo17117e05b1
5'-most EST
                   BLASTX
Method
                   g2827002
NCBI GI
BLAST score
                   662
                   1.0e-69
E value
                   136
Match length
                   93
% identity
                  (AF005993) HSP70 [Triticum aestivum]
NCBI Description
Seq. No.
                   270130
                   23328 1.R1011
Contig ID
5'-most EST
                   xyt700343638.hl
                   270131
Seq. No.
                   23334 1.R1011
Contig ID
5'-most EST
                   rvt700548667.h1
                   270132
Seq. No.
                   23337 1.R1011
Contig ID
5'-most EST
                   uwc700151231.h1
                   BLASTX
Method
                   q3549670
NCBI GI
                   476
BLAST score
                   1.0e-47
E value
Match length
                   125
                   73
% identity
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
Seq. No.
                   270133
Contig ID
                   23350 1.R1011
5'-most EST
                   LIB3150-054-Q1-N1-G1
Method
                   BLASTX
NCBI GI
                   q3334140
BLAST score
                   1181
                   1.0e-130
E value
```

% identity 70

NCBI Description CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5

(GENTROMERE PROPERTY DIVIDING FACTOR 5) (NUCLEOLAR BR)

332

Match length

(CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5) >gi 2737888 (U59148) nucleolar protein AnCbf5p [Emericella



nidulans]

```
270134
Seq. No.
Contig ID
                  23367 1.R1011
                  uC-zmroteosinte120e08b2
5'-most EST
                  BLASTX
Method
                  g2076623
NCBI GI
                   391
BLAST score
E value
                   3.0e-41
Match length
                   321
```

36

% identity (Z95151) PtrB [Mycobacterium leprae] NCBI Description

270135 Seq. No. Contig ID 23367 2.R1011 uer700577363.h1 5'-most EST

270136 Seq. No.

23368 1.R1011 Contig ID

5'-most EST LIB3150-054-Q1-N1-H8

270137 Seq. No.

Contig ID 23369 1.R1011 5'-most EST wty700167279.h1

Method BLASTX NCBI GI q2894598 910 BLAST score 3.0e-98 E value 321 Match length % identity 58

(AL021889) putative protein [Arabidopsis thaliana] NCBI Description

270138 Seq. No.

23371 1.R1011 Contig ID

5'-most EST LIB143-006-Q1-E1-H5

270139 Seq. No.

23371 2.R1011 Contig ID cjh700193171.h1 5'-most EST

Seq. No. 270140

23371_3.R1011 Contig ID

LIB3179-019-P1-K1-B12 5'-most EST

270141 Seq. No.

Contig ID 23373 1.R1011

LIB3150-054-Q1-N1-H9 5'-most EST

Method BLASTX NCBI GI q2507229 BLAST score 270 8.0e-24 E value Match length 67 75 % identity

NCBI Description 40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE)

(ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED

PROTEIN) (ESTROGEN RECEPTOR BINDING CYCLOPHILIN) >gi 423247 pir A46579 estrogen receptor-binding

BLAST score

Match length

% identity

E value

578

161

77

2.0e-59



cyclophilin - bovine >gi_393300_dbj_BAA03159_ (D14074)
cyclophilin [Bos taurus]

270142 Seq. No. 23374 1.R1011 Contig ID $uC-zm\overline{f}lmo17264g05a2$ 5'-most EST BLASTN Method g3821780 NCBI GI BLAST score 36 1.0e-10 E value Match length 36 100 % identity Xenopus laevis cDNA clone 27A6-1 NCBI Description 270143 Seq. No. 23374 2.R1011 Contig ID 5'-most EST ntr700077249.h1 Method BLASTX g2801536 NCBI GI BLAST score 252 2.0e-21 E value 96 Match length 53 % identity (AF039531) lysophospholipase homolog [Oryza sativa] NCBI Description 270144 Seq. No. 23376 1.R1011 Contig ID uC-zmflmo17158h03a1 5'-most EST 270145 Seq. No. 23384 1.R1011 Contig ID LIB3150-111-P2-K1-B11 5'-most EST 270146 Seq. No. 23391 1.R1011 Contig ID 5'-most EST uC-zmflb73247h02a2 Method BLASTX g3341697 NCBI GI BLAST score 254 E value 1.0e-21 59 Match length 78 % identity (AC003672) hypothetical protein [Arabidopsis thaliana] NCBI Description 270147 Seq. No. 23396 1.R1011 Contig ID 5'-most EST LIB3150-055-Q1-N1-D1 270148 Seq. No. 23404 1.R1011 Contig ID uC-zmflb73247a09a2 5'-most EST BLASTX Method NCBI GI q137476

E value

Match length

5.0e-11

40



```
VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT
NCBI Description
                  >gi_82334_pir__A40814 H+-transporting ATPase (EC 3.6.1.35)
                  proteolipid chain, vacuolar - oat >gi_166549 (M73232)
                  H+-ATPase [Avena sativa]
                  270149
Seq. No.
                  23417 1.R1011
Contig ID
                  uC-zmroteosinte068a07b1
5'-most EST
Method
                  BLASTX
                  q3142289
NCBI GI
                  224
BLAST score
E value
                  3.0e-18
Match length
                  56
                  73
% identity
                  (AC002411) Strong similarity to beta-keto-Coa synthase
NCBI Description
                  gb U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
                  270150
Seq. No.
                  23417 2.R1011
Contig ID
                  LIB3150-055-Q1-N1-F1
5'-most EST
Method
                  BLASTX
                  g3142289
NCBI GI
BLAST score
                  289
                  1.0e-25
E value
                  79
Match length
                  66
% identity
                  (AC002411) Strong similarity to beta-keto-Coa synthase
NCBI Description
                  gb U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
                  270151
Seq. No.
                  23418 1.R1011
Contig ID
                  uC-zmroteosinte028a03b1
5'-most EST
                  270152
Seq. No.
Contig ID
                  23418 2.R1011
5'-most EST
                  uC-zmflmo17323e03a1
Method
                  BLASTX
                  g3927831
NCBI GI
BLAST score
                  189
                   4.0e-14
E value
Match length
                   45
                   69
% identity
                  (AC005727) similar to mouse ankyrin 3 [Arabidopsis
NCBI Description
                  thaliana]
                   270153
Seq. No.
Contig ID
                   23418 3.R1011
5'-most EST
                  uC-zmflb73290h07a1
                   270154
Seq. No.
                   23419 1.R1011
Contig ID
5'-most EST
                  LIB3070-008-Q1-N1-F9
Method
                   BLASTX
NCBI GI
                   q585960
BLAST score
                   163
```



% identity 80

NCBI Description PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT

>gi 433665 emb_CAA81412_ (Z26753) Sec61 beta-subunit

homolog [Arabidopsis thaliana]

Seq. No. 270155

Contig ID 23422 1.R1011

5'-most EST uC-zmflmo17354h11a1

Method BLASTX
NCBI GI g2842482
BLAST score 422
E value 2.0e-41
Match length 116
% identity 72

NCBI Description (AL021749) protein phosphatase 2C-like protein [Arabidopsis

thaliana]

Seq. No. 270156

Contig ID 23432 1.R1011 5'-most EST uC-zmflb73085f01a1

Method BLASTX
NCBI GI g1086225
BLAST score 317
E value 5.0e-29
Match length 97
% identity 62

NCBI Description RING-finger protein (C-terminal) - Lotus japonicus

>gi_558545_emb_CAA85321_ (Z36750) protein containing

C-terminal RING-finger [Lotus japonicus]

>gi 1771195_emb_CAA70734_ (Y09539) RING-finger protein

[Lotus japonicus]

Seq. No. 270157 Contig ID 23434_1.R1011

5'-most EST uC-zmroteosinte094h04b2

Seq. No. 270158

Contig ID 23434_2.R1011

5'-most EST uC-zmroteosinte057e12b1

Seq. No. 270159

Contig ID 23434 5.R1011 5'-most EST wyr700238858.h1

Seq. No. 270160

Contig ID 23434_6.R1011 5'-most EST cyk700050618.f1

Seq. No. 270161

Contig ID 23434_7.R1011 5'-most EST pwr700451340.h1

Seq. No. 270162

Contig ID 23436_1.R1011 5'-most EST uer700577979.h1

Method BLASTN NCBI GI g470670



BLAST score 426 E value 0.0e+00 Match length 786 % identity 94

NCBI Description Zea mays transposable element ILS-1

Seq. No. 270163

Contig ID 23438 1.R1011

5'-most EST LIB3157-015-Q1-K1-C8

Seq. No. 270164

Contig ID 23444 1.R1011

5'-most EST uC-zmflb73080f09a1

Method BLASTX
NCBI GI g4432823
BLAST score 392
E value 2.0e-37
Match length 168

% identity 52

NCBI Description (AC006593) hypothetical protein [Arabidopsis thaliana]

Seq. No. 270165

Contig ID 23444 2.R1011

5'-most EST LIB3156-002-Q1-K2-A1

Seq. No. 270166

Contig ID 23454 1.R1011

5'-most EST LIB3180-040-P2-M2-B2

Method BLASTX
NCBI GI g399213
BLAST score 441
E value 2.0e-43
Match length 189
% identity 54

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

CD4B PRECURSOR >gi_100190_pir__B35905 CD4B protein - tomato

>gi_170435 (M32604) ATP-dependent protease (CD4B)

[Lycopersicon esculentum]

Seq. No. 270167

Contig ID 23458 1.R1011

5'-most EST LIB3150-056-Q1-N1-B1

Method BLASTX
NCBI GI g2213591
BLAST score 281
E value 2.0e-24
Match length 189
% identity 35

NCBI Description (AC000348) T7N9.11 [Arabidopsis thaliana]

Seq. No. 270168

Contig ID 23458_3.R1011 5'-most EST uC-zmflb73184c01a1

Seq. No. 270169

Contig ID 23460_1.R1011 5'-most EST xyt700343265.h1



Method BLASTX
NCBI GI 94097690
BLAST score 1005
E value 1.0e-109
Match length 234
% identity 85

NCBI Description (U66592) prohibitin 2 [Arabidopsis thaliana] >gi_4099801 (U89791) prohibitin-like protein [Arabidopsis thaliana] >gi_4204301 (AC003027) prohibitin 2 [Arabidopsis thaliana]

Seq. No. 270170

Contig ID 23460_2.R1011 5'-most EST uC-zmflb73177b07b1

Method BLASTX
NCBI GI 94097690
BLAST score 586
E value 6.0e-61
Match length 166
% identity 76

NCBI Description (U66592) prohibitin 2 [Arabidopsis thaliana] >gi_4099801 (U89791) prohibitin-like protein [Arabidopsis thaliana]

>gi_4204301 (AC003027) prohibitin 2 [Arabidopsis thaliana]

Seq. No. 270171

Contig ID 23469_1.R1011 5'-most EST uC-zmflb73301h10a1

Seq. No. 270172

Contig ID 23471_1.R1011 5'-most EST fC-zmse700616058f1

Method BLASTX
NCBI GI g1653702
BLAST score 860
E value 3.0e-92
Match length 360
% identity 52

NCBI Description (D90915) dihydrolipoamide acetyltransferase component (E2)

of pyruvate dehydrogenase complex [Synechocystis sp.]

Seq. No. 270173

Contig ID 23471_2.R1011 5'-most EST rvt700552129.h1

Method BLASTX
NCBI GI g1653702
BLAST score 158
E value 1.0e-21
Match length 79
% identity 73

NCBI Description (D90915) dihydrolipoamide acetyltransferase component (E2)

of pyruvate dehydrogenase complex [Synechocystis sp.]

Seq. No. 270174

Contig ID 23473_1.R1011 5'-most EST cyk700050435.f1

Seq. No. 270175

Contig ID 23485_1.R1011



```
5'-most EST
                  uC-zmflmo17175g10b1
Seq. No.
                  270176
                  23486 1.R1011
Contig ID
                  wen700334640.hl
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1195465
                  Ī55
BLAST score
                  7.0e-10
E value
                  107
Match length
                   33
% identity
                   (U24677) ras-related protein RAB-4 [Trypanosoma brucei
NCBI Description
                  rhodesiense]
                  270177
Seq. No.
                  23496 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73158a02b2
Method
                  BLASTX
                  g103313
NCBI GI
                  318
BLAST score
                   3.0e-29
E value
                  98
Match length
% identity
                   63
                  probable cell cycle control protein crn - fruit fly
NCBI Description
                   (Drosophila melanogaster) >gi 2827496 emb CAA15705
                   (AL009195) EG:30B8.1 [Drosophila melanogaster]
                   270178
Seq. No.
                   23501 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73199h08b1
Method
                  BLASTX
NCBI GI
                   g2408094
BLAST score
                   150
E value
                   3.0e-09
                  74
Match length
                   39
% identity
NCBI Description
                  (299168) hypothetical protein [Schizosaccharomyces pombe]
                   270179
Seq. No.
Contig ID
                   23511 1.R1011
5'-most EST
                   hvj700622849.h1
Method
                  BLASTX
NCBI GI
                   q4455190
BLAST score
                   434
E value
                   2.0e-42
Match length
                   116
% identity
                   72
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                   270180
Seq. No.
                   23524 1.R1011
Contig ID
5'-most EST
                  LIB3150-057-Q1-N1-A8
```

37617

270181

23532 1.R1011

uC-zmflmo17303f06b1

Seq. No. Contig ID

5'-most EST



Seq. No. 270182

Contig ID 23532 2.R1011

5'-most EST LIB3150-057-Q1-N1-C11

Seq. No. 270183

Contig ID 23539_1.R1011

5'-most EST LIB3150-057-Q1-N1-C7

Seq. No. 270184

Contig ID 23545_1.R1011 5'-most EST cyk700048195.f1

Method BLASTX
NCBI GI g2104558
BLAST score 208
E value 3.0e-16
Match length 159
% identity 30

NCBI Description (AB000216) CCA3 [Rattus norvegicus]

Seq. No. 270185

Contig ID 23562_1.R1011 5'-most EST uC-zmflB73021e12b1

Method BLASTX
NCBI GI g2462781
BLAST score 1156
E value 1.0e-127
Match length 319
% identity 68

NCBI Description (U73175) carbamoyl phosphate synthetase small subunit

[Arabidopsis thaliana]

Seq. No. 270186

Contig ID 23562_2.R1011

5'-most EST LIB143-012-Q1-E1-A12

Seq. No. 270187

Contig ID 23562_3.R1011 5'-most EST LIB84-008-Q1-E1-C7

Seq. No. 270188

Contig ID 23563 1.R1011

5'-most EST LIB3180-005-P2-M1-G1

Seq. No. 270189

Contig ID 23570_1.R1011

5'-most EST LIB189-026-Q1-E1-H9

Seq. No. 270190

Contig ID 23570_2.R1011 5'-most EST wyr700237487.h1

Method BLASTX
NCBI GI g4309740
BLAST score 160
E value 9.0e-11
Match length 111
% identity 34

NCBI Description (AC006439) putative syntaxin [Arabidopsis thaliana]



Seq. No. 270191 Contig ID 23577_1.R1011

5'-most EST LIB3159-017-Q1-K1-G6

Method BLASTX
NCBI GI g2290528
BLAST score 300
E value 1.0e-31
Match length 112
% identity 69

NCBI Description (U94746) ATAN11 [Arabidopsis thaliana]

Seq. No. 270192

Contig ID 23592_1.R1011

5'-most EST LIB3150-058-Q1-N1-A7

Method BLASTX
NCBI GI g4160298
BLAST score 507
E value 4.0e-51
Match length 228
% identity 48

NCBI Description (AJ011892) cyclin D2.1 protein [Nicotiana tabacum]

Seq. No. 270193

Contig ID 23598_1.R1011

5'-most EST LIB3150-058-Q1-N1-B12

Seq. No. 270194

Contig ID 23605_1.R1011 5'-most EST pmx700088676.h1

Method BLASTX
NCBI GI g1946329
BLAST score 988
E value 1.0e-107

Match length 280 % identity 71

NCBI Description (U69154) prohibitin [Nicotiana tabacum]

Seq. No. 270195

Contig ID 23612_1.R1011

5'-most EST LIB3150-058-Q1-N1-C4

Method BLASTX
NCBI GI g100849
BLAST score 1312
E value 1.0e-145
Match length 257
% identity 99

NCBI Description acetolactate synthase (EC 4.1.3.18) (clone pSOG108) - maize

>gi_22139_emb_CAA45116_ (X63553) acetohydroxyacid synthase

[Zea mays]

Seq. No. 270196

Contig ID 23625_1.R1011 5'-most EST ntr700072325.h2

Seq. No. 270197

Contig ID 23628 1.R1011

NCBI Description



```
uC-zmflMo17006c01b1
5'-most EST
                  BLASTX
Method
                  g2660669
NCBI GI
BLAST score
                   285
                   4.0e-25
E value
                   209
Match length
% identity
                   38
                   (AC002342) human Mi-2 autoantigen-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   270198
Seq. No.
                   23635 1.R1011
Contig ID
                   uC-zmrob73005e01b1
5'-most EST
                   270199
Seq. No.
                   23635 2.R1011
Contig ID
                   uC-zmroteosinte063e01b1
5'-most EST
                   BLASTX
Method
                   g1076685
NCBI GI
                   351
BLAST score
                   1.0e-32
E value
Match length
                   282
                   18
% identity
                   SPF1 protein - sweet potato >gi_484261_dbj_BAA06278_
NCBI Description
                   (D30038) SPF1 protein [Ipomoea batatas]
Seq. No.
                   270200
                   23649 1.R1011
Contig ID
5'-most EST
                   xjt700092579.h1
                   270201
Seq. No.
                   23669 1.R1011
Contig ID
5'-most EST
                   bdu70\overline{0}382301.h1
                   BLASTX
Method
NCBI GI
                   g2833220
BLAST score
                   446
E value
                   9.0e-44
Match length
                   165
                   52
% identity
                   HYPOTHETICAL 35.7 KD PROTEIN IN DNL4-SLG1 INTERGENIC REGION
NCBI Description
                   >gi_2132030_pir__S61990 hypothetical protein YOR006c -
                   yeast (Saccharomyces cerevisiae) >gi_1151002 (U43491)
                   hypothetical protein UND313 [Saccharomyces cerevisiae]
                   >gi_1420098_emb_CAA99194_ (Z74914) ORF YOR006c
                   [Saccharomyces cerevisiae]
Seq. No.
                   270202
Contig ID
                   23670 1.R1011
5'-most EST
                   LIB3150-058-Q1-N1-H9
                   BLASTX
Method
NCBI GI
                   q132127
BLAST score
                   380
E value
                   6.0e-36
Match length
                   306
% identity
                   36
```

RIBOKINASE >gi_66667_pir__KIECRB ribokinase (EC 2.7.1.15) -

Escherichia coli >gi_2981974 pdb_1RKD_ E. Coli Ribokinase



Complexed With Ribose And Adp >gi_147516 (M13169) ribokinase [Escherichia coli] >gi_290602 (L10328) ribokinase [Escherichia coli] >gi_1790193 (AE000452) ribokinase [Escherichia coli]

Seq. No. 270203

Contig ID 23676 1.R1011

5'-most EST LIB3151-026-Q1-K1-D4

Method BLASTX
NCBI GI g4580466
BLAST score 988
E value 1.0e-107
Match length 246

% identity 76

NCBI Description (AC006081) putative 50S ribosomal protein L4 [Arabidopsis

thaliana]

Seq. No. 270204

Contig ID 23683 1.R1011

5'-most EST LIB3150-068-P2-K1-C10

Seq. No. 270205

Contig ID 23686 1.R1011

5'-most EST LIB3137-008-Q1-K1-C5

Seq. No. 270206

Contig ID 23692_1.R1011

5'-most EST LIB189-005-Q1-E1-H8

Method BLASTX
NCBI GI g4468979
BLAST score 453
E value 3.0e-45
Match length 106

% identity 75

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 270207

Contig ID 23692 3.R1011

5'-most EST LIB3069-004-Q1-K1-D10

Method BLASTX
NCBI GI 94468979
BLAST score 417
E value 5.0e-41
Match length 95
% identity 76

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 270208

Contig ID 23709 1.R1011

5'-most EST LIB3150-059-Q1-N1-E12

Seq. No. 270209

Contig ID 23717_1.R1011 5'-most EST uC-zmflb73160b09a1

Seq. No. 270210

Contig ID 23717_2.R1011

Seq. No.

Contig ID

270216

23766 1.R1011



```
5'-most EST
                  uC-zmflmo17294f05b1
                   270211
Seq. No.
                   23740 1.R1011
Contig ID
5'-most EST
                  dyk700104211.h1
                  BLASTX
Method
NCBI GI
                   g2460251
BLAST score
                   584
                   3.0e-60
E value
                   186
Match length
                   67
% identity
                   (AF020791) ferrochelatase [Hordeum vulgare]
NCBI Description
Seq. No.
                   270212
                   23748 1.R1011
Contig ID
                   xjt70\overline{0}092431.h1
5'-most EST
Method
                   BLASTX
                   g2104530
NCBI GI
                   878
BLAST score
                   1.0e-94
E value
Match length
                   202
% identity
                   82
                   (AF001308) PROLIFERA [Arabidopsis thaliana] >gi_2104548
NCBI Description
                   (AF001535) AGAA.2, PROLIFERA [Arabidopsis thaliana]
                   270213
Seq. No.
                   23751 1.R1011
Contig ID
                   LIB3150-060-Q1-N1-B3
5'-most EST
                   270214
Seq. No.
                   23765 1.R1011
Contig ID
5'-most EST
                   LIB84-003-Q1-E1-A7
                   BLASTX
Method
                   q3548802
NCBI GI
BLAST score
                   614
                   1.0e-63
E value
Match length
                   234
% identity
                   52
                   (AC005313) axi 1-like protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein
                   [Nicotiana tabacum] [Arabidopsis thaliana]
                   270215
Seq. No.
                   23765 2.R1011
Contig ID
                   uC-zmflb73362e12a2
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3548802
BLAST score
                   243
E value
                   6.0e-25
Match length
                   122
                   51
% identity
                   (AC005313) axi 1-like protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4335769 qb AAD17446 (AC006284) putative axil protein
                   [Nicotiana tabacum] [Arabidopsis thaliana]
```



5'-most EST uC-zmroteosinte042d07b1

Method BLASTX
NCBI GI g3402693
BLAST score 592
E value 3.0e-61
Match length 201
% identity 61

NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 270217

Contig ID 23782 1.R1011

5'-most EST LIB3150-060-Q1-N1-F10

Seq. No. 270218

Contig ID 23783 1.R1011

5'-most EST LIB3180-044-P2-M2-F1

Seq. No. 270219

Contig ID 23791 1.R1011

5'-most EST uC-zmflmo17054d02b1

Seq. No. 270220

Contig ID 23793 1.R1011

5'-most EST uC-zmflmo17044a08b1

Seq. No. 270221

Contig ID 23816_1.R1011 5'-most EST rvt700553122.h1

Seq. No. 270222

Contig ID 23816_2.R1011 5'-most EST uC-zmflb73120c04b1

Seq. No. 270223

Contig ID 23819_1.R1011 5'-most EST cyk700048534.f1

Seq. No. 270224

Contig ID 23830_1.R1011

5'-most EST LIB3150-061-Q1-N1-C12

Method BLASTX
NCBI GI g2498995
BLAST score 153
E value 1.0e-09
Match length 106
% identity 35

NCBI Description QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE

TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)

>gi 1006609_dbj_BAA10764_ (D64005) transfer RNA-guanine

transglycosylase [Synechocystis sp.]

Seq. No. 270225

Contig ID 23834_1.R1011

5'-most EST LIB3159-011-Q1-K1-D7

Method BLASTX NCBI GI g2454182 BLAST score 1163



E value 1.0e-128 Match length 269 % identity 83

NCBI Description (U80185) pyruvate dehydrogenase E1 alpha subunit

[Arabidopsis thaliana]

Seq. No. 270226

Contig ID 23837_1.R1011 5'-most EST yyf700351435.h1

Seq. No. 270227

Contig ID 23842 1.R1011

5'-most EST uC-zmflmo17069d08b1

Seq. No. 270228

Contig ID 23850_1.R1011 5'-most EST cat700019262.r1

Method BLASTX
NCBI GI g119351
BLAST score 1283
E value 1.0e-142
Match length 343
% identity 71

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_84950_pir__S07586

phosphopyruvate hydratase (EC 4.2.1.11) - fruit $f\overline{ly}$

(Drosophila melanogaster) >gi_7946_emb_CAA34895_ (X17034)

enolase (AA 1-433) [Drosophila melanogaster]

Seq. No. 270229

Contig ID 23855_1.R1011

5'-most EST LIB3150-061-Q1-N1-F1

Method BLASTX
NCBI GI g1086586
BLAST score 152
E value 2.0e-22
Match length 166
% identity 34

NCBI Description (U41007) similar to G beta repeats (PROSITE: PS00670)

[Caenorhabditis elegans]

Seq. No. 270230

Contig ID 23862_1.R1011 5'-most EST xsy700211988.h1

Method BLASTX
NCBI GI g4314401
BLAST score 176
E value 1.0e-12
Match length 66
% identity 58

NCBI Description (AC006232) putative beta-1,3-glucanase [Arabidopsis

thaliana]

Seq. No. 270231

Contig ID 23876_1.R1011

5'-most EST LIB3150-063-P2-K1-A3

Method BLASTX



```
g1350795
NCBI GI
                   162
BLAST score
                   1.0e-10
E value
Match length
                   136
                   32
% identity
                  MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L24 PRECURSOR (YML24)
NCBI Description
                   >gi 1078342_pir__S50921 ribosomal protein YmL24,
                  mitochondrial - yeast (Saccharomyces cerevisiae)
                   >gi 642285 emb CAA87814_ (Z47815) ribosomal protein
                   [Saccharomyces cerevisiae]
                   270232
Seq. No.
                   23887 1.R1011
Contig ID
                   uC-zmflmo17398d02a1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3046695
                   192
BLAST score
                   3.0e-14
E value
Match length
                   88
                   51
% identity
                  (AL022224) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   270233
                   23890 1.R1011
Contig ID
                 LIB31\overline{5}0-063-P2-K1-B9
5'-most EST
                   270234
Seq. No.
Contig ID
                   23908 1.R1011
                   uC-zm\overline{f}lmo17202e12a1
5'-most EST
                   BLASTX
Method
                   q3522938
NCBI GI
                   169
BLAST score
                   3.0e-11
E value
                   151
Match length
                   33
% identity
NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]
Seq. No.
                   270235
                   23908 2.R1011
Contig ID
                   uer700583703.hl
5'-most EST
                   BLASTX
Method
                   g3522938
NCBI GI
                   373
BLAST score
E value
                   5.0e-35
                   397
Match length
                   28
% identity
                  (AC004411) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   270236
Contig ID
                   23912 1.R1011
                   wyr700243109.hl
5'-most EST
```

Seq. No. 270237

Contig ID 23930_1.R1011

5'-most EST LIB3150-064-P1-N1-A9

Method BLASTX NCBI GI g2854117



BLAST score 202 E value 3.0e-15 Match length 98 % identity 45

NCBI Description (AF045453) protein kinase YakA [Dictyostelium discoideum]

Seq. No. 270238

Contig ID 23941 1.R1011

5'-most EST LIB189-021-Q1-E1-H9

Seq. No. 270239

Contig ID 23949_1.R1011 5'-most EST xjt700092527.h1

Method BLASTX
NCBI GI g3122861
BLAST score 346
E value 6.0e-32
Match length 279
% identity 32

NCBI Description D-3-PHOSPHOGLYCERATE DEHYDROGENASE (PGDH) >gi_2649798

(AE001048) phosphoglycerate dehydrogenase (serA)

[Archaeoglobus fulgidus]

Seq. No. 270240

Contig ID 23949_2.R1011 5'-most EST vmj700053763.r1

Seq. No. 270241

Contig ID 23949 3.R1011 5'-most EST uC-zmflb73121c04b2

Seq. No. 270242

Contig ID 23962_1.R1011

5'-most EST LIB3180-021-P2-M1-G12

Seq. No. 270243

Contig ID 23982_1.R1011

5'-most EST LIB3150-064-P2-K1-A7

Seq. No. 270244

Contig ID 23990_1.R1011

5'-most EST LIB3150-064-P2-K1-C3

Seq. No. 270245

Contig ID 24004_1.R1011

5'-most EST uC-zmflb73038g12b1

Seq. No. 270246

Contig ID 24039_1.R1011 5'-most EST uC-zmrob73050a05b1

Seq. No. 270247

Contig ID 24042_1.R1011

5'-most EST LIB3150-065-P2-K1-C4

Method BLASTX
NCBI GI g3882183
BLAST score 271



```
2.0e-23
E value
Match length
                  91
                  53
% identity
NCBI Description (AB018274) KIAA0731 protein [Homo sapiens]
                  270248
Seq. No.
                  24042 2.R1011
Contig ID
5'-most EST
                  LIB3059-053-Q1-K1-A2
                  BLASTX
Method
                  q3882183
NCBI GI
                  306
BLAST score
                  2.0e-27
E value
Match length
                  103
% identity
                  52
                  (AB018274) KIAA0731 protein [Homo sapiens]
NCBI Description
Seq. No.
                  270249
                  24048 1.R1011
Contig ID
5'-most EST
                  LIB3150-065-P2-K1-D2
                  270250
Seq. No.
                  24051 1.R1011
Contig ID
5'-most EST
                  LIB3150-065-P2-K1-D6
                  270251
Seq. No.
                  24055 1.R1011
Contig ID
5'-most EST
                  uC-zmromo17096c12a1
Seq. No.
                  270252
Contig ID
                  24061 1.R1011
                  LIB3150-065-P2-K1-E8
5'-most EST
                  270253
Seq. No.
Contig ID
                  24061 2.R1011
                  uC-zmflmo17375d07a1
5'-most EST
                  270254
Seq. No.
                  24073 1.R1011
Contig ID
                  LIB3150-089-P2-K1-H7
5'-most EST
Method
                  BLASTX
                  g1279640
NCBI GI
BLAST score
                   551
                   6.0e-56
E value
                  171
Match length
                   60
% identity
NCBI Description (X92204) NAM [Petunia x hybrida]
                   270255
Seq. No.
                   24073 2.R1011
Contig ID
5'-most EST
                  LIB3059-035-Q1-K1-B10
                   BLASTX
Method
NCBI GI
                   g1944132
```

BLAST score 345 E value 5.0e-49 Match length 178 58 % identity

(AB002560) CUC2 [Arabidopsis thaliana] NCBI Description



```
270256
Seq. No.
Contig ID
                   24073 3.R1011
5'-most EST
                  LIB3060-032-Q1-K1-A1
Method
                  BLASTX
NCBI GI
                  g1944132
BLAST score
                  426
E value
                   5.0e-42
Match length
                  100
% identity
                  76
                  (AB002560) CUC2 [Arabidopsis thaliana]
NCBI Description
                   270257
Seq. No.
Contig ID
                   24076 1.R1011
5'-most EST
                  uC-zmrob73034b05a1
Method
                  BLASTX
NCBI GI
                   g4521249
BLAST score
                  767
                   1.0e-81
E value
                   203
Match length
                   71
% identity
                  (AB013912) DNA helicase [Mus musculus]
NCBI Description
                   270258
Seq. No.
                   24076 2.R1011
Contig ID
5'-most EST
                   uC-zmrob73039f07a1
Method
                   BLASTX
NCBI GI
                   g4521249
BLAST score
                   151
                   9.0e-10
E value
                   46
Match length
                   57
% identity
NCBI Description
                  (AB013912) DNA helicase [Mus musculus]
                   270259
Seq. No.
                   24081 1.R1011
Contig ID
5'-most EST
                   cat70\overline{0}017170.r1
                   270260
Seq. No.
                   24092 1.R1011
Contig ID
5'-most EST
                   pwr700452827.h1
Method
                   BLASTX
NCBI GI
                   g4191784
                   373
BLAST score
E value
                   1.0e-35
Match length
                   138
                   52
% identity
NCBI Description
                  (AC005917) putative WD-40 repeat protein [Arabidopsis
                   thaliana]
                   270261
Seq. No.
```

Contig ID 24129_2.R1011
5'-most EST uC-zmflb73062f03b1
Method BLASTX
NCBI GI g2335108
BLAST score 1377
E value 1.0e-153



Match length 440 % identity 55

NCBI Description (AC002339) putative isulinase [Arabidopsis thaliana]

Seq. No. 270262

Contig ID 24134_1.R1011

5'-most EST LIB3150-066-P2-K1-A11

Seq. No. 270263

Contig ID 24139_1.R1011

5'-most EST LIB3150-066-P2-K1-A7

Method BLASTX
NCBI GI g2244822
BLAST score 445
E value 8.0e-44
Match length 157
% identity 52

NCBI Description (Z97336) RNA polymerase II fifth largest subunit homolog

[Arabidopsis thaliana]

Seq. No. 270264

Contig ID 24140_1.R1011

5'-most EST LIB3150-066-P2-K1-A8

Method BLASTX
NCBI GI g3193330
BLAST score 432
E value 4.0e-42
Match length 209

% identity 49

NCBI Description (AF069299) contains similarity to Medicago sativa corC

(GB:L22305) [Arabidopsis thaliana]

Seq. No. 270265

Contig ID 24152_1.R1011

5'-most EST uC-zmflmo17264f09a2

Method BLASTX
NCBI GI g3548818
BLAST score 235
E value 2.0e-19
Match length 64
% identity 67

NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 270266

Contig ID 24153_1.R1011 5'-most EST pwr700453207.h1

Seq. No. 270267

Contig ID 24153_2.R1011 5'-most EST gwl700614007.h1

Seq. No. 270268

Contig ID 24155_1.R1011

5'-most EST LIB3150-066-P2-K1-D6

Seq. No. 270269

Contig ID 24157 1.R1011



5'-most EST nbm700469215.h1 BLASTX Method g4103324 NCBI GI BLAST score 216 2.0e-17 E value Match length 43 98 % identity (AF022716) GDP-mannose pyrophosphorylase [Solanum NCBI Description tuberosum] 270270 Seq. No. 24157 2.R1011 Contig ID LIB3150-107-P2-K1-G2 5'-most EST Seq. No. 270271 Contig ID 24159 1.R1011 LIB3150-066-P2-K1-E10 5'-most EST 270272 Seq. No. 24170 1.R1011 Contig ID ntr700077152.h1 5'-most EST Seq. No. 270273 24171 1.R1011 Contig ID cat700016087.rl 5'-most EST 270274 Seq. No. Contig ID 24192 1.R1011 LIB3150-066-P2-K1-H8 5'-most EST 270275 Seq. No. 24194 1.R1011 Contig ID LIB83-012-Q1-E1-D7 5'-most EST BLASTX Method g2623297 NCBI GI BLAST score 401 9.0e-39 E value Match length 137 58 % identity (AC002409) unknown protein [Arabidopsis thaliana] NCBI Description >gi_3790583 (AF079180) RING-H2 finger protein RHC1a [Arabidopsis thaliana] 270276 Seq. No. Contig ID 24208 1.R1011 $xsy70\overline{0}208180.h1$ 5'-most EST Method BLASTX g3219969 NCBI GI BLAST score 151 2.0e-09 E value Match length 56

43 % identity

HYPOTHETICAL 22.4 KD PROTEIN C6G10.10C IN CHROMOSOME I NCBI Description >qi 2330874 emb CAB11296 (Z98603) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 270277



Contig ID 24212 1.R1011

uC-zmflmo17100e10b1 5'-most EST

Method BLASTN g3819228 NCBI GI 55 BLAST score 8.0e-22 E value Match length 71 94 % identity

Hordeum vulgare partial mRNA; clone cMWG0741 NCBI Description

Seq. No. 270278

Contig ID 24214 1.R1011 pmx700091117.h1 5'-most EST

Seq. No. 270279

Contig ID 24216 1.R1011

uC-zmflMo17005d09b1 5'-most EST

BLASTX Method g2244988 NCBI GI BLAST score 316 8.0e-29 E value Match length 181

43 % identity

(Z97340) hypothetical protein [Arabidopsis thaliana] NCBI Description

270280 Seq. No.

24216 3.R1011 Contig ID

5'-most EST LIB3152-049-P1-K1-H11

Method BLASTX NCBI GI q542182 BLAST score 1573 1.0e-176 E value 408 Match length 77 % identity

vicilin-like storage protein Glb1-L, embryo - maize NCBI Description

>gi_22284_emb_CAA41809_ (X59083) vicilin-like embryo

storage protein [Zea mays]

270281 Seq. No.

24216 7.R1011 Contig ID $xmt70\overline{0}265495.h1$ 5'-most EST

BLASTX Method NCBI GI q542182 208 BLAST score 1.0e-16 E value 34 Match length 100 % identity

vicilin-like storage protein Glb1-L, embryo - maize NCBI Description

>gi_22284_emb_CAA41809_ (X59083) vicilin-like embryo

storage protein [Zea mays]

270282 Seq. No.

24219 1.R1011 Contig ID

LIB3150-067-P2-K1-A11 5'-most EST

270283 Seq. No.

Contig ID 24240_1.R1011

Match length

% identity



```
5'-most EST
                   LIB3150-067-P2-K1-D1
Seq. No.
                   270284
                   24241 1.R1011
Contig ID
                   LIB3150-067-P2-K1-D12
5'-most EST
                   270285
Seq. No.
                   24241 2.R1011
Contig ID
                   uC-zm\overline{f}1b73201d01b1
5'-most EST
Seq. No.
                   270286
                   24243 1.R1011
Contig ID
                   LIB3067-002-Q1-K1-B7
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2668742
BLAST score
                   239
E value
                   8.0e-20
                   49
Match length
                   96
% identity
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                   270287
Seq. No.
Contig ID
                   24243 3.R1011
                   LIB3150-114-P2-K1-F12
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2668741
BLAST score
                   189
E value
                   1.0e-102
                   249
Match length
                   94
% identity
                   Zea mays glycine-rich RNA binding protein (GRP) mRNA,
NCBI Description
                   complete cds
                   270288
Seq. No.
Contig ID
                   24243 4.R1011
5'-most EST
                   xsy70\overline{0}208468.h1
Method
                   BLASTX
NCBI GI
                   g2668742
BLAST score
                   262
                   1.0e-22
E value
Match length
                   53
% identity
                   100
NCBI Description
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
                   270289
Seq. No.
Contig ID
                   24244 1.R1011
5'-most EST
                   LIB3150-067-P2-K1-D9
Seq. No.
                   270290
Contig ID
                   24251_1.R1011
                   LIB3150-067-P2-K1-E6
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2760839
BLAST score
                   1057
                   1.0e-115
E value
```



```
(AC003105) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   270291
Contig ID
                   24257 1.R1011
                  LIB3150-067-P2-K1-F12
5'-most EST
Seq. No.
                   270292
                   24272 1.R1011
Contig ID
                  LIB3150-067-P2-K1-G8
5'-most EST
                   270293
Seq. No.
                   24302 1.R1011
Contig ID
5'-most EST
                   uwc700153138.h1
                   BLASTX
Method
NCBI GI
                   g1628482
BLAST score
                   214
E value
                   4.0e-17
Match length
                   156
% identity
                   9
                  (X97570) embryogenesis transmembrane protein [Zea mays]
NCBI Description
                   270294
Seq. No.
                   24337 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73134a06a2
Method
                   BLASTX
NCBI GI
                   g4455294
BLAST score
                   275
E value
                   4.0e-24
Match length
                   69
% identity
                   64
                  (AL035528) putative protein [Arabidopsis thaliana]
NCBI Description
                   270295
Seq. No.
Contig ID
                   24340 1.R1011
                   LIB3150-068-P2-K1-D1
5'-most EST
Method
                   BLASTX
                   g2462911
NCBI GI
BLAST score
                   165
                   2.0e-11
E value
                   44
Match length
                   77
% identity
                  (Z83832) UDP-glucose:sterol glucosyltransferase [Avena
NCBI Description
                   sativa]
                   270296
Seq. No.
                   24346_1.R1011
Contig ID
5'-most EST
                   LIB3150-068-P2-K1-E12
                   270297
Seq. No.
Contig ID
                   24350 1.R1011
5'-most EST
                   uC-zm\overline{f}lb73317e11b1
                   BLASTX
Method
                   g4558591
NCBI GI
                   320
BLAST score
                   3.0e-29
E value
```

37633

99

62

Match length

% identity



```
(AC006555) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                  thaliana]
                  270298
Seq. No.
                  24357 1.R1011
Contig ID
                  vux700158436.h1
5'-most EST
                  BLASTX
Method
                  g2499614
NCBI GI
                  501
BLAST score
                  2.0e-50
E value
Match length
                  119
                  74
% identity
                  MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG NTF3 (P43)
NCBI Description
                  >gi_481830_pir__S39559 mitogen-activated protein kinase 3
                  homolog ntf3 - common tobacco >gi 406751 emb CAA49592_
                   (X69971) NTF3 [Nicotiana tabacum]
                  270299
Seq. No.
                  24366 1.R1011
Contig ID
                  LIB3150-094-P2-K1-H6
5'-most EST
                  BLASTX
Method
NCBI GI
                  g4567232
                  303
BLAST score
                  3.0e-27
E value
                  72
Match length
                  81
% identity
NCBI Description
                  (AC007119) putative 40S ribosomal protein S25 [Arabidopsis
                  thaliana]
                   270300
Seq. No.
                  24366 2.R1011
Contig ID
                   fC-zmle700444748b1
5'-most EST
                  BLASTX
Method
                   g4567232
NCBI GI
                   307
BLAST score
                   9.0e-28
E value
Match length
                   72
                   83
% identity
                  (AC007119) putative 40S ribosomal protein S25 [Arabidopsis
NCBI Description
                   thalianal
                   270301
Seq. No.
                   24376 1.R1011
Contig ID
5'-most EST
                   tfd700574061.h1
Seq. No.
                   270302
Contig ID
                   24379 1.R1011
5'-most EST
                   uC-zmflb73346b09a2
```

Method BLASTX
NCBI GI g2708741
BLAST score 1288
E value 1.0e-142
Match length 338
% identity 74

NCBI Description (AC003952) hypothetical protein [Arabidopsis thaliana]

Seq. No. 270303

Match length



```
24381 1.R1011
Contig ID
                  uC-zm\overline{f}lmo17132e01b1
5'-most EST
                   270304
Seq. No.
                   24382 1.R1011
Contig ID
                  LIB3182-016-P2-M1-H11
5'-most EST
                   BLASTX
Method
                   g2129579
NCBI GI
                   1554
BLAST score
                   0.0e+00
E value
                   559
Match length
                   77
% identity
                   Dwarf1 protein - Arabidopsis thaliana >gi 516043 (U12400)
NCBI Description
                   Dwarf1 [Arabidopsis thaliana]
                   270305
Seq. No.
                   24382 2.R1011
Contig ID
                   wty700163239.hl
5'-most EST
                   BLASTX
Method
                   g2129579
NCBI GI
                   365
BLAST score
                   6.0e-35
E value
Match length
                   81
                   77
% identity
                   Dwarfl protein - Arabidopsis thaliana >gi 516043 (U12400)
NCBI Description
                   Dwarf1 [Arabidopsis thaliana]
Seq. No.
                   270306
                   24389 1.R1011
Contig ID
                   LIB3061-014-Q1-K1-H8
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4539145
                   358
BLAST score
                   1.0e-33
E value
                   168
Match length
                   42
% identity
NCBI Description
                  (AJ133748) major intrinsic protein [Picea abies]
                   270307
Seq. No.
                   24402 1.R1011
Contig ID
5'-most EST
                   pmx700087945.h1
                   BLASTX
Method
                   q1001263
NCBI GI
                   521
BLAST score
                   5.0e-53
E value
Match length
                   161
                   60
% identity
NCBI Description (D64003) hypothetical protein [Synechocystis sp.]
                   270308
Seq. No.
Contig ID
                   24408 1.R1011
                   LIB3150-069-P1-N1-G4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g134889
BLAST score
                   255
                    3.0e-36
E value
```



% identity 34

NCBI Description SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68) >gi 108065 pir S12981 68K protein - gray wolf

>gi_227342_prf__1702226A SRP68 protein [Canis familiaris]

Seq. No. 270309

Contig ID 24412_1.R1011 5'-most EST yyf700350570.h1

Method BLASTX
NCBI GI g3548819
BLAST score 153
E value 7.0e-10
Match length 58
% identity 53

NCBI Description (AC005313) putative heterogeneous nuclear ribonucleoprotein

[Arabidopsis thaliana]

Seq. No. 270310

Contig ID 24412_2.R1011 5'-most EST uC-zmflmo17134a02b1

Seq. No. 270311

Contig ID 24417 1.R1011

5'-most EST LIB3150-069-P2-K1-A10

Method BLASTX
NCBI GI g2944180
BLAST score 508
E value 3.0e-51
Match length 137
% identity 70

NCBI Description (AF007779) trehalose-6-phosphate phosphatase [Arabidopsis

thaliana]

Seq. No. 270312

Contig ID 24419 1.R1011

5'-most EST LIB3150-069-P2-K1-A12

Seq. No. 270313

Contig ID 24424 1.R1011

5'-most EST LIB3150-072-P2-K1-F11

Seq. No. 270314

Contig ID 24424 2.R1011

5'-most EST LIB3150-069-P2-K1-B1

Seq. No. 270315

Contig ID 24424_3.R1011 5'-most EST gct701179876.h1

Seq. No. 270316

Contig ID 24431 1.R1011

5'-most EST LIB3150-069-P2-K1-C7

Method BLASTX
NCBI GI g534982
BLAST score 312
E value 4.0e-28
Match length 216



% identity 40 (X75898) phosphoglucomutase [Spinacia oleracea] NCBI Description 270317 Seq. No. 24436 1.R1011 Contig ID LIB3150-069-P2-K1-E11 5'-most EST Method BLASTX g2982293 NCBI GI 304 BLAST score 2.0e-27 E value 74 Match length % identity 72 (AF051231) ISP42-like protein [Picea mariana] NCBI Description Seq. No. 270318 Contig ID 24436 3.R1011 ntr700073703.h1 5'-most EST Method BLASTX q2982293 NCBI GI 230 BLAST score 8.0e-19 E value 54 Match length % identity 80 (AF051231) ISP42-like protein [Picea mariana] NCBI Description 270319 Seq. No. 24440 1.R1011 Contig ID 5'-most EST LIB3150-069-P2-K1-F10 270320 Seq. No. 24442 2.R1011 Contig ID LIB3150-114-P2-K1-D10 5'-most EST BLASTX Method g567893 NCBI GI 148 BLAST score 2.0e-09 E value Match length 96 % identity 43 (L37382) beta-galactosidase-complementation protein NCBI Description [Cloning vector] 270321 Seq. No. Contig ID 24449 1.R1011 LIB3150-069-P2-K1-G12 5'-most EST 270322 Seq. No. 24451_1.R1011 Contig ID 5'-most EST LIB3059-058-Q1-K1-C11

Method BLASTX
NCBI GI g3183094
BLAST score 1334
E value 1.0e-147
Match length 330
% identity 79

NCBI Description ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR (OTCASE)

(ORNITHINE TRANSCARBAMYLASE) >gi_971168 (U13684) ornithine

carbamoyltransferase [Pisum sativum]

Contig ID

NCBI GI BLAST score

5'-most EST Method



```
270323
Seq. No.
                  24451 2.R1011
Contig ID
                  LIB3150-069-P2-K1-G7
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3914234
                  240
BLAST score
                  4.0e-20
E value
                  60
Match length
                  78
% identity
NCBI Description
                  ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR (OTCASE)
                   (ORNITHINE TRANSCARBAMYLASE) >gi_2764518_emb_CAA04115
                   (AJ000476) Ornithine carbamoyltransferase [Arabidopsis
                  thaliana] >gi_2764737_emb_CAA05510 (AJ002524) ornithine
                  carbamoyltransferase [Arabidopsis thaliana]
Seq. No.
                  270324
                  24461 1.R1011
Contig ID
                  uC-zmflb73309a09a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g940288
BLAST score
                  633
                  2.0e-65
E value
Match length
                  218
                  56
% identity
                  (L43510) protein localized in the nucleoli of pea nuclei;
NCBI Description
                  ORF; putative [Pisum sativum]
                  270325
Seq. No.
                  24498 1.R1011
Contig ID
5'-most EST
                  LIB3150-070-P1-N1-G4
Method
                  BLASTX
NCBI GI
                  q2244904
BLAST score
                  317
E value
                  3.0e-29
Match length
                  128
% identity
                  48
NCBI Description
                  (Z97339) similar to hypothetical protein C02F5.7 - Caenorha
                   [Arabidopsis thaliana]
                  270326
Seq. No.
Contig ID
                  24502 1.R1011
                  uC-zmflb73239g02b2
5'-most EST
Method
                  BLASTX
NCBI GI
                  q4309889
BLAST score
                  150
E value
                  2.0e-09
Match length
                  77
% identity
NCBI Description
                  (AC004983) similar to PID:g3877944 [Homo sapiens]
Seq. No.
                  270327
```

37638

24512 1.R1011

BLASTX q1706714

387

LIB3060-027-Q1-K1-C1



E value 3.0e-37 146 Match length % identity 59

ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT (BETA-ETF) NCBI Description (ELECTRON TRANSFER FLAVOPROTEIN SMALL SUBUNIT) (ETFSS)

>gi 1209054 (U32230) EtfS [Bradyrhizobium japonicum]

270328 Seq. No.

24513 1.R1011 Contia ID tfd700569256.h2 5'-most EST

Method BLASTX NCBI GI g2842477 BLAST score 342 8.0e-32 E value Match length 109 % identity 59

(AL021749) copper-binding protein-like [Arabidopsis NCBI Description

thaliana]

270329 Seq. No.

24520 1.R1011 Contig ID $xsy70\overline{0}207839.h1$ 5'-most EST

Method BLASTX NCBI GI g2244898 BLAST score 1735 0.0e+00E value Match length 501 % identity 66

(Z97338) strong similarity to protein phosphatase 2A NCBI Description

regulatory chain, 74K [Arabidopsis thaliana]

270330 Seq. No.

24520 2.R1011 Contig ID

uC-zmflmo17025g10a1 5'-most EST

270331 Seq. No.

24522 1.R1011 Contig ID

5'-most EST LIB3150-071-P1-N1-C2

270332 Seq. No.

24523 1.R1011 Contig ID 5'-most EST xsy700209259.hl

Method BLASTX NCBI GI g3328101 165 BLAST score 4.0e-11 E value Match length 118 % identity 33

(AF073995) beta-galactosidase [synthetic construct] NCBI Description

270333 Seq. No.

24525 1.R1011 Contig ID

5'-most EST LIB3150-071-P1-N1-C5

BLASTX Method NCBI GI g2655291 BLAST score 295 E value 1.0e-26



Match length 70 % identity 81

NCBI Description (AF032974) germin-like protein 4 [Oryza sativa]

Seq. No. 270334

Contig ID 24528_1.R1011

5'-most EST LIB3059-002-Q1-K2-G10

Seq. No. 270335

Contig ID 24534_1.R1011 5'-most EST wyr700241420.h1

Seq. No. 270336

Contig ID 24534_2.R1011 5'-most EST qmh700028254.f1

Seq. No. 270337

Contig ID 24548 1.R1011

5'-most EST LIB3150-071-P1-N1-E8

Seq. No. 270338

Contig ID 24555_1.R1011 5'-most EST uwc700150712.h1

Method BLASTX
NCBI GI g3334405
BLAST score 631
E value 1.0e-65
Match length 206
% identity 65

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)

>qi 2267583 (AF009338) vacuolar H+-ATPase subunit E

[Gossypium hirsutum]

Seq. No. 270339

Contig ID 24561_1.R1011

5'-most EST uC-zmroteosinte095f07b2

Seq. No. 270340

Contig ID 24561_2.R1011

5'-most EST uC-zmflmo17051a10b1

Seq. No. 270341

Contig ID 24564 1.R1011

5'-most EST LIB3068-025-Q1-K1-D8

Method BLASTX
NCBI GI g1703091
BLAST score 373
E value 3.0e-35
Match length 90
% identity 78

NCBI Description ACYL CARRIER PROTEIN, MITOCHONDRIAL PRECURSOR (ACP)

(NADH-UBIQUINONE OXIDOREDUCTASE 9.6 KD SUBUNIT) (MTACP-1)

>gi_903689 (L23574) acyl carrier protein precursor

[Arabidopsis thaliana] >gi 3341682 (AC003672) acyl carrier

protein [Arabidopsis thaliana]

Seq. No. 270342



Contig ID 24564 2.R1011 fC-zmle700431965a1 5'-most EST Method BLASTX q1703091 NCBI GI BLAST score 341 4.0e-32 E value Match length 81 79 % identity ACYL CARRIER PROTEIN, MITOCHONDRIAL PRECURSOR (ACP) NCBI Description (NADH-UBIQUINONE OXIDOREDUCTASE 9.6 KD SUBUNIT) (MTACP-1) >gi 903689 (L23574) acyl carrier protein precursor [Arabidopsis thaliana] >gi_3341682 (AC003672) acyl carrier protein [Arabidopsis thaliana] Seq. No. 270343 Contig ID 24567 1.R1011 uC-zmroteosinte028b02b1 5'-most EST BLASTX Method q2689030 NCBI GI BLAST score 280 1.0e-24 E value Match length 222 35 % identity (AF034568) RNA guanylyltransferase [Mus musculus] NCBI Description >gi_2697127 (AF025653) mRNA capping enzyme [Mus musculus] 270344 Seq. No. Contig ID 24570 1.R1011 LIB3067-028-Q1-K1-E4 5'-most EST 270345 Seq. No. 24574 1.R1011 Contig ID 5'-most EST pmx700082904.h1 270346 Seq. No. 24579 1.R1011 Contig ID 5'-most EST qmh700026657.f1 270347 Seq. No. 24591 1.R1011 Contig ID LIB3150-072-P2-K1-B6 5'-most EST BLASTX Method g691752 NCBI GI 284 BLAST score 3.0e-25E value 81 Match length 60 % identity NCBI Description (D29803) preproMP27-MP32 [Cucurbita sp.] Seq. No. 270348 24608 1.R1011 Contig ID uC-zmroteosinte104h11b2 5'-most EST

Method BLASTX
NCBI GI g2388585
BLAST score 538
E value 9.0e-55
Match length 147



% identity 73

NCBI Description (AC000098) Similar to Caenorhabditis unknown protein

T03F1.1 (gb U88169). [Arabidopsis thaliana]

Seq. No. 270349

Contig ID 24616 1.R1011

5'-most EST uC-zmflmo17222e12a1

Method BLASTX
NCBI GI g3334349
BLAST score 296
E value 1.0e-26
Match length 88
% identity 62

NCBI Description GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS)

>gi_2564215_emb_CAA05162_ (AJ002062) glycyl-tRNA synthetase

[Arabidopsis thaliana]

Seq. No. 270350

Contig ID 24618 1.R1011

5'-most EST uC-zmroteosinte008d11b1

Method BLASTX
NCBI GI g2500378
BLAST score 341
E value 7.0e-32
Match length 73
% identity 82

NCBI Description 60S RIBOSOMAL PROTEIN L37

Seq. No. 270351

Contig ID 24618 2.R1011 5'-most EST tfd700571543.h1

Method BLASTX
NCBI GI g1350736
BLAST score 197
E value 5.0e-15
Match length 46
% identity 85

NCBI Description 60S RIBOSOMAL PROTEIN L37 >gi_629673_pir__S44313 ribosomal

protein L37 - tomato >gi 483586 emb CAA55674 (X79074)

ribosomal protein L37 [Lycopersicon esculentum]

Seq. No. 270352

Contig ID 24618_3.R1011 5'-most EST dyk700102539.h1

Seq. No. 270353

Contig ID 24620 1.R1011

5'-most EST uC-zmflmo17180g09a1

Seq. No. 270354

Contig ID 24620_2.R1011 5'-most EST wuj700282066.h1

Method BLASTX
NCBI GI g3335335
BLAST score 702
E value 9.0e-74
Match length 200



% identity

(AC004512) ESTs gb F14113 and gb T42122 come from this NCBI Description

region. [Arabidopsis thaliana]

Seq. No. 270355

24620 4.R1011 Contig ID

5'-most EST uC-zmflb73009c02a2

270356 Seq. No.

Contig ID 24622_1.R1011 5'-most EST rvt700550701.h1

270357 Seq. No.

24638 1.R1011 Contig ID

5'-most EST LIB3150-072-P2-K1-G9

Method BLASTX NCBI GI q4567197 BLAST score 1426 E value 1.0e-158

Match length 648 % identity 48

(AC007168) unknown protein [Arabidopsis thaliana] NCBI Description

270358 Seq. No.

Contig ID 24647 1.R1011

5'-most EST LIB3150-072-P2-K1-H9

270359 Seq. No.

24654 1.R1011 Contig ID

5'-most EST LIB3059-040-Q1-K1-E8

Method BLASTX NCBI GI g1514639 BLAST score 1126 E value 1.0e-123 Match length 252

81 % identity

NCBI Description (X85181) alpha-glucan phosphorylase [Spinacia oleracea]

270360 Seq. No.

24658 1.R1011 Contig ID

5'-most EST LIB3180-003-P2-M1-E11

270361 Seq. No.

24669 1.R1011 Contig ID wen700334641.hl 5'-most EST

Method BLASTX NCBI GI q1709205 BLAST score 796 E value 4.0e-85 Match length 202 % identity 76

NCBI Description MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 3 (IMP 3) (INOSITOL

MONOPHOSPHATASE 3) >gi_1098971 (U39059) myo-inositol

monophosphatase 3 [Lycopersicon esculentum]

270362 Seq. No.

Contig ID 24684 1.R1011



```
5'-most EST
                  xyt700344659.h1
                  270363
Seq. No.
                  24691 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73186h07a1
Method
                  BLASTX
NCBI GI
                  q3549669
BLAST score
                  908
E value
                  4.0e-98
Match length
                  226
% identity
                  77
NCBI Description
                  (AL031394) putative protein [Arabidopsis thaliana]
                  270364
Seq. No.
Contig ID
                  24701 1.R1011
5'-most EST
                  uC-zmflmo17269d11b1
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  37
E value
                  3.0e-11
Match length
                  37
% identity
                  100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  270365
Seq. No.
                  24718 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73267f06a1
                  270366
Seq. No.
                  24731 1.R1011
Contig ID
5'-most EST
                  LIB3150-073-P2-K1-D9
                  270367
Seq. No.
                  24732 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17213d08a1
Method
                  BLASTX
                  g3287683
NCBI GI
                  754
BLAST score
                  7.0e-80
E value
Match length
                  348
                  27
% identity
NCBI Description
                  (AC003979) Similar to apoptosis protein MA-3 gb D50465 from
                  Mus musculus. [Arabidopsis thaliana]
Seq. No.
                  270368
                  24750 1.R1011
Contig ID
5'-most EST
                  LIB3150-073-P2-K1-G3
Method
                  BLASTX
NCBI GI
                  g3763917
BLAST score
                  359
E value
                  8.0e-34
Match length
                  142
% identity
                  51
                  (AC004450) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

>gi_4531438_gb_AAD22123.1_AC006224_5 (AC006224)
hypothetical protein [Arabidopsis thaliana]



```
Seq. No.
                   270369
                  24760 1.R1011
Contig ID
                  LIB3150-073-P2-K1-H8
5'-most EST
Method
                  BLASTX
NCBI GI
                  q2262165
BLAST score
                  415
E value
                  2.0e-40
Match length
                  104
% identity
                  76
                   (AC002329) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
                   270370
Seq. No.
Contig ID
                   24768 1.R1011
5'-most EST
                  LIB3062-039-Q1-K1-G11
                  BLASTX
Method
                   g3560144
NCBI GI
BLAST score
                   249
                   3.0e-21
E value
Match length
                   151
% identity
                   39
                  (AL031534) putative asparagine synthase
NCBI Description
                   [Schizosaccharomyces pombe]
Seq. No.
                   270371
Contig ID
                   24769 1.R1011
5'-most EST
                   uC-zmflmo17179e02b1
Method
                   BLASTX
NCBI GI
                   q1711572
                   1311
BLAST score
                   1.0e-145
E value
Match length
                   292
                   85
% identity
                  SUCCINYL-COA LIGASE (GDP-FORMING), ALPHA-CHAIN PRECURSOR
NCBI Description
                   (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA)
                   >gi 1076415_pir__S30579 succinate--CoA ligase (GDP-forming)
                   (EC 6.2.1.4) alpha chain - Arabidopsis thaliana (fragment)
                   >gi 16510_emb_CAA48891_ (X69138) succinate--CoA ligase
                   (GDP-forming) [Arabidopsis thaliana]
                   270372
Seq. No.
                   24769 2.R1011
Contig ID
5'-most EST
                   uC-zmflb73276d09a1
                   BLASTX
Method
                   g3660467
NCBI GI
                   305
BLAST score
                   9.0e-28
E value
```

Match length 75 77 % identity

(AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis NCBI Description

thaliana]

Seq. No. 270373

24783 1.R1011 Contig ID

 $uC-zm\overline{f}lmo17130f07b1$ 5'-most EST

Method BLASTX NCBI GI g2244781



```
BLAST score
                    581
, E value
                    2.0e-59
 Match length
                    451
 % identity
                    22
                    (Z97335) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    270374
 Seq. No.
                    24784 2.R1011
 Contig ID
                    LIB3150-074-P1-N1-E1
 5'-most EST
                    BLASTN
 Method
                    q2894376
 NCBI GI
                    73
 BLAST score
 E value
                    1.0e-32
                    220
 Match length
                    88
 % identity
 NCBI Description Hordeum vulgare DNA for chromosome 4H
                    270375
 Seq. No.
 Contig ID
                    24799 1.R1011
                    LIB83-012-Q1-E1-E3
 5'-most EST
                    BLASTX
 Method
                    q1208454
 NCBI GI
                    160
 BLAST score
                    3.0e-21
 E value
                    116
 Match length
                    53
 % identity
                    (D64004) hypothetical protein [Synechocystis sp.]
 NCBI Description
 Seq. No.
                    270376
 Contig ID
                    24801 1.R1011
 5'-most EST
                    uC-zmflb73307b10b1
                    270377
 Seq. No.
 Contig ID
                    24801 2.R1011
                    nwy700444377.h1
  5'-most EST
 Method
                    BLASTX
                    g4325382
 NCBI GI
  BLAST score
                    1112
  E value
                    1.0e-122
  Match length
                    408
  % identity
                    52
                    (AF129075) T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA)
  NCBI Description
                    [Homo sapiens]
                    270378
  Seq. No.
                    24807 1.R1011
  Contig ID
                    fdz701161456.h1
  5'-most EST
                    270379
  Seq. No.
  Contig ID
                    24830 1.R1011
                    LIB3150-074-P2-K1-C3
  5'-most EST
                    270380
  Seq. No.
  Contig ID
                    24848 1.R1011
                    cat700016486.rl
  5'-most EST
```

BLASTX

g462234

Method NCBI GI



BLAST score 397 E value 2.0e-38 Match length 122 % identity 72

NCBI Description HISTONE H2A >gi_419741_pir__S30155 histone H2A - Norway spruce >gi 297871_emb CAA48030_ (X67819) histone H2A [Picea

abies]

Seq. No. 270381

Contig ID 24856_1.R1011

5'-most EST uC-zmflmo17158h11a1

Method BLASTX
NCBI GI g1730502
BLAST score 353
E value 7.0e-33
Match length 251
% identity 37

NCBI Description TRANSMEMBRANE PROTEIN PFT27 >gi_110903_pir__A31351 probable

transmembrane protein FT27 - mouse >gi_535682 (M23568)

transmembrane protein [Mus musculus]

Seq. No. 270382

Contig ID 24856 2.R1011

5'-most EST LIB3150-078-P1-N1-D3

Method BLASTX
NCBI GI g1730502
BLAST score 191
E value 2.0e-14
Match length 96
% identity 47

NCBI Description TRANSMEMBRANE PROTEIN PFT27 >gi_110903_pir__A31351 probable

transmembrane protein FT27 - mouse >gi_535682 (M23568)

transmembrane protein [Mus musculus]

Seq. No. 270383

Contig ID 24857_1.R1011 5'-most EST uer700581331.h1

Method BLASTX
NCBI GI g1168493
BLAST score 405
E value 2.0e-39
Match length 86
% identity 92

NCBI Description ARGINASE >gi 602422 (U15019) arginase [Arabidopsis

thaliana] $>g\overline{1}_4325373_gb_AAD17369_ (AF128396)$ Arabidopsis thaliana arginase (SW:P46637) (Pfam: PF00491, Score=419.6,

E=3.7e-142 N=1) [Arabidopsis thaliana]

Seq. No. 270384

Contig ID 24871_1.R1011 5'-most EST uC-zmflb73341b08a2

Seq. No. 270385

Contig ID 24884_1.R1011 5'-most EST wty700165274.h1

Method BLASTX NCBI GI g1352316



BLAST score 562 E value 1.0e-57 Match length 139 % identity 80

NCBI Description DR1 PROTEIN HOMOLOG >gi_633026_dbj_BAA07288_ (D38110) Dr1

[Arabidopsis thaliana]

Seq. No. 270386

Contig ID 24890 1.R1011

5'-most EST LIB3180-042-P2-M2-C2

Method BLASTX
NCBI GI g4539343
BLAST score 386
E value 3.0e-37
Match length 176
% identity 49

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 270387

Contig ID 24891 1.R1011

5'-most EST LIB3066-024-Q1-K1-G1

Seq. No. 270388

Contig ID 24891 2.R1011

5'-most EST uC-zmflmo17220h06b1

Seq. No. 270389

Contig ID 24894_1.R1011

5'-most EST uC-zmflMo17019g12b1

Method BLASTX
NCBI GI g2088647
BLAST score 1694
E value 0.0e+00
Match length 569
% identity 58

NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

>gi_3158394 (AF036340) LRR-containing F-box protein

[Arabidopsis thaliana]

Seq. No. 270390

Contig ID 24894 2.R1011

5'-most EST uC-zmflmo17190f07b1

Method BLASTX
NCBI GI g2088647
BLAST score 416
E value 9.0e-41
Match length 146
% identity 54

NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]

>gi_3158394 (AF036340) LRR-containing F-box protein

[Arabidopsis thaliana]

Seq. No. 270391

Contig ID 24894_4.R1011 5'-most EST uC-zmflb73276h11a1

Method BLASTX NCBI GI g2088647



BLAST score 145 E value 5.0e-09 Match length 58 % identity 60

NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana] >gi_3158394 (AF036340) LRR-containing F-box protein

[Arabidopsis thaliana]

Seq. No. 270392

Contig ID 24894_5.R1011

5'-most EST uC-zmflmo17314h05a1

Seq. No. 270393

Contig ID 24897 1.R1011

5'-most EST uC-zmflmo17041g09b1

Method BLASTX
NCBI GI 94586117
BLAST score 388
E value 4.0e-37
Match length 164
% identity 50

NCBI Description (AL049638) putative protein [Arabidopsis thaliana]

Seq. No. 270394

Contig ID 24932 1.R1011

5'-most EST LIB3136-036-Q1-K1-E4

Method BLASTX
NCBI GI g3334276
BLAST score 1299
E value 1.0e-143
Match length 474
% identity 54

NCBI Description AUTOANTIGEN NGP-1 >gi_179285 (L05425) autoantigen [Homo

sapiens]

Seq. No. 270395

Contig ID 24939 1.R1011 5'-most EST nbm700472966.h1

Method BLASTX
NCBI GI g2104908
BLAST score 1403
E value 1.0e-156
Match length 331

% identity 82

NCBI Description (Y07632) potassium channel [Zea mays]

Seq. No. 270396

Contig ID 24943_1.R1011 5'-most EST gwl700618084.h1

Method BLASTX
NCBI GI g2104535
BLAST score 780
E value 3.0e-83
Match length 193
% identity 77

NCBI Description (AF001308) T10M13.13 [Arabidopsis thaliana]



Seq. No. 270397

24946 1.R1011 Contig ID 5'-most EST ypc700805842.h1

270398 Seq. No.

24947 1.R1011 Contig ID

LIB3150-075-P2-N2-C4 5'-most EST

Method BLASTX g3924606 NCBI GI BLAST score 154 5.0e-10 E value Match length 60 % identity 55

(AF069442) hypothetical protein [Arabidopsis thaliana] NCBI Description

270399 Seq. No.

24952 1.R1011 Contig ID

5'-most EST LIB3150-095-P1-N1-F1

270400 Seq. No.

24956 1.R1011 Contig ID

uC-zmflmo17163b10b1 5'-most EST

270401 Seq. No.

24957 1.R1011 Contig ID

LIB3150-094-P1-N1-F7 5'-most EST

BLASTX Method NCBI GI g2129726 BLAST score 1101 1.0e-120 E value 305 Match length 73

% identity

NCBI Description RNA polymerase II third largest chain RPB35.5A -

Arabidopsis thaliana >gi 514318 (L34770) RNA polymerase II

third largest subunit [Arabidopsis thaliana]

>gi_4544370_gb_AAD22281.1_AC006920_5 (AC006920) RNA

polymerase II, third largest subunit [Arabidopsis thaliana]

270402 Seq. No.

24961 1.R1011 Contig ID qmh700026185.f15'-most EST BLASTX

Method NCBI GI q401238 BLAST score 993 1.0e-108 E value Match length 207 88 % identity

NCBI Description UBIQUITIN-ACTIVATING ENZYME E1 3 >gi 170686 (M90664)

ubiquitin activating enzyme [Triticum aestivum]

270403 Seq. No.

24991 1.R1011 Contig ID

uC-zmromo17009d08a1 5'-most EST

270404 Seq. No.

24991 3.R1011 Contig ID

5'-most EST LIB3150-075-P2-N2-G8



Seq. No. 270405

Contig ID 24992 1.R1011

5'-most EST LIB3150-075-P2-N2-G9

Method BLASTX
NCBI GI g3608155
BLAST score 412
E value 3.0e-40
Match length 169
% identity 50

NCBI Description (AC005314) putative RNA helicase [Arabidopsis thaliana]

Seq. No. 270406

Contig ID 24995 2.R1011

5'-most EST LIB3279-051-P1-K1-H12

Method BLASTX
NCBI GI g1730666
BLAST score 250
E value 3.0e-21
Match length 102
% identity 50

NCBI Description HYPOTHETICAL 32.2 KD PROTEIN IN ARE2-SWP73 INTERGENIC

REGION >gi 2131968 pir S63351 hypothetical protein YNR020c

- yeast (Saccharomyces cerevisiae)

>gi 1302506 emb CAA96299 (Z71635) ORF YNR020c

[Saccharomyces cerevisiae]

Seq. No. 270407

Contig ID 24997 1.R1011

5'-most EST LIB3150-075-P2-N2-H6

Seq. No. 270408

Contig ID 25004 1.R1011

5'-most EST LIB3069-004-Q1-K1-C11

Seq. No. 270409

Contig ID 25004_2.R1011 5'-most EST pwr700449346.h1

Seq. No. 270410

Contig ID 25006 1.R1011

5'-most EST LIB3182-001-P1-M1-A8

Method BLASTX
NCBI GI g3183237
BLAST score 239
E value 1.0e-19
Match length 264
% identity 27

NCBI Description HYPOTHETICAL 103.4 KD TRP-ASP REPEATS CONTAINING PROTEIN

C3D6.12 IN CHROMOSOME II >gi 2117308 emb_CAB09121.1_

(Z95620) trp asp repeat protein [Schizosaccharomyces pombe]

Seq. No. 270411

Contig ID 25007 1.R1011

5'-most EST LIB3150-076-P1-N1-A4

Method BLASTX NCBI GI g3395431



BLAST score 277 E value 1.0e-24 Match length 75 % identity 68

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 270412

Contig ID 25008 1.R1011 5'-most EST xjt700093452.h1

Seq. No. 270413

Contig ID 25008_2.R1011 5'-most EST fwa700100405.h1

Seq. No. 270414

Contig ID 25012_1.R1011

5'-most EST LIB3279-049-P1-K1-A8

Seq. No. 270415

Contig ID 25014 1.R1011

5'-most EST LIB3136-060-Q1-K1-D4

Seq. No. 270416

Contig ID 25028 1.R1011

5'-most EST LIB3136-013-Q1-K1-B12

Seq. No. 270417

Contig ID 25037_1.R1011 5'-most EST ymt700223870.h1

Seq. No. 270418

Contig ID 25045_1.R1011 5'-most EST xyt700343342.h1

Method BLASTX
NCBI GI g3600051
BLAST score 178
E value 1.0e-12
Match length 44
% identity 73

NCBI Description (AF080120) contains similarity to the single-strand binding

proteins family (Pfam: SSB.hmm, score: 24.02) [Arabidopsis

thaliana]

Seq. No. 270419

Contig ID 25061_1.R1011 5'-most EST fdz701165805.h1

Method BLASTX
NCBI GI g2102679
BLAST score 1045
E value 1.0e-114
Match length 272
% identity 69

NCBI Description (U07424) putative tRNA synthetase-like protein [Homo

sapiens] >gi_4104935_gb_AAD02221_ (AF042347) putative
phenylalanyl-tRNA synthetase alpha-subunit; PheHA [Homo

sapiens]



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270420
Seq. No.
                   25072 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73125c11b2
Method
                   BLASTX
NCBI GI
                   q984756
                   530
BLAST score
                   4.0e-67
E value
                   389
Match length
                   60
% identity
                  (Z54153) chilling-inducible protein [Oryza sativa]
NCBI Description
Seq. No.
                   270421
                   25072 4.R1011
Contig ID
5'-most EST
                   uC-zmflmo17261a09b1
                   270422
Seq. No.
Contig ID
                   25077 1.R1011
5'-most EST
                  LIB3059-036-Q1-K1-E12
                   270423
Seq. No.
                   25077 2.R1011
Contig ID
5'-most EST
                  LIB3059-038-Q1-K1-G8
Seq. No.
                   270424
                   25085_1.R1011
Contig ID
5'-most EST
                   uC-zmflb73362g12a2
Method
                   BLASTX
NCBI GI
                   g2760839
                   732
BLAST score
                   3.0e-77
E value
Match length
                   367
% identity
                   47
                  (AC003105) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
                   270425
Seq. No.
Contig ID
                   25105_1.R1011
5'-most EST
                   ymt700220280.h1
Method
                   BLASTX
                   g3043596
NCBI GI
BLAST score
                   408
E value
                   2.0e-39
Match length
                   150
% identity
                   55
NCBI Description
                  (AB011108) KIAA0536 protein [Homo sapiens]
                   270426
Seq. No.
Contig ID
                   25105 2.R1011
5'-most EST
                   xsy700209763.h1
Method
                   BLASTX
```

Method BLASTX
NCBI GI g2829911
BLAST score 227
E value 1.0e-18
Match length 80
% identity 54

NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No. 270427



Contig ID 25105_4.R1011 5'-most EST uC-zmflb73193d12b1

Method BLASTN
NCBI GI g22118
BLAST score 102
E value 8.0e-50
Match length 134
% identity 94

NCBI Description Z.mays DNA for Adh1-Cm allele

Seq. No. 270428

Contig ID 25105_8.R1011 5'-most EST afb700381737.h1

Seq. No. 270429

Contig ID 25112 1.R1011 5'-most EST ypc700803077.h1

Method BLASTX
NCBI GI g1495251
BLAST score 649
E value 4.0e-68
Match length 159
% identity 77

NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No. 270430

Contig ID 25115_1.R1011 5'-most EST pwf700321634.h1

Method BLASTX
NCBI GI g3334349
BLAST score 2229
E value 0.0e+00
Match length 538
% identity 79

NCBI Description GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS)

>gi_2564215_emb_CAA05162_ (AJ002062) glycyl-tRNA synthetase

[Arabidopsis thaliana]

Seq. No. 270431

Contig ID 25119_1.R1011 5'-most EST cyk700050849.f1

Seq. No. 270432

Contig ID 25126 1.R1011

5'-most EST LIB3150-076-P2-N2-H7

Method BLASTX
NCBI GI g2781345
BLAST score 418
E value 1.0e-40
Match length 230
% identity 41

NCBI Description (AC003113) F2401.2 [Arabidopsis thaliana]

Seq. No. 270433

Contig ID 25127_1.R1011 5'-most EST pmx700090410.h1

Method BLASTX



NCBI GI g2829894
BLAST score 265
E value 6.0e-33
Match length 158
% identity 46
NCBI Description (AC00231

NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No. 270434

Contig ID 25134 1.R1011

5'-most EST LIB3150-077-P1-N1-A3

Method BLASTX
NCBI GI g3128181
BLAST score 403
E value 3.0e-39
Match length 113
% identity 73

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 270435

Contig ID 25146 1.R1011

5'-most EST LIB3062-005-Q1-K1-G5

Seq. No. 270436

Contig ID 25149 2.R1011

5'-most EST LIB3150-077-P1-N1-D5

Seq. No. 270437

Contig ID 25158_1.R1011 5'-most EST fC-zmle700445240f7

Method BLASTX
NCBI GI g3341679
BLAST score 187
E value 2.0e-13
Match length 100
% identity 38

NCBI Description (AC003672) dynamin-like protein phragmoplastin 12

[Arabidopsis thaliana]

Seq. No. 270438

Contig ID 25161_1.R1011

5'-most EST LIB3150-077-P1-N1-F3

Seq. No. 270439

Contig ID 25161 2.R1011

5'-most EST uC-zmflmo17199b03b1

Method BLASTX
NCBI GI g3738310
BLAST score 207
E value 2.0e-16
Match length 137
% identity 36

NCBI Description (AC005309) putative nuclear protein [Arabidopsis thaliana]

Seq. No. 270440

Contig ID 25162_1.R1011

5'-most EST LIB3159-016-Q1-K1-H11

Method BLASTX

BLAST score

E value

245 1.0e-20



```
NCBI GI
                   q4567275
BLAST score
                   534
                   2.0e-54
E value
                   191
Match length
% identity
                   58
                  (AC006841) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   270441
Contig ID
                   25165 1.R1011
                   LIB3060-047-Q1-K1-G6
5'-most EST
Seq. No.
                   270442
                   25170 1.R1011
Contig ID
                   nbm70\overline{0}477251.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1531758
BLAST score
                   892
                   3.0e-96
E value
Match length
                   185
% identity
                   89
                   (X98772) AUX1 [Arabidopsis thaliana] >qi 3335360 (AC003028)
NCBI Description
                   unknown protein [Arabidopsis thaliana]
                   270443
Seq. No.
                   25170_2.R1011
Contig ID
                   wyr700240022.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1531758
BLAST score
                   620
                   1.0e-64
E value
Match length
                   147
                   78
% identity
NCBI Description
                  (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)
                   unknown protein [Arabidopsis thaliana]
                   270444
Seq. No.
Contig ID
                   25170 3.R1011
5'-most EST
                   LIB3150-077-P1-N1-G4
                   BLASTX
Method
                   g1531758
NCBI GI
BLAST score
                   737
E value
                   2.0e-78
Match length
                   157
                   87
% identity
NCBI Description
                  (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)
                   unknown protein [Arabidopsis thaliana]
Seq. No.
                   270445
Contig ID
                   25175 1.R1011
                   cat700021406.rl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4263776
```

Match length 82 % identity 57 NCBI Description (AC006068) unknown protein [Arabidopsis thaliana]



>gi_4510390_gb_AAD21478.1_ (AC007017) unknown protein
[Arabidopsis thaliana]

 Seq. No.
 270446

 Contig ID
 25198_1.R1011

 5'-most EST
 uC-zmflb73030c04b1

Seq. No. 270447

Contig ID 25213 1.R1011

5'-most EST uC-zmroteosinte005a06b1

Method BLASTX
NCBI GI g2209087
BLAST score 499
E value 4.0e-50
Match length 236
% identity 46

NCBI Description (AF000309) putative serine/threonine kinase [Colletotrichum

lindemuthianum]

Seq. No. 270448

Contig ID 25215 1.R1011

5'-most EST uC-zmflmo17235d02b1

Method BLASTX
NCBI GI g461753
BLAST score 352
E value 5.0e-33
Match length 82
% identity 87

NCBI Description ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

PRECURSOR >gi 419773 pir S31164 ATP-dependent ClpB

proteinase regulatory chain homolog precursor, chloroplast - garden pea >gi 169128 (L09547) nuclear encoded precursor

to chloroplast protein [Pisum sativum]

Seq. No. 270449

Contig ID 25230 1.R1011

5'-most EST LIB3150-107-P2-K1-B9

Method BLASTX
NCBI GI g4508082
BLAST score 275
E value 4.0e-24
Match length 64
% identity 80

NCBI Description (AC005882) Putative RNA polymerase II subunit Rpb10

[Arabidopsis thaliana]

Seq. No. 270450

Contig ID 25230 2.R1011

5'-most EST LIB3067-057-Q1-K1-G2

Method BLASTX
NCBI GI g2833375
BLAST score 343
E value 4.0e-32
Match length 71
% identity 89

NCBI Description DNA-DIRECTED RNA POLYMERASE II 8.2 KD POLYPEPTIDE (RPB10)

(RP10) (ABC10) >gi 533690 (U12133) RNA polymerase II



subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica napus]

 Seq. No.
 270451

 Contig ID
 25230_3.R1011

 5'-most EST
 xsy700209552.h1

 Method
 BLASTX

 NCBI GI
 g2833375

 BLAST score
 343

 E value
 4.0e-32

Match length 71 % identity 89

NCBI Description DNA-DIRECTED RNA POLYMERASE II 8.2 KD POLYPEPTIDE (RPB10)

(RP10) (ABC10) >gi_533690 (U12133) RNA polymerase II

subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica

napus]

Seq. No. 270452

Contig ID 25230_4.R1011 5'-most EST uC-zmflb73150g08b1

Method BLASTX
NCBI GI g2833375
BLAST score 254
E value 2.0e-25
Match length 71
% identity 86

NCBI Description DNA-DIRECTED RNA POLYMERASE II 8.2 KD POLYPEPTIDE (RPB10)

(RP10) (ABC10) >gi 533690 (U12133) RNA polymerase II

subunit RPB10 homolog; similar to yeast RNA polymerase II subunit RPB10, Swiss-Prot Accession Number P22139 [Brassica

napus]

Seq. No. 270453

Contig ID 25236_1.R1011 5'-most EST fwa700097642.h1

Method BLASTX
NCBI GI g1805617
BLAST score 699
E value 1.0e-100
Match length 242
% identity 79

NCBI Description (D49704) OSH44 transcript; homeobox gene [Oryza sativa]

Seq. No. 270454

Contig ID 25238_1.R1011

5'-most EST LIB3062-039-Q1-K1-A8

Method BLASTX
NCBI GI g1616741
BLAST score 299
E value 6.0e-27
Match length 120

% identity 49

NCBI Description (U60276) hASNA-I [Homo sapiens]

Seq. No. 270455



25238 2.R1011 Contig ID xsy700210153.hl 5'-most EST

Seq. No. 270456

Contig ID 25252 1.R1011 $wty70\overline{0}169381.h1$ 5'-most EST

270457 Seq. No.

25257 1.R1011 Contig ID $qmh70\overline{0}030066.f1$ 5'-most EST

270458 Seq. No.

Contig ID 25257 2.R1011 5'-most EST pmx700086106.hl

Method BLASTX g129916 NCBI GI BLAST score 304 E value 1.0e-27 Match length 65 94 % identity

PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY NCBI Description

phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase

(AA 1 - 401) [Triticum aestivum]

270459 Seq. No.

Contig ID 25258 1.R1011

5'-most EST LIB3069-029-Q1-K1-A7

Method BLASTX NCBI GI g3878119 372 BLAST score E value 2.0e-35 Match length 135 % identity 54

(Z49068) similar to GTP-binding protein; cDNA EST NCBI Description

> EMBL: M89111 comes from this gene; cDNA EST EMBL: D27709 comes from this gene; cDNA EST EMBL: D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST

yk353

Seq. No. 270460

25258 2.R1011 Contig ID 5'-most EST dyk700106138.h1

Method BLASTX NCBI GI g629881 BLAST score 234 E value 2.0e-22 Match length 183 % identity 38

myosin-related protein - slime mold (Physarum polycephalum)
>gi_511053_emb_CAA79924_ (Z21878) myosin-related protein NCBI Description

[Physarum polycephalum]

270461 Seq. No.

25276 1.R1011 Contig ID

5'-most EST uC-zmflmo17278g06b1

Method BLASTX



NCBI GI g2244847
BLAST score 552
E value 5.0e-56
Match length 370
% identity 37
NCBI Description (297337)

NCBI Description (Z97337) hydroxyproline-rich glycoprotein homolog

[Arabidopsis thaliana]

Seq. No. 270462

Contig ID 25276 2.R1011

5'-most EST LIB3150-078-P1-N1-D5

Seq. No. 270463

Contig ID 25284_1.R1011 5'-most EST hvj700618954.h1

Method BLASTX
NCBI GI g3335361
BLAST score 431
E value 1.0e-42
Match length 100
% identity 81

NCBI Description (AC003028) putative acyltransferase [Arabidopsis thaliana]

Seq. No. 270464

Contig ID 25307 1.R1011

5'-most EST LIB3150-078-P2-N2-C2

Method BLASTX
NCBI GI g2244850
BLAST score 496
E value 7.0e-50
Match length 178
% identity 61

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 270465

Contig ID 25307_2.R1011 5'-most EST LIB143-020-Q1-E1-F1

Method BLASTX
NCBI GI g2244850
BLAST score 239
E value 1.0e-19
Match length 76
% identity 58

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 270466

Contig ID 25313 1.R1011

5'-most EST LIB3060-054-Q1-K1-C12

Method BLASTX
NCBI GI g1170029
BLAST score 1198
E value 1.0e-132
Match length 245
% identity 94

NCBI Description GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA)

(GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)

>gi 100581 pir A35789 glutamate-1-semialdehyde

Seq. No.

Contig ID

5'-most EST



2,1-aminomutase (EC 5.4.3.8) - barley >gi 506383 (M31545) glutamate 1-semialdehyde aminotransferase [Hordeum vulgare]

```
270467
Seq. No.
                  25315 1.R1011
Contig ID
                  yyf700349183.hl
5'-most EST
Method
                  BLASTX
                  g2117355
NCBI GI
                  1530
BLAST score
                  1.0e-170
E value
                  505
Match length
                  59
% identity
                  mitochondrial processing peptidase (EC 3.4.99.41) alpha-II
NCBI Description
                  chain precursor - potato >gi_587562_emb_CAA56520_ (X80236)
                  mitochondrial processing peptidase [Solanum tuberosum]
                   270468
Seq. No.
                   25321 1.R1011
Contig ID
                  LIB3062-049-Q1-K1-H3
5'-most EST
                   BLASTX
Method
                   g4567247
NCBI GI
BLAST score
                   265
                   4.0e-23
E value
Match length
                   77
                   64
% identity
                   (AC007070) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   270469
                   25323 1.R1011
Contig ID
                   LIB3137-030-Q1-K1-E2
5'-most EST
                   BLASTX
Method
                   g2578033
NCBI GI
BLAST score
                   163
                   4.0e-11
E value
                   64
Match length
                   55
% identity
                  (X97016) omega-6 desaturase [Gossypium hirsutum]
NCBI Description
                   270470
Seq. No.
                   25332 1.R1011
Contig ID
                   LIB3150-079-P1-N1-A12
5'-most EST
                   BLASTX
Method
                   g1477480
NCBI GI
BLAST score
                   531
E value
                   7.0e-76
                   186
Match length
                   48
% identity
                   (U40341) carbamoyl phosphate synthetase large chain
NCBI Description
                   [Arabidopsis thaliana]
                   270471
Seq. No.
                   25337 1.R1011
Contig ID
                   LIB3069-053-Q1-K1-C5
5'-most EST
                   270472
```

37661

25337 3.R1011

uwc700150174.h1



Seq. No. 270473

Contig ID 25352 1.R1011

5'-most EST uC-zmroteosinte038a02b1

Method BLASTX
NCBI GI g3928869
BLAST score 160
E value 1.0e-10
Match length 154
% identity 32

NCBI Description (AF093420) Hsp70 binding protein HspBP1 [Homo sapiens]

Seq. No. 270474

Contig ID 25352_2.R1011 5'-most EST rvt700552355.h1

Seq. No. 270475

Contig ID 25374_1.R1011

5'-most EST LIB3150-079-P2-N2-C10

Seq. No. 270476

Contig ID 25384_1.R1011

5'-most EST LIB3150-079-P2-N2-F10

Seq. No. 270477

Contig ID 25388 1.R1011

5'-most EST LIB3180-035-P2-M2-C3

Method BLASTX
NCBI GI g3763917
BLAST score 273
E value 4.0e-24
Match length 110
% identity 52

NCBI Description (AC004450) hypothetical protein [Arabidopsis thaliana]

>gi_4531438_gb_AAD22123.1_AC006224_5 (AC006224)

hypothetical protein [Arabidopsis thaliana]

Seq. No. 270478

Contig ID 25393_1.R1011 5'-most EST uC-zmflb73069c10a1

Method BLASTX
NCBI GI g2282584
BLAST score 1006
E value 1.0e-109
Match length 209
% identity 91

NCBI Description (U76259) elongation factor 1-alpha [Zea mays]

Seq. No. 270479

Contig ID 25399 1.R1011

5'-most EST LIB3067-030-Q1-K1-H4

Method BLASTX
NCBI GI g2462834
BLAST score 222
E value 9.0e-18
Match length 142
% identity 40



NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 270480

25405 1.R1011 Contig ID

LIB3150-080-P2-N2-B11 5'-most EST

Seq. No. 270481

25407 1.R1011 Contig ID

LIB3150-080-P2-N2-B4 5'-most EST

270482 Seq. No.

Contig ID 25422 1.R1011

LIB3150-080-P2-N2-D10 5'-most EST

Seq. No. 270483

Contig ID 25459 1.R1011

uC-zmflmo17068b11b2 5'-most EST

Method BLASTX g2739044 NCBI GI BLAST score 932

1.0e-101 E value Match length 234

% identity 73 (AF024651) polyphosphoinositide binding protein Sshlp NCBI Description

[Glycine max]

270484 Seq. No.

Contig ID 25481 1.R1011 5'-most EST xjt700095259.h1

BLASTX Method g2773363 NCBI GI 153 BLAST score 2.0e-09 E value 318 Match length

24 % identity

(AF041382) microtubule binding protein D-CLIP-190 NCBI Description

[Drosophila melanogaster]

270485 Seq. No.

25483 1.R1011 Contig ID

5'-most EST LIB3150-081-P1-N1-G1

270486 Seq. No.

25492 1.R1011 Contig ID

5'-most EST LIB3150-081-P2-N2-A11

270487 Seq. No.

Contig ID 25493 1.R1011

5'-most EST LIB3150-081-P2-N2-A12

Seq. No. 270488

25498 1.R1011 Contig ID

5'-most EST uC-zmflmo17054a01a1

BLASTX Method NCBI GI q4558563 BLAST score 358 E value 1.0e-33



Match length 84 % identity 81

NCBI Description (AC007138) putative NifU-like metallocluster assembly

factor [Arabidopsis thaliana]

Seq. No. 270489

Contig ID 25508_1.R1011 5'-most EST uC-zmflb73276e10a1

Seq. No. 270490

Contig ID 25524_1.R1011 5'-most EST hvj700623438.h1

Method BLASTX
NCBI GI g3913464
BLAST score 539
E value 5.0e-55
Match length 120

% identity 78

NCBI Description BETAINE-ALDEHYDE DEHYDROGENASE (BADH)

>gi 2244604 dbj_BAA21098_ (AB001348) betaine aldehyde

dehydrogenase [Oryza sativa]

Seq. No. 270491

Contig ID 25538_1.R1011 5'-most EST nbm700472668.h1

Method BLASTX
NCBI GI g3132477
BLAST score 978
E value 1.0e-106
Match length 315

Match length 315 % identity 35

NCBI Description (AC003096) unknown protein [Arabidopsis thaliana]

Seq. No. 270492

Contig ID 25541_1.R1011 5'-most EST qmh700026585.f1

Method BLASTX
NCBI GI g1077251
BLAST score 268
E value 4.0e-23
Match length 83
% identity 53

NCBI Description hypothetical protein YDL008w - yeast (Saccharomyces

cerevisiae) >gi_683689_emb_CAA88351_ (Z48432) unknown [Saccharomyces cerevisiae] >gi_1430969_emb_CAA98564_

(Z74056) ORF YDL008w [Saccharomyces cerevisiae]

Seq. No. 270493

Contig ID 25544 1.R1011

5'-most EST LIB3150-082-P1-N1-A4

Seq. No. 270494

Contig ID 25546_1.R1011 5'-most EST uC-zmflb73012d12b1

Method BLASTX NCBI GI g2618684 BLAST score 173



E value 3.0e-12 Match length 67 % identity 54

NCBI Description (AC002510) putative

UDP-N-acetylglucosamine--dolichyl-phosphate

N-acetylglucosaminephosphotransferase [Arabidopsis thaliana] >gi 3241947 (AC004625) putative

UDP-N-acetylglucosamine--dolichyl-phosphate

N-acetylglucosaminephosphotransferase [Arabidopsis

thaliana]

Seq. No. 270495

Contig ID 25550_1.R1011 5'-most EST uC-zmflb73068f07b1

Seq. No. 270496

Contig ID 25561 1.R1011

5'-most EST LIB3150-082-P1-N1-D2

Seq. No. 270497

Contig ID 25587_1.R1011

5'-most EST uC-zmflmo17355g03a1

Seq. No. 270498

Contig ID 25590 1.R1011

5'-most EST LIB3150-082-P2-N2-C2

Seq. No. 270499

Contig ID 25592 1.R1011

5'-most EST uC-zmflmo17157h05a1

Seq. No. 270500

Contig ID 25594 1.R1011

5'-most EST LIB3150-082-P2-N2-D11

Seq. No. 270501

Contig ID 25594_2.R1011 5'-most EST clt700043791.f1

Seq. No. 270502

Contig ID 25666 1.R1011

5'-most EST LIB3150-083-P2-N2-B2

Method BLASTX
NCBI GI g4454011
BLAST score 806
E value 6.0e-86
Match length 355
% identity 50

NCBI Description (AL035396) putative protein [Arabidopsis thaliana]

Seq. No. 270503

Contig ID 25666_2.R1011 5'-most EST dyk700103782.h1

Method BLASTX
NCBI GI g4454011
BLAST score 198
E value 5.0e-15



Match length 168 % identity 35

NCBI Description (AL035396) putative protein [Arabidopsis thaliana]

Seq. No. 270504

Contig ID 25669 1.R1011

5'-most EST uC-zmflmo17171h10b1

Seq. No. 270505

Contig ID 25672_1.R1011 5'-most EST uC-zmflb73171b01b1

Method BLASTX
NCBI GI g1841357
BLAST score 511
E value 2.0e-51
Match length 213
% identity 58

NCBI Description (D85382) mitochondrial ribosomal protein S11 (nuclear

encoded) [Oryza sativa]

Seq. No. 270506

Contig ID 25672 2.R1011

5'-most EST LIB3150-083-P2-N2-B9

Seq. No. 270507

Contig ID 25675 1.R1011

5'-most EST uC-zmflmo17223c05a1

Seq. No. 270508

Contig ID 25684_1.R1011

5'-most EST LIB3150-083-P2-N2-D3

Method BLASTX
NCBI GI g3327196
BLAST score 389
E value 5.0e-37
Match length 151
% identity 49

NCBI Description (AB014591) KIAA0691 protein [Homo sapiens]

Seq. No. 270509

Contig ID 25692 1.R1011

5'-most EST LIB3150-083-P2-N2-E12

Method BLASTX
NCBI GI g3786009
BLAST score 1013
E value 1.0e-110
Match length 272
% identity 74

NCBI Description (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No. 270510

Contig ID 25697 1.R1011

5'-most EST uC-zmflmo17101c02b1

Seq. No. 270511

Contig ID 25703 1.R1011

5'-most EST LIB3150-110-P2-K1-H12



Seq. No. 270512

25704 1.R1011 Contig ID

5'-most EST LIB3150-083-P2-N2-F8

270513 Seq. No.

25705 1.R1011 Contig ID

5'-most EST LIB3150-083-P2-N2-F9

Seq. No. 270514

25708 1.R1011 Contig ID uC-zmflb73021e12a2 5'-most EST

BLASTX Method q2462781 NCBI GI 352 BLAST score 4.0e-33 E value Match length 87 % identity

(U73175) carbamoyl phosphate synthetase small subunit NCBI Description

[Arabidopsis thaliana]

270515 Seq. No.

25708 3.R1011 Contig ID 5'-most EST $xjt70\overline{0}096989.h1$

270516 Seq. No.

25709 1.R1011 Contig ID

LIB3150-083-P2-N2-G3 5'-most EST

Method BLASTN NCBI GI q3763846 BLAST score 43 6.0e-15 E value Match length 59

93 % identity

NCBI Description Oryza sativa OsENOD93a mRNA for early nodulin, complete cds

270517 Seq. No.

25727 1.R1011 Contig ID 5'-most EST uC-zmflb73151f04a2

270518 Seq. No.

25732 1.R1011 Contig ID

 $LIB31\overline{5}0-094-P2-K1-B3$ 5'-most EST

Method BLASTX NCBI GI g126896 BLAST score 1007 1.0e-109 E value Match length 218 % identity 91

NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR

>gi_319831_pir__DEPUMW malate dehydrogenase (EC 1.1.1.37)

precursor, mitochondrial - watermelon

>gi 18297_emb_CAA35239_ (X17362) precursor protein (AA -27

to 320) [Citrullus lanatus]

270519 Seq. No.

25732 2.R1011 Contig ID



95

79

Match length

NCBI Description

% identity

```
5'-most EST
                  LIB3150-084-P2-N2-B12
Method
                  BLASTN
NCBI GI
                  g18296
BLAST score
                  39
E value
                  1.0e-12
                  79
Match length
                  87
% identity
                  Water melon mMDH mRNA for mitochondrial malate
NCBI Description
                  dehydrogenase (EC 1.1.1.37)
                  270520
Seq. No.
                  25746 1.R1011
Contig ID
                  LIB3150-084-P2-N2-C5
5'-most EST
                  270521
Seq. No.
                  25747 1.R1011
Contig ID
                  LIB3150-109-P2-K1-H5
5'-most EST
Seq. No.
                   270522
Contig ID
                   25747 2.R1011
                   uC-zmflb73041q09b1
5'-most EST
                   BLASTX
Method
                   g2194123
NCBI GI
BLAST score
                   209
                   3.0e-16
E value
                   115
Match length
                   44
% identity
                   (AC002062) Similar to Secale chloroplast ribosomal protein
NCBI Description
                   L12 (gb SCL121A). EST gb H36579 comes from this gene.
                   [Arabidopsis thaliana]
                   270523
Seq. No.
                   25747 3.R1011
Contig ID
                   bdu700382915.h1
5'-most EST
                   270524
Seq. No.
                   25749 1.R1011
Contig ID
5'-most EST
                   LIB3150-084-P2-N2-D11
                   BLASTX
Method
                   g3641252
NCBI GI
                   289
BLAST score
                   8.0e-26
E value
Match length
                   100
                   58
% identity
                  (AF053127) leucine-rich receptor-like protein kinase [Malus
NCBI Description
                   domestica]
                   270525
Seq. No.
                   25749 2.R1011
Contig ID
5'-most EST
                   yyf700349624.hl
Method
                   BLASTX
                   g3641252
NCBI GI
                   388
BLAST score
                   7.0e-38
E value
```

(AF053127) leucine-rich receptor-like protein kinase [Malus



domestica]

270526 Seq. No. 25766 1.R1011 Contig ID LIB3150-094-P2-K1-F3 5'-most EST BLASTX Method NCBI GI g3413717 BLAST score 147 4.0e-09 E value Match length 37 70 % identity NCBI Description

NCBI Description (AC004747) unknown protein [Arabidopsis thaliana] >gi 3643590 (AC005395) unknown protein [Arabidopsis

thaliana]

Seq. No. 270527

Contig ID 25766 2.R1011

5'-most EST LIB3150-084-P2-N2-F9

Seq. No. 270528

Contig ID 25781 1.R1011

5'-most EST LIB3150-085-P1-N1-A3

Seq. No. 270529

Contig ID 25790_1.R1011

5'-most EST LIB3150-085-P1-N1-E2

Seq. No. 270530

Contig ID 25792 1.R1011

5'-most EST LIB3150-085-P1-N1-F2

Seq. No. 270531

Contig ID 25817_1.R1011

5'-most EST LIB3150-086-P1-N1-E4

Seq. No. 270532

Contig ID 25829_1.R1011 5'-most EST yyf700351011.h1

Method BLASTX
NCBI GI g2119045
BLAST score 406
E value 1.0e-39

E value 1.00 Match length 112 % identity 70

NCBI Description small nuclear ribonucleoprotein U1A - potato

>gi 1050840_emb_CAA90282_ (Z49990) UlsnRNP-specific

protein, U1A [Solanum tuberosum]

Seq. No. 270533

Contig ID 25852 1.R1011

5'-most EST LIB3150-086-P2-N2-C8

Seq. No. 270534

Contig ID 25853_1.R1011 5'-most EST cyk700051069.f1

Method BLASTX NCBI GI 94158230



BLAST score 1473 E value 1.0e-164 Match length 306 % identity 89

NCBI Description (Y18625) amylogenin [Triticum aestivum]

Seq. No. 270535

Contig ID 25853 2.R1011

5'-most EST LIB3180-017-P2-M1-H12

Method BLASTX
NCBI GI g4158219
BLAST score 370
E value 3.0e-35
Match length 85
% identity 87

NCBI Description (Y18623) amylogenin [Oryza sativa]

Seq. No. 270536

Contig ID 25862 1.R1011

5'-most EST LIB3150-086-P2-N2-E12

Method BLASTX
NCBI GI g4519671
BLAST score 198
E value 4.0e-15
Match length 65
% identity 62

NCBI Description (AB017693) transfactor [Nicotiana tabacum]

Seq. No. 270537

Contig ID 25877 1.R1011

5'-most EST LIB3150-087-P2-K1-A12

Seq. No. 270538

Contig ID 25926 1.R1011

5'-most EST LIB3150-088-P2-K1-A5

Method BLASTX
NCBI GI g3927836
BLAST score 346
E value 3.0e-32
Match length 171
% identity 40

NCBI Description (AC005727) unknown protein [Arabidopsis thaliana]

Seq. No. 270539

Contig ID 25926_2.R1011

5'-most EST uC-zmflmo17202a03a1

Method BLASTX
NCBI GI g3927836
BLAST score 172
E value 5.0e-12
Match length 81
% identity 42

NCBI Description (AC005727) unknown protein [Arabidopsis thaliana]

Seq. No. 270540

Contig ID 25928_1.R1011 5'-most EST cat700021821.r1



Seq. No. 270541

Contig ID 25928_2.R1011 5'-most EST uC-zmflb73167d07a1

Seq. No. 270542

Contig ID 25948 1.R1011

5'-most EST LIB3150-088-P2-K1-D6

Seq. No. 270543

Contig ID 25952_1.R1011

5'-most EST LIB3150-088-P2-K1-E1

Seq. No. 270544

Contig ID 25953_1.R1011 5'-most EST uC-zmflb73412d01a1

Seq. No. 270545

Contig ID 25963 1.R1011

5'-most EST LIB3157-011-Q1-K1-E11

Seq. No. 270546

Contig ID 25967 2.R1011 5'-most EST uC-zmflb73023g10a1

Method BLASTX
NCBI GI g4115937
BLAST score 278
E value 1.0e-24
Match length 67
% identity 70

NCBI Description (AF118223) contains similarity to human PCF11p homolog

(GB:AF046935) [Arabidopsis thaliana]

Seq. No. 270547

Contig ID 25968_1.R1011 5'-most EST hbs701185127.h1

Method BLASTX
NCBI GI g2499614
BLAST score 1617
E value 0.0e+00
Match length 365
% identity 81

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG NTF3 (P43)

>gi_481830_pir__S39559 mitogen-activated protein kinase 3
homolog ntf3 - common tobacco >gi 406751 emb CAA49592_

(X69971) NTF3 [Nicotiana tabacum]

Seq. No. 270548

Contig ID 25968 2.R1011

5'-most EST LIB3150-088-P2-K1-F3

Method BLASTX
NCBI GI g2499606
BLAST score 290
E value 8.0e-26
Match length 70
% identity 79

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 2 (MAP KINASE 2)



(ATMPK2) >gi_533281_dbj_BAA03536_ (D14714) ATMPK2 [Arabidopsis thaliana]

Seq. No. 270549

Contig ID 25970 1.R1011

5'-most EST LIB3150-088-P2-K1-F5

Seq. No. 270550

Contig ID 25974 1.R1011

5'-most EST LIB3150-088-P2-K1-G1

Seq. No. 270551

Contig ID 25984 1.R1011

5'-most EST LIB3157-003-Q1-K1-H9

Seq. No. 270552

Contig ID 25984 2.R1011

5'-most EST LIB3150-088-P2-K1-H6

Seq. No. 270553

Contig ID 25985 1.R1011

5'-most EST uC-zmflmo17398h08a1

Seq. No. 270554

Contig ID 25985 2.R1011

5'-most EST LIB3150-088-P2-K1-H9

Seq. No. 270555

Contig ID 26000_1.R1011 5'-most EST wty700165457.h1

Method BLASTX
NCBI GI g2982297
BLAST score 598
E value 7.0e-62
Match length 129
% identity 88

NCBI Description (AF051233) KIAA0107-like protein [Picea mariana]

Seq. No. 270556

Contig ID 26002 1.R1011

5'-most EST LIB3150-089-P1-N1-D11

Method BLASTX
NCBI GI 94262183
BLAST score 752
E value 9.0e-80
Match length 186
% identity 79

NCBI Description (AC005508) 51434 [Arabidopsis thaliana]

Seq. No. 270557

Contig ID 26009_1.R1011

5'-most EST LIB3067-043-Q1-K1-D1

Method BLASTX
NCBI GI g2098575
BLAST score 427
E value 2.0e-41
Match length 112

NCBI GI

BLAST score

g4406775



```
% identity
NCBI Description
                  (AC002115) F25451_2 [Homo sapiens]
                  270558
Seq. No.
Contig ID
                  26009 2.R1011
5'-most EST
                  LIB3136-050-Q1-K1-D8
Method
                  BLASTX
                  q2098575
NCBI GI
                  210
BLAST score
                  2.0e-16
E value
                  62
Match length
                  65
% identity
                  (AC002115) F25451 2 [Homo sapiens]
NCBI Description
                  270559
Seq. No.
                  26009 3.R1011
Contig ID
5'-most EST
                  tzu700205047.h1
Seq. No.
                  270560
                  26021 1.R1011
Contig ID
                  LIB3150-089-P1-N1-F7
5'-most EST
Method
                  BLASTX
                  q3293547
NCBI GI
BLAST score
                  218
E value
                  3.0e-17
Match length
                  224
                  29
% identity
NCBI Description (AF072709) putative oxidoreductase [Streptomyces lividans]
Seq. No.
                  270561
                  26027 1.R1011
Contig ID
5'-most EST
                  LIB3118-006-Q1-K1-G1
                  BLASTX
Method
NCBI GI
                  a3688172
BLAST score
                  170
                  5.0e-12
E value
Match length
                  54
% identity
NCBI Description
                  (AL031804) putative protein [Arabidopsis thaliana]
Seq. No.
                  270562
                  26041 1.R1011
Contig ID
5'-most EST
                  ceu700431154.h1
Method
                  BLASTX
NCBI GI
                  g4567228
BLAST score
                  159
                  4.0e-10
E value
Match length
                  45
                  62
% identity
NCBI Description
                  (AC007119) unknown protein [Arabidopsis thaliana]
                  270563
Seq. No.
                  26048 1.R1011
Contig ID
5'-most EST
                  yne700379317.h1
Method
                  BLASTX
```



E value 4.0e-14
Match length 81
% identity 51
NCBI Description (AC00683

CBI Description (AC006836) unknown protein [Arabidopsis thaliana]

Seq. No. 270564 Contig ID 26048_2.R1011

5'-most EST uC-zmroteosinte074a04b1

Method BLASTX
NCBI GI g4406775
BLAST score 178
E value 1.0e-12
Match length 180
% identity 32

NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]

Seq. No. 270565

Contig ID 26062_1.R1011 5'-most EST uC-zmflmo17056d12a1

Method BLASTX
NCBI GI g2501603
BLAST score 167
E value 2.0e-11
Match length 123
% identity 36

NCBI Description HYPOTHETICAL 77.0 KD PROTEIN IN HES1-SEC63 INTERGENIC

REGION >gi_2132095_pir__S67136 hypothetical protein YOR243c

- yeast (Saccharomyces cerevisiae)

>gi 1420554 emb CAA99464 (Z75151) ORF YOR243c

[Saccharomyces cerevisiae]

Seq. No. 270566

Contig ID 26073_1.R1011

5'-most EST LIB31 $\overline{5}0-090-P2-K1-B9$

Method BLASTX
NCBI GI g2191141
BLAST score 465
E value 3.0e-46
Match length 162
% identity 62

NCBI Description (AF007269) A_IG002N01.21 gene product [Arabidopsis

thaliana]

Seq. No. 270567

Contig ID 26073_2.R1011 5'-most EST uC-zmflb73284h03a1

Method BLASTX
NCBI GI g2191141
BLAST score 180
E value 3.0e-13
Match length 45
% identity 87

NCBI Description (AF007269) A IG002N01.21 gene product [Arabidopsis

thaliana]

Seq. No. 270568

Contig ID 26086 1.R1011



uC-zmroteosinte082e02b2 5'-most EST Method BLASTX q322639 NCBI GI BLAST score 248 6.0e-21E value 79 Match length 52 % identity beta-1,3-glucanase homolog (clone A20) - rape (fragment) NCBI Description >gi_17734_emb_CAA49515_ (X69889) beta-1,3-glucanase homologue [Brassica napus] 270569 Seq. No. Contig ID 26088 1.R1011 uC-zmflmo17019f10a1 5'-most EST BLASTX Method q3241943 NCBI GI BLAST score 1115 1.0e-122 E value Match length 251 % identity (AC004625) hypothetical protein [Arabidopsis thaliana] NCBI Description 270570 Seq. No. Contig ID 26095 1.R1011 LIB3150-090-P2-K1-G4 5'-most EST 270571 Seq. No. 26096 1.R1011 Contig ID 5'-most EST LIB3150-090-P2-K1-H11 270572 Seq. No. 26106 1.R1011 Contig ID ymt700219340.h1 5'-most EST BLASTX Method q3170230 NCBI GI BLAST score 455 4.0e-45 E value 210 Match length % identity 48 (AF041848) fructose-6-phosphate 2-kinase NCBI Description /fructose-2,6-bisphosphatase [Spinacia oleracea] 270573 Seq. No. 26110 1.R1011 Contig ID $uC-zm\overline{f}1b73202e06b1$ 5'-most EST 270574 Seq. No. 26116 1.R1011 Contig ID LIB3150-091-P1-N1-C11 5'-most EST 270575 Seq. No.

26120 1.R1011 Contig ID

LIB3150-091-P1-N1-D2 5'-most EST

270576 Seq. No.

26122 1.R1011 Contig ID 5'-most EST qmh700027177.f1



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270577
Seq. No.
                  26129 1.R1011
Contig ID
                  pmx700083308.hl
5'-most EST
                  BLASTX
Method
                  g3283220
NCBI GI
                  274
BLAST score
                  9.0e-24
E value
                  237
Match length
                  29
% identity
                  (AF061241) splicing factor hPRP17 [Homo sapiens]
NCBI Description
                  270578
Seq. No.
                  26131 1.R1011
Contig ID
                  ymt700221352.h1
5'-most EST
Method
                  BLASTX
                  g2335108
NCBI GI
BLAST score
                  1585
                  1.0e-177
E value
                   465
Match length
% identity
                   64
                  (AC002339) putative isulinase [Arabidopsis thaliana]
NCBI Description
                  270579
Seq. No.
                   26131 2.R1011
Contig ID
                  uC-zmflmo17161q04b1
5'-most EST
Method
                  BLASTX
                  g2335108
NCBI GI
                   566
BLAST score
                   3.0e-58
E value
Match length
                  157
% identity
                   61
                  (AC002339) putative isulinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   270580
                   26132 1.R1011
Contig ID
                   LIB3150-091-P1-N1-E7
5'-most EST
                   270581
Seq. No.
Contig ID
                   26133 1.R1011
5'-most EST
                   uwc700152366.h1
Seq. No.
                   270582
                   26138 1.R1011
Contig ID
                   pmx700083474.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1330254
BLAST score
                   1467
                   0.0e+00
E value
Match length
                   590
```

NCBI Description (D85039) calcium-dependent protein kinase [Zea mays]

 Seq. No.
 270583

 Contig ID
 26138_2.R1011

 5'-most EST
 uC-zmflmo17240g08a1

96

Method BLASTX

% identity



NCBI GI g1330254 BLAST score 262 E value 8.0e-23 Match length 54 % identity 94

NCBI Description (D85039) calcium-dependent protein kinase [Zea mays]

Seq. No. 270584

Contig ID 26138_3.R1011 5'-most EST xsy700209923.h1

Method BLASTN
NCBI GI g1330253
BLAST score 194
E value 1.0e-105
Match length 361
% identity 89

% identity 89
NCBI Description Zea mays calcium-dependent protein kinase mRNA, complete

cds

Seq. No. 270585

Contig ID 26145_1.R1011 5'-most EST nbm700475303.h1

Seq. No. 270586

Contig ID 26148_1.R1011 5'-most EST clt700045416.f1

Method BLASTX
NCBI GI g1351834
BLAST score 761
E value 1.0e-80
Match length 243
% identity 59

NCBI Description PROBABLE ATP-DEPENDENT TRANSPORTER YCF16 >gi_1016162

(U30821) ABC transporter subunit [Cyanophora paradoxa]

Seq. No. 270587

Contig ID 26148 2.R1011

5'-most EST LIB3180-024-P2-M1-A3

Method BLASTX
NCBI GI g3024873
BLAST score 155
E value 3.0e-10
Match length 50
% identity 64

NCBI Description PROBABLE ATP-DEPENDENT TRANSPORTER SLR0075

>gi 1001706 dbj BAA10543 (D64004) ABC transporter subunit

[Synechocystis sp.]

Seq. No. 270588

Contig ID 26152 1.R1011

5'-most EST uC-zmflmo17166d08b1

Seq. No. 270589

Contig ID 26172_1.R1011

5'-most EST LIB3150-092-P1-N1-C6

Seq. No. 270590



Contig ID 26175_1.R1011 5'-most EST pmx700086532.h1

Method BLASTX
NCBI GI g2244834
BLAST score 637
E value 6.0e-66
Match length 457
% identity 40

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

5'-most EST wty70016602 Method BLASTX NCBI GI g4220485

BLAST score 206 E value 7.0e-16 Match length 79 % identity 47

NCBI Description (AC006069) putative beta-1,3-glucanase [Arabidopsis

thaliana]

Seq. No. 270592

Contig ID 26192_1.R1011 5'-most EST uwc700149612.h1

Method BLASTN
NCBI GI g1402874
BLAST score 58

E value 2.0e-23
Match length 114
% identity 88

NCBI Description A.thaliana 81kb genomic sequence

Seq. No. 270593

Contig ID 26196 1.R1011

5'-most EST uC-zmflmo170114e05b1

Seq. No. 270594

Contig ID 26196_3.R1011 5'-most EST uC-zmflb73055d10b1

Seq. No. 270595

Contig ID 26202 1.R1011

5'-most EST LIB3150-092-P2-K1-A5

Seq. No. 270596

Contig ID 26203_1.R1011 5'-most EST uC-zmflb73031f09b1

Method BLASTX
NCBI GI g2497540
BLAST score 1187
E value 1.0e-130
Match length 297

Match length 297 % identity 78

NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME G

Seq. No. 270597



Contig ID 26203 2.R1011

5'-most EST LIB30 $\overline{6}1-054-Q1-K1-F9$

Method BLASTX
NCBI GI g2497542
BLAST score 1174
E value 1.0e-129
Match length 263
% identity 86

NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR

>gi_629696_pir__S44287 pyruvate kinase, plastid - common tobacco >gi_482938_emb_CAA82223_ (Z28374) Pyruvate kinase;

plastid isozyme [Nicotiana tabacum]

Seq. No. 270598

Contig ID 26206 1.R1011

5'-most EST LIB3150-092-P2-K1-B1

Seq. No. 270599

Contig ID 26210 1.R1011

5'-most EST LIB3150-092-P2-K1-C1

Seq. No. 270600

Contig ID 26211 1.R1011

5'-most EST LIB3067-051-Q1-K1-D8

2.-WOSE F21 PIP2001-021-AI-VI-DG

Seq. No. 270601

Contig ID 26233 1.R1011

5'-most EST LIB3150-092-P2-K1-F4

Seq. No. 270602

Contig ID 26243 1.R1011

5'-most EST uC-zmflmo17427g02a1

Seq. No. 270603

Contig ID 26243 2.R1011

5'-most EST LIB31\overline{5}0-092-P2-K1-G8
Method BLASTN

NCBI GI g1373000

BLAST score 47
E value 5.0e-17
Match length 107

Match length 107 % identity 86

NCBI Description Oryza sativa ubiquitin conjugating enzyme (UBC) gene,

complete cds

Seq. No. 270604

Contig ID 26243_3.R1011

5'-most EST uC-zmflb73167b12a1

Seq. No. 270605

Contig ID 26253 1.R1011

5'-most EST LIB3150-092-P2-K1-H8

Method BLASTN
NCBI GI g2832242
BLAST score 114
E value 4.0e-57
Match length 368



```
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                  270606
Seq. No.
                  26271 1.R1011
Contig ID
5'-most EST
                  uC-zmflm017207f09b1
                  BLASTX
Method
                  q2499087
NCBI GI
BLAST score
                  513
                  1.0e-51
E value
                  340
Match length
                  37
% identity
                 UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR
NCBI Description
                  (DUGT) >gi_1085170_pir__S54723 UDP-glucose--glycoprotein
                  glucosyltransferase - fruit fly (Drosophila sp.) >gi 790585
                  (U20554) UDP-glucose:glycoprotein glucosyltransferase
                  precursor [Drosophila melanogaster]
                  270607
Seq. No.
Contig ID
                  26271 2.R1011
                  uC-zmflmo17052d08b1
                  BLASTX
                  g2499087
                  474
                  2.0e-47
```

5'-most EST Method NCBI GI BLAST score E value 185 Match length 52 % identity

NCBI Description UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT) >gi_1085170_pir__S54723 UDP-glucose--glycoprotein glucosyltransferase - fruit fly (Drosophila sp.) >gi 790585 (U20554) UDP-glucose:glycoprotein glucosyltransferase

precursor [Drosophila melanogaster]

270608 Seq. No. Contig ID 26272 1.R1011 5'-most EST LIB3150-093-P1-N1-C4

BLASTX Method q4106984 NCBI GI BLAST score 144 E value 5.0e-09Match length 80 % identity

NCBI Description (AC003038) R30923 1 [Homo sapiens]

Seq. No. 270609 Contig ID 26275 1.R1011 5'-most EST ntr700074895.h1

Method BLASTX NCBI GI g3123209 BLAST score 1066 1.0e-116 E value Match length 372 % identity 58

NCBI Description ELONGATION FACTOR G, MITOCHONDRIAL 1 PRECURSOR (MEF-G-1) >gi_2119928_pir__S61642 translation elongation factor G,

> mitochondrial - yeast (Saccharomyces cerevisiae) >gi 1181289 emb CAA64315 (X94607) Mef1 protein



[Saccharomyces cerevisiae] >gi_1360422_emb_CAA97626_(Z73241) ORF YLR069c [Saccharomyces cerevisiae]

```
Seq. No.
                   270610
                   26281 1.R1011
Contig ID
                  LIB3067-032-Q1-K1-B8
5'-most EST
                  BLASTN
Method
NCBI GI
                   q3821780
BLAST score
                   36
                   1.0e-10
E value
                   48
Match length
                   67
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   270611
Seq. No.
                   26287 1.R1011
Contig ID
5'-most EST
                   uC-zmflm017026d10b1
                   BLASTX
Method
NCBI GI
                   q1619300
BLAST score
                   677
                   6.0e-71
E value
                   190
Match length
                   65
% identity
                  (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   270612
                   26287 2.R1011
Contig ID
5'-most EST
                   LIB3136-050-Q1-K1-A12
Method
                   BLASTX
NCBI GI
                   g1619300
BLAST score
                   352
                   3.0e - 33
E value
                   105
Match length
% identity
                   65
                  (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
                   270613
Seq. No.
                   26287 3.R1011
Contig ID
5'-most EST
                   wyr700238963.h1
                   BLASTX
Method
                   g1619300
NCBI GI
                   238
BLAST score
                   7.0e-20
E value
                   63
Match length
                   67
% identity
                  (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
                   270614
Seq. No.
                   26294 1.R1011
Contig ID
                   pmx700086939.h1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g2062705
BLAST score
                   37
E value
                   2.0e-11
                   37
Match length
                   100
% identity
```

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds



```
270615
Seq. No.
                  26308 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17070b02a1
Seq. No.
                  270616
                  26327 1.R1011
Contig ID
                  LIB3150-093-P2-K1-E5
5'-most EST
                  270617
Seq. No.
                  26337 1.R1011
Contig ID
                  LIB3150-093-P2-K1-F6
5'-most EST
Seq. No.
                   270618
                  26340 1.R1011
Contig ID
                  LIB3150-093-P2-K1-F9
5'-most EST
                  BLASTX
Method
NCBI GI
                   g2271477
BLAST score
                   1449
E value
                   1.0e-161
                   294
Match length
                   93
% identity
                  (AF009631) AP47/50p [Arabidopsis thaliana]
NCBI Description
                   270619
Seq. No.
                   26354 1.R1011
Contig ID
5'-most EST
                   uC-zm\overline{f}lB73004a05b1
                   270620
Seq. No.
Contig ID
                   26364 1.R1011
5'-most EST
                   uC-zmflmo17127h02b1
                   270621
Seq. No.
                   26378 2.R1011
Contig ID
5'-most EST
                   ntr700076553.h1
                   BLASTX
Method
NCBI GI
                   q4469020
BLAST score
                   209
                   1.0e-16
E value
Match length
                   66
                   55
% identity
NCBI Description
                  (AL035602) putative protein (fragment) [Arabidopsis
                   thaliana]
Seq. No.
                   270622
Contig ID
                   26381 1.R1011
5'-most EST
                   uC-zmflmo17168a04b1
                   270623
Seq. No.
Contig ID
                   26382 1.R1011
```

5'-most EST 26382_1.RIUI1 UC-zmflmo17029g01b1

Seq. No. 270624

Contig ID 26391_1.R1011

5'-most EST uC-zmroteosinte100f05b2

Method BLASTX NCBI GI g3212861



BLAST score 348
E value 1.0e-32
Match length 124
% identity 51

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 270625

Contig ID 26396_1.R1011 5'-most EST uC-zmflb73144b01b1

Seq. No. 270626

Contig ID 26396_2.R1011 5'-most EST cyk700049836.f1

Method BLASTX
NCBI GI 94585987
BLAST score 1062
E value 1.0e-116
Match length 363
% identity 58

NCBI Description (AC005287) Similar to nucleolar protein [Arabidopsis

thaliana]

Seq. No. 270627

Contig ID 26403 1.R1011

5'-most EST LIB3066-012-Q1-K1-E4

Method BLASTX
NCBI GI g4559387
BLAST score 239
E value 8.0e-20
Match length 158
% identity 53

NCBI Description (AC006526) putative oxal protein [Arabidopsis thaliana]

Seq. No. 270628

Contig ID 26403_2.R1011 5'-most EST qmh700029841.f1

Method BLASTX
NCBI GI g2462077
BLAST score 426
E value 4.0e-42
Match length 116
% identity 70

NCBI Description (Y11871) Oxal protein [Arabidopsis thaliana]

Seq. No. 270629

Contig ID 26404_1.R1011 5'-most EST wty700162971.h1

Method BLASTX
NCBI GI g3355465
BLAST score 447
E value 2.0e-44
Match length 148
% identity 57

NCBI Description (AC004218) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 270630



Contig ID 26404_3.R1011 5'-most EST rvt700550562.h1

Seq. No. 270631

Contig ID 26406 1.R1011

5'-most EST uC-zmroteosinte083h03b1

Method BLASTX
NCBI GI g3702632
BLAST score 374
E value 1.0e-35
Match length 240
% identity 37

NCBI Description (AL031824) putative transcriptional regulator

[Schizosaccharomyces pombe] >gi 3859080 emb CAA21957

(AL033406) putative alcohol dehydrogenase repressor protein

[Schizosaccharomyces pombe]

Seq. No. 270632

Contig ID 26412 1.R1011

5'-most EST LIB3150-094-P2-K1-A4

Method BLASTX
NCBI GI g3212871
BLAST score 1731
E value 0.0e+00
Match length 369
% identity 87

NCBI Description (AC004005) putative translation initiation factor

[Arabidopsis thaliana]

Seq. No. 270633

Contig ID 26412_3.R1011 5'-most EST uC-zmrob73006h10a1

Method BLASTX
NCBI GI g3023282
BLAST score 218
E value 1.0e-17
Match length 44
% identity 84

NCBI Description METHIONINE AMINOPEPTIDASE 2 (METAP 2) (PEPTIDASE M 2)

(INITIATION FACTOR 2 ASSOCIATED 67 KD GLYCOPROTEIN) (P67) >gi_2055254_dbj_BAA19789_ (AB003144) initiation factor

2-associated 67kDa protein [Mus musculus]

Seq. No. 270634

Contig ID 26414_1.R1011

5'-most EST LIB3150-094-P2-K1-A6

Seq. No. 270635

Contig ID 26418_1.R1011 5'-most EST uC-zmflb73208e09a2

Seq. No. 270636

Contig ID 26418_2.R1011 5'-most EST uC-zmflb73297c10a1

Seq. No. 270637

Contig ID 26421 1.R1011



5'-most EST LIB3069-020-Q1-K1-C4

Seq. No. 270638

Contig ID 26437 1.R1011

5'-most EST LIB3150-094-P2-K1-D6

Seq. No. 270639

Contig ID 26437 2.R1011 5'-most EST uC-zmflb73122f09a1

Seq. No. 270640

26454 1.R1011 Contig ID

5'-most EST LIB3279-053-P1-K1-E6

Method BLASTX NCBI GI g3560261 BLAST score 229 E value 2.0e-18 108

Match length % identity 42

NCBI Description (AL031535) RNA binding protein [Schizosaccharomyces pombe]

Seq. No. 270641

26455 1.R1011 Contig ID

5'-most EST uC-zmflmo17024g04a1

Seq. No. 270642

Contig ID 26456 1.R1011

5'-most EST uC-zmrob73055d03a1

Method BLASTX NCBI GI g4376158 BLAST score 472 E value 5.0e-47Match length 122

% identity

NCBI Description (X98873) aspartate kinase [Arabidopsis thaliana]

Seq. No. 270643

Contig ID 26457 2.R1011 5'-most EST uC-zmflb73080a03a1

Seq. No. 270644

Contig ID 26462 1.R1011

LIB3150-094-P2-K1-H11 5'-most EST

Seq. No. 270645

26463 1.R1011 Contig ID

5'-most EST LIB3150-100-P2-K1-H3

Seq. No. 270646

Contig ID 26472 1.R1011 5'-most EST $cjh70\overline{0}193284.h1$

Method BLASTX NCBI GI q2894598 BLAST score 310 E value 2.0e-28 Match length 153 % identity 46

Contiq ID

5'-most EST



```
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                  270647
                  26476 1.R1011
Contig ID
                  LIB3150-095-P1-N1-A8
5'-most EST
                  270648
Seq. No.
                  26480 1.R1011
Contig ID
                  LIB3150-095-P1-N1-B3
5'-most EST
Method
                  BLASTX
                  g3834306
NCBI GI
BLAST score
                  155
                  3.0e-10
E value
                  48
Match length
                  56
% identity
                  (AC005679) EST gb_R65024 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  270649
Seq. No.
Contig ID
                  26500 1.R1011
                  bdu700382841.h1
5'-most EST
                  BLASTX
Method
                  g4101473
NCBI GI
BLAST score
                  558
                  6.0e-90
E value
                  279
Match length
% identity
                  65
NCBI Description (AF003382) KEA1 [Arabidopsis thaliana]
Seq. No.
                  270650
Contig ID
                  26506 1.R1011
5'-most EST
                  wty700171280.h1
                  BLASTX
Method
NCBI GI
                  g3947854
BLAST score
                  513
E value
                  1.0e-51
Match length
                  257
                  43
% identity
                  (AL034381) conserved hypothetical PFAM UPF0031 containing
NCBI Description
                  protein [Schizosaccharomyces pombe]
Seq. No.
                  270651
                  26513 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73236c10b1
                  BLASTX
Method
NCBI GI
                  q3309066
BLAST score
                  231
                   4.0e-19
E value
Match length
                   63
% identity
NCBI Description
                  (AF073488) bifunctional dihydrofolate reductase-thymidylate
                  synthase [Zea mays]
Seq. No.
                  270652
```

26519 1.R1011

LIB3059-043-Q1-K1-H1



```
270653
Seq. No.
                  26524 1.R1011
Contig ID
                  LIB3150-095-P2-K1-C11
5'-most EST
                  270654
Seq. No.
                  26530 1.R1011
Contig ID
                  LIB3150-095-P2-K1-E6
5'-most EST
                  BLASTX
Method
                  g417769
NCBI GI
BLAST score
                   325
                   1.0e-29
E value
                   279
Match length
                   31
% identity
NCBI Description GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)
                   (FALDH) (ALCOHOL DEHYDROGENASE SFA) >gi 320091_pir__S31140
                   alcohol dehydrogenase (EC 1.1.1.1) SFA - yeast
                   (Saccharomyces cerevisiae) >gi 288591 emb CAA48161.1_
                   (X68020) SFA [Saccharomyces cerevisiae]
                   >qi 1061271 emb CAA91578 (Z67750) alcohol dehydrogenase
                   [Saccharomyces cerevisiae] >gi 1431268 emb CAA98742_
                   (Z74216) ORF YDL168w [Saccharomyces cerevisiae]
                   270655
Seq. No.
                   26548 1.R1011
Contig ID
5'-most EST
                  LIB3060-001-Q1-K2-G9
Seq. No.
                   270656
                   26559 1.R1011
Contig ID
                   xsy70\overline{0}211163.h1
5'-most EST
Method
                   BLASTX
                   q3169091
NCBI GI
                   622
BLAST score
                   2.0e-64
E value
                   368
Match length
% identity
                   35
NCBI Description (AL023706) hypothetical protein [Schizosaccharomyces pombe]
                   270657
Seq. No.
                   26564 1.R1011
Contig ID
5'-most EST
                   qct701172959.h2
Method
                   BLASTX
NCBI GI
                   q4309734
BLAST score
                   277
                   2.0e-24
E value
Match length
                   114
% identity
                   54
                  (AC006439) putative 26S proteosome regulatory subunit 8
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   270658
                   26570 1.R1011
Contig ID
```

5'-most EST uC-zmroteosinte033f08b1

Method BLASTX
NCBI GI g2894598
BLAST score 646
E value 4.0e-67
Match length 329



% identity

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

270659 Seq. No.

Contig ID 26570 2.R1011 xmt700263953.h1 5'-most EST

BLASTX Method q2947312 NCBI GI 177 BLAST score 1.0e-20 E value 476

Match length 27 % identity

(AF051398) nucleoporin [Drosophila melanogaster] NCBI Description

>gi 2981204 (AF051396) nucleoporin [Drosophila

melanogaster]

270660 Seq. No.

26570 3.R1011 Contig ID 5'-most EST cat700020355.rl

Seq. No. 270661

26570 4.R1011 Contig ID

5'-most EST uC-zmflm017089c09b1

270662 Seq. No.

26570 5.R1011 Contig ID

uC-zmflmo17041b04a1 5'-most EST

270663 Seq. No.

Contig ID 26572 1.R1011

uC-zmromo17096g03a1 5'-most EST

BLASTX Method q3024991 NCBI GI 192 BLAST score E value 2.0e-14 Match length 103 43

% identity

HYPOTHETICAL AMINOTRANSFERASE YBDL >gi 1778518 (U82598) NCBI Description

hypothetical protein [Escherichia coli] >gi 1786816 (AE000165) putative aminotransferase [Escherichia coli] >gi 4062217 dbj BAA35230 (D90701) Aspartate transaminase

(EC 2.6.1.1) [Escherichia coli]

270664 Seq. No.

Contig ID 26590 1.R1011

LIB3150-097-P1-N1-B6 5'-most EST

270665 Seq. No.

26595 1.R1011 Contig ID

uC-zmflmo17264c05a2 5'-most EST

270666 Seq. No.

26596 1.R1011 Contig ID

LIB3150-097-P1-N1-C4 5'-most EST

270667 Seq. No.

26601 1.R1011 Contig ID



```
xmt700257573.h1
5'-most EST
Method
                  BLASTX
                  g3450889
NCBI GI
BLAST score
                  1315
                  1.0e-145
E value
                  408
Match length
                   67
% identity
                 (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
NCBI Description
                   270668
Seq. No.
                   26601 2.R1011
Contig ID
                  uC-zmflb73397f01a1
5'-most EST
                  BLASTX
Method
                  g3450889
NCBI GI
BLAST score
                  268
                  2.0e-23
E value
                  65
Match length
                  80
% identity
NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
Seq. No.
                   270669
                   26601 6.R1011
Contig ID
5'-most EST
                  uC-zmflmo17075g05b2
                   270670
Seq. No.
                   26646 1.R1011
Contig ID
                  uwc700155283.h1
5'-most EST
                  BLASTX
Method
                  g3643594
NCBI GI
BLAST score
                   868
E value
                   3.0e-93
                  249
Match length
                   69
% identity
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                   270671
                   26646 2.R1011
Contig ID
                   uC-zm\overline{f}lb73173g06b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3643594
BLAST score
                   311
E value
                   2.0e-28
                   81
Match length
% identity
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
                   270672
Contig ID
                   26647 1.R1011
5'-most EST
                   uC-zmflmo17222a07b1
Seq. No.
                   270673
Contig ID
                   26651 1.R1011
```

5'-most EST ymt700222905.h1

Method BLASTX
NCBI GI g3859548
BLAST score 342
E value 3.0e-40



Match length 88 % identity 94

NCBI Description (AF097182) protein phosphatase 2A catalytic subunit [Oryza

sativa]

Seq. No. 270674

Contig ID 26659 1.R1011

5'-most EST LIB3150-098-P1-N1-F2

Method BLASTX
NCBI GI g4220472
BLAST score 398
E value 2.0e-40
Match length 152
% identity 56

NCBI Description (AC006069) similar to yeast cccl protein [Arabidopsis

thaliana]

Seq. No. 270675

Contig ID 26661_1.R1011 5'-most EST uC-zmflb73112e10a1

Method BLASTX
NCBI GI g461736
BLAST score 1311
E value 1.0e-145
Match length 374
% identity 68

NCBI Description MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR

>gi_478786_pir__S29316 chaperonin 60 - cucurbit

>gi_12546_emb_CAA50218_ (X70868) chaperonin 60 [Cucurbita

sp.]

Seq. No. 270676

Contig ID 26667 1.R1011

5'-most EST LIB1 $4\overline{3}$ -044-Q1-E1-E11

Seq. No. 270677

Contig ID 26668_1.R1011 5'-most EST uC-zmflb73182g05b1

Method BLASTX
NCBI GI g1723242
BLAST score 152
E value 1.0e-09
Match length 70
% identity 47

NCBI Description HYPOTHETICAL 36.8 KD PROTEIN C26A3.16 IN CHROMOSOME I

>gi_1177363_emb_CAA93239_ (Z69240) yeast dsk2 homolog,

ubiquitin-like protein [Schizosaccharomyces pombe]

Seq. No. 270678

Contig ID 26679_1.R1011 5'-most EST LIB83-014-Q1-E1-G10

62

Method BLASTX
NCBI GI g3582334
BLAST score 222
E value 2.0e-29
Match length 92

% identity

NCBI GI

E value Match length

BLAST score

q2618731

149 3.0e-09

50



```
NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  270679
                  26713 1.R1011
Contig ID
5'-most EST
                  clt700042260.f1
Method
                  BLASTX
NCBI GI
                  q3876473
BLAST score
                  194
E value
                   3.0e-14
Match length
                  137
% identity
                  28
NCBI Description (Z72508) F28H7.4 [Caenorhabditis elegans]
Seq. No.
                  270680
Contig ID
                  26723 1.R1011
5'-most EST
                  LIB3150-100-P1-N1-D4
Seq. No.
                  270681
Contig ID
                  26731 1.R1011
5'-most EST
                  fdz701158591.h1
Method
                  BLASTX
NCBI GI
                  g2832625
BLAST score
                  256
E value
                  1.0e-21
Match length
                  81
% identity
                  58
NCBI Description
                  (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  270682
Contig ID
                  26742 1.R1011
5'-most EST
                  LIB3151-057-Q1-K1-G4
Method
                  BLASTX
NCBI GI
                  g1071913
BLAST score
                  237
E value
                  1.0e-19
                  72
Match length
% identity
                  61
NCBI Description
                  cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial
                  - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine
                  synthase [Spinacia oleracea]
                  270683
Seq. No.
Contig ID
                  26743 1.R1011
5'-most EST
                  LIB3150-100-P2-K1-A1
                  270684
Seq. No.
Contig ID
                  26765 1.R1011
5'-most EST
                  LIB3157-009-Q1-K1-F5
Seq. No.
                  270685
                  26789 1.R1011
Contig ID
5'-most EST
                  LIB3150-100-P2-K1-G2
Method
                  BLASTX
```



% identity 56

NCBI Description (U49077) IAA21 [Arabidopsis thaliana]

Seq. No. 270686

Contig ID 26801_1.R1011 5'-most EST uC-zmflb73292f05b1

Seq. No. 270687

Contig ID 26802 1.R1011

5'-most EST LIB3279-007-P1-K1-H4

Method BLASTX
NCBI GI g3080401
BLAST score 1179
E value 1.0e-129
Match length 293
% identity 72

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

>gi 4455265 emb CAB36801.1_ (AL035527) putative protein

[Arabidopsis thaliana]

Seq. No. 270688

Contig ID 26802 2.R1011

5'-most EST LIB3157-011-Q1-K1-C12

Method BLASTX
NCBI GI g3080401
BLAST score 182
E value 2.0e-13
Match length 53
% identity 62

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

>gi_4455265_emb_CAB36801.1_ (AL035527) putative protein

[Arabidopsis thaliana]

Seq. No. 270689

Contig ID 26806_1.R1011 5'-most EST uC-zmflb73152c10b1

Method BLASTX
NCBI GI g4107009
BLAST score 765
E value 2.0e-81
Match length 152
% identity 97

NCBI Description (D82039) OSK1 [Oryza sativa]

Seq. No. 270690

Contig ID 26806_2.R1011 5'-most EST tzu700204782.h1

Method BLASTX
NCBI GI g4107009
BLAST score 493
E value 7.0e-50
Match length 102
% identity 94

NCBI Description (D82039) OSK1 [Oryza sativa]

Seq. No. 270691

Contig ID 26813 1.R1011



```
LIB3150-108-P1-N1-H2
5'-most EST
Method
                  BLASTX
                  q1209020
NCBI GI
BLAST score
                  205
                  2.0e-15
E value
Match length
                  221
                  30
% identity
NCBI Description (U09584) PL6 protein [Homo sapiens]
                  270692
Seq. No.
                  26813 4.R1011
Contig ID
                  uC-zmflmo17112c01a1
5'-most EST
                  270693
Seq. No.
                  26816 1.R1011
Contig ID
                  LIB3066-020-Q1-K1-B5
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2160692
BLAST score
                  394
E value
                  4.0e-38
                  157
Match length
                  53
% identity
                  (U73527) B' regulatory subunit of PP2A [Arabidopsis
NCBI Description
                  thaliana]
                  270694
Seq. No.
                  26820 1.R1011
Contig ID
                  LIB143-034-Q1-E1-G12
5'-most EST
                  BLASTX
Method
NCBI GI
                  q1169451
BLAST score
                  319
                  3.0e-60
E value
Match length
                  233
                  53
% identity
NCBI Description PROBABLE GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A6 PRECURSOR
                   ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                   (BETA-1, 3-ENDOGLUCANASE) >gi_322510_pir__S31906
                  beta-1,3-glucanase homolog - Arabidopsis thaliana
                   >gi_22677_emb_CAA49853_ (X70409) A6 [Arabidopsis thaliana]
                   >qi 2244764 emb CAB10187 (Z97335) AMP-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                   270695
                   26821 1.R1011
Contig ID
5'-most EST
                   LIB3136-025-Q1-K1-A11
Method
                  BLASTX
NCBI GI
                   g2781361
BLAST score
                   586
                   1.0e-60
E value
Match length
                  180
% identity
                   76
NCBI Description (AC003113) F2401.17 [Arabidopsis thaliana]
```

Seq. No. 270696

Contig ID 26823 1.R1011 5'-most EST tfd700575886.h1



270697 Seq. No.

26823 2.R1011 Contig ID

5'-most EST uC-zmroteosinte012f09b1

Seq. No. 270698

26824 1.R1011 Contig ID

uC-zmflm017016f10b1 5'-most EST

Method BLASTX q173419 NCBI GI 882 BLAST score 3.0e-99 E value 284 Match length 64 % identity

(L11574) p68 RNA helicase [Schizosaccharomyces pombe] NCBI Description

>gi 3810840_emb_CAA21801_ (AL032684) p68-like protein.

[Schizosaccharomyces pombe]

270699 Seq. No.

26831 1.R1011 Contig ID

LIB3150-102-P2-K1-A2 5'-most EST

270700 Seq. No.

26841 1.R1011 Contig ID

LIB84-030-Q1-E1-C4 5'-most EST BLASTX Method

NCBI GI q1653791 **1**76 BLAST score 1.0e-12 E value 105 Match length 35

% identity

(D90916) hypothetical protein [Synechocystis sp.] NCBI Description

270701 Seq. No.

26852 1.R1011 Contig ID

5'-most EST LIB3150-102-P2-K1-D5

270702 Seq. No.

26856 2.R1011 Contig ID

5'-most EST uC-zmromo17026a02a1

Seq. No. 270703

Contig ID 26861 1.R1011

5'-most EST uC-zmroteosinte013g12b1

Method BLASTX NCBI GI q1416514 BLAST score 186 1.0e-13 E value Match length 46 67 % identity

(D63168) CTP:phosphocholine cytidylyltransferase [Brassica NCBI Description

napus]

Seq. No. 270704

26861 2.R1011 Contig ID

LIB3150-102-P2-K1-F6 5'-most EST

Method BLASTX NCBI GI g1418127



BLAST score 172 6.0e-14 E value 56 Match length 77 % identity (D63166) CTP:phosphocholine cytidylyltransferase [Brassica NCBI Description napus] 270705 Seq. No. 26876 1.R1011 Contig ID 5'-most EST LIB3150-102-P2-K1-H11 BLASTN Method g2668737 NCBI GI BLAST score 94 2.0e-45 E value Match length 260 % identity 84 NCBI Description Zea mays translation initiation factor 5A (TIF5A) mRNA, complete cds 270706 Seq. No. 26889 1.R1011 Contig ID LIB3150-103-P2-K1-B10 5'-most EST Method BLASTX q1084454 NCBI GI BLAST score 409 5.0e-40E value Match length 92 85 % identity peptidylprolyl isomerase (EC 5.2.1.8) Cyp1 - rice NCBI Description >gi 600765 (L29471) cyclophilin 1 [Oryza sativa] 270707 Seq. No. Contig ID 26898_1.R1011 5'-most EST LIB3150-103-P2-K1-C2 Method BLASTX NCBI GI g3738297 BLAST score 274 E value 9.0e-24 Match length 203 % identity 24 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana] Seq. No. 270708 Contig ID 26911_1.R1011 5'-most EST LIB3150-103-P2-K1-E11 Method BLASTX NCBI GI q1653293 BLAST score 184

E value 1.0e-13 Match length 67 % identity 58

NCBI Description (D90912) ornithine acetyltransferase [Synechocystis sp.]

270709 Seq. No.

Contig ID 26915 1.R1011

5'-most EST LIB3150-103-P2-K1-E4

% identity

NCBI Description



```
Seq. No.
                  270710
                  26921 1.R1011
Contig ID
5'-most EST
                  LIB3150-103-P2-K1-F10
                  270711
Seq. No.
                  26932 1.R1011
Contig ID
5'-most EST
                  LIB3150-103-P2-K1-H11
                  270712
Seq. No.
                  26943 1.R1011
Contig ID
                  LIB3150-104-P2-K1-B5
5'-most EST
Method
                  BLASTN
                  q498642
NCBI GI
BLAST score
                  345
E value
                  0.0e + 00
Match length
                  387
                   97
% identity
NCBI Description Zea mays G-box binding factor 1 (GBF1) mRNA, complete cds
Seq. No.
                  270713
                  26961 1.R1011
Contiq ID
                  uC-zmflb73106c12a1
5'-most EST
Method
                  BLASTN
                  g4589412
NCBI GI
                   47
BLAST score
                  7.0e-17
E value
                  95
Match length
% identity
                  87
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  F6N7, complete sequence
                   270714
Seq. No.
                   26962 1.R1011
Contig ID
5'-most EST
                  LIB3150-104-P2-K1-E5
                   270715
Seq. No.
Contig ID
                   26964 1.R1011
5'-most EST
                   uC-zmflmo17238g04b1
Method
                   BLASTX
NCBI GI
                   q3978578
BLAST score
                   625
E value
                   1.0e-64
Match length
                   300
                   44
% identity
                  (AB020528) Polygalacturonase inhibitor [Poncirus
NCBI Description
                   trifoliata]
Seq. No.
                   270716
                   26964_2.R1011
Contig ID
                  LIB3068-016-Q1-K1-A10
5'-most EST
Method
                  BLASTX
NCBI GI
                   q1679733
BLAST score
                   173
                   3.0e-19
E value
Match length
                   178
```

(U77041) polygalacturonase-inhibiting protein [Malus



domestica]

Seq. No. 270717

Contig ID 26964_3.R1011

5'-most EST uC-zmflmo17180c01b1

Method BLASTX
NCBI GI g1076591
BLAST score 200
E value 2.0e-15
Match length 108
% identity 41

NCBI Description polygalacturonase inhibitor protein - tomato >gi_469457

(L26529) polygalacturonase inhibitor protein [Lycopersicon

esculentum]

Seq. No. 270718

Contig ID 26964 4.R1011

5'-most EST LIB3150-104-P2-K1-F12

Method BLASTX
NCBI GI g3978578
BLAST score 217
E value 3.0e-17
Match length 93
% identity 45

NCBI Description (AB020528) Polygalacturonase inhibitor [Poncirus

trifoliata]

Seq. No. 270719

Contig ID 26964_7.R1011

5'-most EST uC-zmflmo17001f12b1

Seq. No. 270720

Contig ID 26971 1.R1011

5'-most EST LIB3150-104-P2-K1-G3

Seq. No. 270721

Contig ID 26975_1.R1011

5'-most EST uC-zmflb73196c02a2

Seq. No. 270722

Contig ID 26979 1.R1011

5'-most EST LIB3150-104-P2-K1-H12

Method BLASTX
NCBI GI g3763917
BLAST score 241
E value 2.0e-20
Match length 54
% identity 78

NCBI Description (AC004450) hypothetical protein [Arabidopsis thaliana]

>gi_4531438 gb_AAD22123.1_AC006224_5 (AC006224)

hypothetical protein [Arabidopsis thaliana]

Seq. No. 270723

Contig ID 26989 1.R1011

5'-most EST uC-zmromo17119c10a1

Seq. No. 270724



Contig ID 26994_1.R1011

5'-most EST LIB3150-105-P2-K1-D2

Seq. No. 270725

Contig ID 27010_1.R1011

5'-most EST LIB3150-105-P2-K1-G11

Method BLASTN
NCBI GI g22379
BLAST score 100
E value 7.0e-49
Match length 314
% identity 84

NCBI Description Z.mays mRNA for CAAT-box DNA binding protein subunit B

(NF-YB)

Seq. No. 270726

Contig ID 27016_1.R1011

5'-most EST LIB3156-001-Q1-K1-G4

Method BLASTN
NCBI GI g3449322
BLAST score 38
E value 2.0e-11
Match length 170
% identity 86

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MXC17, complete sequence [Arabidopsis thaliana]

Seq. No. 270727

Contig ID 27039 1.R1011

5'-most EST uC-zmflmo17141f07a1

Method BLASTX
NCBI GI g4589726
BLAST score 374
E value 5.0e-73
Match length 221
% identity 62

NCBI Description (AB003137) DnaJ homolog protein [Salix gilgiana]

>gi 4589739_dbj BAA76888.1_ (AB003138) DnaJ homolog protein

[Salix gilgiana]

Seq. No. 270728

Contig ID 27040 1.R1011

5'-most EST uC-zmflb73016g07a1

Seq. No. 270729

Contig ID 27047_1.R1011

5'-most EST LIB3066-045-Q1-K1-G3

Method BLASTX
NCBI GI g2842744
BLAST score 414
E value 3.0e-40
Match length 100
% identity 74

NCBI Description ENHANCER OF RUDIMENTARY HOMOLOG >gi 1595812 (U67398)

enhancer of rudimentary homolog ATER [Arabidopsis thaliana]

Seq. No. 270730

BLAST score

E value Match length 148 1.0e-77



```
27076 1.R1011
Contig ID
                   uC\text{-}zmroteosinte045g03b2\\
5'-most EST
                   BLASTX
Method
NCBI GI
                   q2642158
BLAST score
                   338
                   4.0e-31
E value
                   190
Match length
% identity
                   42
                   (AC003000) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   270731
                   27076 2.R1011
Contig ID
                   LIB3067-033-Q1-K1-B11
5'-most EST
                   BLASTX
Method
                   q1076534
NCBI GI
BLAST score
                   919
                   4.0e-99
E value
                   434
Match length
% identity
                   66
                   monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - garden
NCBI Description
                   pea >gi 497120 (U06461) monodehydroascorbate reductase
                   [Pisum sativum]
                   270732
Seq. No.
                   27086 1.R1011
Contig ID
                   LIB3150-107-P1-N1-D2
5'-most EST
                   BLASTX
Method
                   g3150239
NCBI GI
BLAST score
                   183
E value
                   5.0e-13
Match length
                   126
                   37
% identity
                   (AL023635) hypothetical protein MLCB1243.38 [Mycobacterium
NCBI Description
                   leprae]
                   270733
Seq. No.
                   27093 1.R1011
Contig ID
                   uC-zm\overline{f}1b73080a09b2
5'-most EST
Method
                   BLASTX
                   g1076821
NCBI GI
                   503
BLAST score
                   9.0e-51
E value
                   113
Match length
                   88
% identity
                   probable 1-acyl-glycerol-3-phosphate acyltransferase -
NCBI Description
                   maize >gi_575960_emb_CAA82638_ (Z29518)
                   1-acyl-glycerol-3-phosphate acyltransferase (putative) [Zea
                   mays]
                   270734
Seq. No.
                   27093 2.R1011
Contig ID
                   xmt700259174.h2
5'-most EST
                   BLASTN
Method
NCBI GI
                   q575959
```



93 % identity Z.mays (Black Mexican Sweet) mRNA for NCBI Description 1-acyl-glycerol-3-phosphate acyltransferase (putative) Seq. No. 270735 27106 1.R1011 Contig ID ypc700806469.hl 5'-most EST BLASTX Method q4138581 NCBI GI 1116 BLAST score 1.0e-122 E value 356 Match length 41 % identity (X98474) mitochondrial energy transfer protein [Solanum NCBI Description tuberosum] 270736 Seq. No. 27116 1.R1011 Contig ID LIB3150-108-P2-K1-G10 5'-most EST 270737 Seq. No. 27126 1.R1011 Contig ID uC-zmflb73100f03b1 5'-most EST Method BLASTN q3821780 NCBI GI 36 BLAST score 2.0e-10 E value 48 Match length 67 % identity NCBI Description Xenopus laevis cDNA clone 27A6-1 270738 Seq. No. 27160 1.R1011 Contig ID $uC-zm\overline{f}lb73414b02a1$ 5'-most EST 270739 Seq. No. 27165 1.R1011 Contig ID $xdb70\overline{0}340421.h1$ 5'-most EST BLASTX Method g4579913 NCBI GI 568 BLAST score 4.0e-58 E value 224 Match length 47 % identity NCBI Description (AB023423) sulfate transporter [Arabidopsis thaliana] 270740 Seq. No. 27166 1.R1011 Contig ID LIB3150-107-P2-K1-F4 5'-most EST 270741 Seq. No. 27171 1.R1011

Contig ID

5'-most EST LIB3150-107-P2-K1-G10

BLASTX Method g4006829 NCBI GI 216 BLAST score 3.0e-17 E value



Match length 66 % identity 65

NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No. 270742

Contig ID 27175_1.R1011 5'-most EST nbm700475612.h1

Seq. No. 270743

Contig ID 27183_1.R1011

5'-most EST LIB3150-107-P2-K1-H5

Method BLASTX
NCBI GI g4586033
BLAST score 810
E value 1.0e-86
Match length 244
% identity 60

NCBI Description (AC007109) unknown protein [Arabidopsis thaliana]

Seq. No. 270744

Contig ID 27184 1.R1011

5'-most EST LIB3150-107-P2-K1-H6

Seq. No. 270745

Contig ID 27186_1.R1011

5'-most EST LIB3150-107-P2-K1-H8

Seq. No. 270746

Contig ID 27199_1.R1011

5'-most EST LIB3151-024-Q1-K1-D4

Method BLASTX
NCBI GI g2815493
BLAST score 148
E value 2.0e-09
Match length 51
% identity 61

NCBI Description SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)

(CP-MI) >gi_1731988_emb_CAA70816_ (Y09603) serine

carboxypeptidase I, CP-MI [Hordeum vulgare]

Seq. No. 270747

Contig ID 27201 1.R1011

5'-most EST LIB3150-108-P1-N1-B3

Method BLASTX
NCBI GI g1722933
BLAST score 246
E value 9.0e-21
Match length 123
% identity 44

NCBI Description HYPOTHETICAL 39.2 KD PROTEIN CY427.09C

>gi 1261930_emb_CAA94651_ (Z70692) hypothetical protein

Rv2228c [Mycobacterium tuberculosis]

Seq. No. 270748

Contig ID 27218_1.R1011 5'-most EST LIB143-003-Q1-E1-B4

Method BLASTX



NCBI GI g2689221 185 BLAST score 9.0e-14 E value Match length 68 % identity 54 (Y10098) 7-ethoxycoumarin O-deethylase [Helianthus NCBI Description tuberosus] 270749 Seq. No. 27244_1.R1011 Contig ID LIB3150-108-P2-K1-B12 5'-most EST BLASTX Method g2126240 NCBI GI 325 BLAST score 5.0e-30 E value 162 Match length % identity 41 NCBI Description Prolyl Aminopeptidase - Aeromonas sobria (fragment) 270750 Seq. No. 27274_1.R1011 Contig ID LIB3150-108-P2-K1-E2 5'-most EST BLASTX Method g2952433 NCBI GI 1047 BLAST score 1.0e-114 E value 307 Match length 64 % identity (AF051135) putative ubiquitin activating enzyme E1 NCBI Description [Arabidopsis thaliana] 270751 Seq. No. 27274 2.R1011 Contig ID uC-zmflb73369h12a1 5'-most EST 270752 Seq. No. 27275 1.R1011 Contig ID LIB3150-108-P2-K1-E4 5'-most EST 270753 Seq. No. 27294 1.R1011 Contig ID 5'-most EST LIB3150-108-P2-K1-G5 270754 Seq. No. 27301 1.R1011 Contig ID LIB3150-108-P2-K1-H12 5'-most EST Seq. No. 270755 27313 1.R1011 Contig ID LIB3150-109-P2-K1-A6 5'-most EST BLASTN Method q312178 NCBI GI BLAST score 209 1.0e-114 E value

37702

470

NCBI Description Z.mays GapC2 gene

Match length % identity



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270756
Seq. No.
                   27321 1.R1011
Contig ID
                   uC-zmflmo17324g04a1
5'-most EST
                   BLASTX
Method
                    q4309698
NCBI GI
                    991
BLAST score
                    1.0e-108
E value
                    296
Match length
                    68
% identity
                    (AC006266) putative glucosyltransferase [Arabidopsis
NCBI Description
                    thaliana]
                    270757
Seq. No.
                    27326 1.R1011
Contig ID
                    LIB3150-109-P2-K1-C10
5'-most EST
                    270758
Seq. No.
                    27347 1.R1011
Contig ID
                    LIB3150-109-P2-K1-D9
5'-most EST
                    270759
Seq. No.
Contig ID
                    27348 1.R1011
                    uC-zm\overline{f}1b73005g09a1
5'-most EST
                    270760
Seq. No.
                    27349 1.R1011
Contig ID
                    LIB3150-109-P2-K1-E11
5'-most EST
                    270761
Seq. No.
                    27355 1.R1011
Contig ID
                    LIB3150-109-P2-K1-E8
5'-most EST
                    BLASTX
Method
                    g2462760
NCBI GI
                    169
BLAST score
                    1.0e-11
E value
                    75
Match length
                    47
% identity
                   (AC002292) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    270762
Seq. No.
                    27361 1.R1011
Contig ID
                    uC-zm\overline{f}lmo17071c01b1
5'-most EST
                    BLASTX
Method
                    q2225877
NCBI GI
                    200
BLAST score
                    3.0e-15
E value
                    74
Match length
                    49
 % identity
                    (AB002406) TIP49 [Rattus norvegicus] >gi_4106528 (AF100694)
NCBI Description
                    Pontin52 [Mus musculus] >gi_4521276_dbj_BAA76313.1_ (AB001581) DNA helicase p50 [Rattus norvegicus]
```

270763 Seq. No. Contig ID

27361_2.R1011

LIB3150-109-P2-K1-F4 5'-most EST

BLASTX Method



NCBI GI g2225877 149 BLAST score 3.0e-09 E value 56 Match length 46 % identity (AB002406) TIP49 [Rattus norvegicus] >gi_4106528 (AF100694) NCBI Description Pontin52 [Mus musculus] >gi_4521276_dbj_BAA76313.1_(AB001581) DNA helicase p50 [Rattus norvegicus] 270764 Seg. No. 27361 3.R1011 Contig ID uC-zmflb73121f06a1 5'-most EST 270765 Seq. No. 27362 1.R1011 Contig ID LIB3150-109-P2-K1-F5 5'-most EST BLASTN Method g4140643 NCBI GI 38 BLAST score 1.0e-11 E value 66 Match length 89 % identity Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, NCBI Description complete sequence 270766 Seq. No. 27362 2.R1011 Contig ID $xyt70\overline{0}342991.h1$ 5'-most EST BLASTX Method g3372864 NCBI GI 226 BLAST score 2.0e-18 E value 179 Match length 34 % identity (AF068201) aminopeptidase-1 [Caenorhabditis elegans] NCBI Description >gi 3859874 (AF068200) aminopeptidase-1 [Caenorhabditis elegans] 270767 Seq. No. 27407 1.R1011 Contig ID LIB3150-110-P2-K1-C12 5'-most EST 270768 Seq. No. 27411_1.R1011 Contig ID LIB3150-110-P2-K1-C5 5'-most EST BLASTX Method g4454472 NCBI GI BLAST score 505 1.0e-50 E value 216 Match length

55 % identity

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

270769 Seq. No. 27425 1.R1011 Contig ID

LIB3150-110-P2-K1-D9 5'-most EST

BLASTX Method



```
NCBI GI
                  g1531541
BLAST score
                   456
                   6.0e-70
E value
Match length
                  140
                   99
% identity
                  (D83391) uroporphyrinogen III methyltransferase [Zea mays]
NCBI Description
                   270770
Seq. No.
                   27458 1.R1011
Contig ID
                   LIB3150-110-P2-K1-H2
5'-most EST
                   BLASTX
Method
                   q4544383
NCBI GI
                   177
BLAST score
                   4.0e-12
E value
Match length
                   101
                   42
% identity
                  (AC007047) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   270771
Seq. No.
                   27458 2.R1011
Contig ID
                   LIB143-015-Q1-E1-B11
5'-most EST
                   270772
Seq. No.
                   27494 1.R1011
Contig ID
                   LIB3150-112-P2-K1-B8
5'-most EST
                   BLASTX
Method
                   g2909783
NCBI GI
BLAST score
                   786
                   9.0e - 84
E value
                   231
Match length
                   68
% identity
                  (AF020289) MgATP-energized glutathione S-conjugate pump
NCBI Description
                   [Arabidopsis thaliana]
                   270773
Seq. No.
                   27501_1.R1011
Contig ID
                   LIB3150-112-P2-K1-C5
5'-most EST
                   BLASTX
Method
                   g4544386
NCBI GI
                   1066
BLAST score
                   1.0e-116
E value
                   288
Match length
                   76
% identity
                   (AC007047) putative cell division control protein
NCBI Description
                   [Arabidopsis thaliana]
                   270774
Seq. No.
                   27505 2.R1011
Contig ID
5'-most EST
                   LIB3150-112-P2-K1-C9
                   270775
Seq. No.
                   27508 1.R1011
Contig ID
5'-most EST
                   LIB3150-112-P2-K1-D11
                   270776
Seq. No.
```

37705

27510 1.R1011

LIB3067-058-Q1-K1-E10

Contig ID

5'-most EST



Seq. No. 270777

Contig ID 27523_1.R1011 5'-most EST uC-zmflb73131c07a1

Seq. No. 270778

Contig ID 27531 1.R1011

5'-most EST LIB3150-112-P2-K1-G10

Method BLASTX
NCBI GI g3551954
BLAST score 323
E value 2.0e-29
Match length 157
% identity 39

NCBI Description (AF082030) senescence-associated protein 5 [Hemerocallis

hybrid cultivar]

Seq. No. 270779

Contig ID 27535 1.R1011

5'-most EST LIB3150-112-P2-K1-G4

Method BLASTX
NCBI GI g3157943
BLAST score 244
E value 3.0e-20
Match length 128
% identity 40

NCBI Description (AC002131) Contains similarity to BAP31 protein gb_X81816

from Mus musculus. [Arabidopsis thaliana]

Seq. No. 270780

Contig ID 27535_2.R1011 5'-most EST uC-zmflb73090h01a2

Seq. No. 270781

Contig ID 27543 1.R1011

5'-most EST uC-zmflmo17123h02a1

Seq. No. 270782

Contig ID 27574_1.R1011

5'-most EST LIB3150-113-P2-K1-F12

Seq. No. 270783

Contig ID 27578_1.R1011

5'-most EST LIB3150-113-P2-K1-G12

Seq. No. 270784

Contig ID 27586_1.R1011

5'-most EST uC-zmflb731216g09a1

Seq. No. 270785

Contig ID 27586 2.R1011

5'-most EST LIB31 $\overline{5}$ 0-113-P2-K1-H2

Seq. No. 270786

Contig ID 27590_1.R1011

5'-most EST LIB3154-003-Q1-K1-F11



Seq. No. 270787

Contig ID 27595_1.R1011

5'-most EST LIB3150-114-P2-K1-B4

Seq. No. 270788

Contig ID 27595 2.R1011 5'-most EST xmt700266531.h1

Seq. No. 270789

Contig ID 27597_1.R1011 5'-most EST fC-zmle700430654r4

Seq. No. 270790

Contig ID 27599_1.R1011 5'-most EST LIB84-015-Q1-E1-A5

Seq. No. 270791

Contig ID 27599 2.R1011

5'-most EST LIB3150-114-P2-K1-C11

Seq. No. 270792

Contig ID 27611 1.R1011

5'-most EST LIB3150-114-P2-K1-D2

Seq. No. 270793

Contig ID 27616 1.R1011

5'-most EST LIB3150-114-P2-K1-E11

Method BLASTX
NCBI GI g3513726
BLAST score 549
E value 6.0e-56
Match length 258
% identity 45

NCBI Description

(AF080118) F8M12.23 gene product [Arabidopsis thaliana] >gi_4539354_emb_CAB40048.1 (AL049525) putative protein

[Arabidopsis thaliana]

Seq. No. 270794

Contig ID 27621 1.R1011

5'-most EST LIB3150-114-P2-K1-E5

Method BLASTX
NCBI GI g872116
BLAST score 1412
E value 1.0e-157
Match length 330
% identity 79

NCBI Description (X79770) sti (stress inducible protein) [Glycine max]

Seq. No. 270795

Contig ID 27621 2.R1011

5'-most EST uC-zmflmo17138c07b1

Seq. No. 270796

Contig ID 27626 1.R1011

5'-most EST LIB3150-114-P2-K1-F2

Method BLASTX NCBI GI g2583108



BLAST score 184 3.0e-25E value Match length 113 % identity 53

(AC002387) putative surface protein [Arabidopsis thaliana] NCBI Description

Seq. No. 270797

27631 1.R1011 Contig ID

LIB3150-114-P2-K1-G10 5'-most EST

Method BLASTX g3201680 NCBI GI BLAST score 276 2.0e-24 E value Match length 116 % identity 47

(AF060941) extra-large G-protein [Arabidopsis thaliana] NCBI Description

Seq. No. 270798

27638 1.R1011 Contig ID

LIB3150-114-P2-K1-H12 5'-most EST

270799 Seq. No.

Contig ID 27642 1.R1011

LIB3150-114-P2-K1-H8 5'-most EST

270800 Seq. No.

27642 2.R1011 Contig ID

5'-most EST uC-zmflb73159f09a2

270801 Seq. No.

27643 1.R1011 Contig ID

5'-most EST LIB3150-116-P2-K1-A12

Method BLASTX NCBI GI g4432846 BLAST score 295 3.0e - 37E value Match length 94 % identity 81

(AC006283) unknown protein [Arabidopsis thaliana] NCBI Description

270802 Seq. No.

27675 1.R1011 Contig ID

LIB3150-116-P2-K1-E10 5'-most EST

270803 Seq. No.

27681 1.R1011 Contig ID 5'-most EST ntr700072829.h1

Method BLASTX NCBI GI g3142292 BLAST score 305 1.0e-27 E value Match length 73 % identity 74

(AC002411) Contains similarity to tetratricopeptide repeat NCBI Description protein gb_U46571 from home sapiens. EST gb Z47802 and

gb Z48402 come from this gene. [Arabidopsis thaliana]



```
Seq. No.
                  270804
Contig ID
                  27685 1.R1011
5'-most EST
                  LIB3150-116-P2-K1-F1
Method
                  BLASTX
NCBI GI
                  q2213584
BLAST score
                  182
                  3.0e-19
E value
Match length
                  84
                  60
% identity
                  (AC000348) T7N9.4 [Arabidopsis thaliana]
NCBI Description
                  270805
Seq. No.
Contig ID
                  27714 1.R1011
5'-most EST
                  LIB3150-117-P2-K1-A4
                  BLASTX
Method
NCBI GI
                  q4314390
BLAST score
                  231
                  8.0e-19
E value
Match length
                  85
                  53
% identity
                  (AC006232) putative calcium binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  270806
Contig ID
                  27720 1.R1011
5'-most EST
                  LIB3150-117-P2-K1-B2
Seq. No.
                  270807
Contig ID
                  27732 1.R1011
                  uC-zmflmo17241g12a1
5'-most EST
Method
                  BLASTN
                  q2655097
NCBI GI
BLAST score
                  60
                  5.0e-25
E value
                  132
Match length
                  88
% identity
                  Hordeum vulgare peptide transporter (ptr1) mRNA, complete
NCBI Description
                  cds
                  270808
Seq. No.
                  27737 1.R1011
Contig ID
5'-most EST
                  LIB3150-117-P2-K1-D12
                  270809
Seq. No.
                  27755 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17069h06a1
Method
                  BLASTX
NCBI GI
                  q2997686
BLAST score
                  260
E value
                  5.0e-22
```

Match length 124 % identity 63

NCBI Description (AF053303) putative transcriptional co-activator

[Arabidopsis thaliana] $>gi_3513735$ (AF080118) contains similarity to RNA polymerase II transcription cofactor p15

[Arabidopsis thaliana] >gi_4539366_emb_CAB40060.1_(AL049525) putative protein [Arabidopsis thaliana]



Seq. No. 270810

Contig ID 27776 1.R1011

5'-most EST LIB3150-118-P2-K1-A11

Seq. No. 270811

Contig ID 27790_1.R1011

5'-most EST LIB3150-118-P2-K1-C11

Seq. No. 270812

Contig ID 27804_1.R1011

5'-most EST LIB3150-118-P2-K1-D8

Seq. No. 270813

Contig ID 27820_1.R1011

5'-most EST LIB3150-118-P2-K1-G6

Method BLASTX
NCBI GI g3256066
BLAST score 220
E value 1.0e-17

Match length 68 % identity 62

NCBI Description (Y13987) chloroplast NAD-MDH [Arabidopsis thaliana]

Seq. No. 270814

Contig ID 27825 1.R1011

5'-most EST LIB3150-118-P2-K1-H8

Seq. No. 270815

Contig ID 27832 1.R1011

5'-most EST LIB3180-007-P2-M1-H3

Method BLASTX
NCBI GI g4572673
BLAST score 352
E value 3.0e-33
Match length 143
% identity 52

NCBI Description (AC006954) putative sarcosine oxidase [Arabidopsis

thaliana]

Seq. No. 270816

Contig ID 27838_1.R1011

5'-most EST LIB3151-001-P1-K1-B3

Method BLASTX
NCBI GI g2653446
BLAST score 654
E value 1.0e-68
Match length 167
% identity 72

NCBI Description (AB009077) proton pyrophosphatase [Vigna radiata]

Seq. No. 270817

Contig ID 27847_1.R1011 5'-most EST uC-zmflb73286g04b1

Method BLASTX
NCBI GI g3641863
BLAST score 451



E value 8.0e-45 Match length 108 % identity 70

NCBI Description (AJ005042) beta-galactosidase [Cicer arietinum]

Seq. No. Contig ID

270818 27878_1.R1011

5'-most EST uC-zmflb73069b11b1

Seq. No. 270819

Contig ID 27891_1.R1011 5'-most EST ypc700806493.h1

Method BLASTX
NCBI GI g132589
BLAST score 459
E value 3.0e-49
Match length 111
% identity 95

NCBI Description RIBOSOME-INACTIVATING PROTEIN 9 (RRNA N-GLYCOSIDASE) (B-32

PROTEIN) >gi_320205_pir__JQ1673 albumin b-32 - maize >gi 168453 (M83927) ribosome-inactivating protein [Zea

mays]

Seq. No. 270820

Contig ID 27916_1.R1011

5'-most EST LIB3066-030-Q1-E1-H5

Method BLASTX
NCBI GI g136757
BLAST score 1584
E value 0.0e+00
Match length 364
% identity 88

NCBI Description GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR

>gi 100881 pir S07314 UDPglucose--starch

glucosyltransferase (EC 2.4.1.11) precursor - maize
>gi_168653 (M24258) amyloplast-specific transit protein
[Zea mays] >gi_1644339_emb_CAA27574_ (X03935) glucosyl

transferase [Zea mays]

Seq. No. 270821

Contig ID 27916_8.R1011 5'-most EST LIB3181-007-P1-K2-B11

5'-most EST LIB3181Method BLASTX
NCBI GI g136757
BLAST score 188
E value 2.0e-14
Match length 34

% identity 100

NCBI Description GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR

>gi_100881_pir__S07314 UDPglucose--starch

glucosyltransferase (EC 2.4.1.11) precursor - maize >gi_168653 (M24258) amyloplast-specific transit protein [Zea mays] >gi_1644339_emb_CAA27574_ (X03935) glucosyl

transferase [Zea mays]

Seq. No. 270822

Contig ID 27931 1.R1011



```
LIB3151-003-Q1-K1-D2
5'-most EST
                  270823
Seq. No.
                  27985 1.R1011
Contig ID
                  xsy700213877.h1
5'-most EST
                  270824
Seq. No.
                  27990 1.R1011
Contig ID
5'-most EST
                  LIB3151-004-Q1-K1-E1
                  270825
Seq. No.
Contig ID
                  28002 1.R1011
                  LIB3151-004-Q1-K1-F6
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2194142
BLAST score
                  179
                   5.0e-13
E value
                   67
Match length
                   55
% identity
                  (AC002062) ESTs gb N38288, gb T43486, gb AA395242 come from
NCBI Description
                   this gene. [Arabidopsis thaliana]
                   270826
Seq. No.
                   28008 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17042e09b1
                   270827
Seq. No.
                   28010 1.R1011
Contig ID
                   LIB3154-014-Q1-K1-A12
5'-most EST
                   BLASTX
Method
NCBI GI
                   g22216
BLAST score
                   162
                   3.0e-11
E value
                   99
Match length
                   40
% identity
NCBI Description
                  (X55722) 22kD zein [Zea mays]
                   270828
Seq. No.
                   28023 1.R1011
Contig ID
5'-most EST
                   LIB3151-005-Q1-K1-B12
                   BLASTX
Method
                   g3212867
NCBI GI
BLAST score
                   374
                   7.0e - 36
E value
Match length
                   127
                   55
% identity
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                   270829
Seq. No.
                   28032 1.R1011
Contig ID
                   LIB3151-005-Q1-K1-D10
5'-most EST
                   270830
Seq. No.
                   28038 1.R1011
Contig ID
```

BLASTX

g1708463

5'-most EST Method

NCBI GI

LIB3151-008-Q1-K1-H1



```
389
BLAST score
                  1.0e-37
E value
                  118
Match length
                  64
% identity
                  IAA-AMINO ACID HYDROLASE >qi 887785 (U23794) ILR1
NCBI Description
                   [Arabidopsis thaliana]
                  270831
Seq. No.
Contig ID
                  28057 1.R1011
5'-most EST
                  yyf700348213.h1
                  270832
Seq. No.
Contig ID
                  28062_1.R1011
5'-most EST
                  LIB3151-006-Q1-K1-A6
Seq. No.
                  270833
                  28069 1.R1011
Contig ID
5'-most EST
                  wyr700240631.h1
Method
                  BLASTX
NCBI GI
                  g4079809
BLAST score
                  245
                  3.0e-20
E value
                  167
Match length
                   6
% identity
NCBI Description
                  (AF071172) HERC2 [Homo sapiens]
Seq. No.
                   270834
Contig ID
                  28087 1.R1011
                  LIB3180-049-P2-M1-F8
5'-most EST
Method
                  BLASTX
NCBI GI
                   g4539459
                   279
BLAST score
                   9.0e-25
E value
Match length
                   71
                   70
% identity
NCBI Description (AL049500) putative protein [Arabidopsis thaliana]
Seq. No.
                   270835
Contig ID
                   28100 1.R1011
5'-most EST
                   nbm700466614.hl
Method
                   BLASTX
NCBI GI
                   g3098603
BLAST score
                   149
E value
                   3.0e-09
Match length
                   111
% identity
                   30
NCBI Description
                  (AF052191) katanin p60 subunit [Strongylocentrotus
                   purpuratus]
                   270836
Seq. No.
```

28110 1.R1011 Contig ID 5'-most EST uC-zmflb73290c07b1

BLASTX Method NCBI GI g4455367 BLAST score 664 4.0e-69 E value 315 Match length

Match length

% identity

165



```
% identity
                   (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   270837
Seq. No.
                   28110 2.R1011
Contig ID
                   dyk700102305.h1
5'-most EST
Method
                   BLASTN
                   g2062705
NCBI GI
                   36
BLAST score
                   9.0e-11
E value
                   36
Match length
                   100
% identity
                   Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
                   270838
Seq. No.
Contig ID
                   28133 2.R1011
                   pmx700085689.hl
5'-most EST
                   270839
Seq. No.
                   28165 1.R1011
Contig ID
                   xmt700264445.h1
5'-most EST
                   270840
Seq. No.
                   28167 1.R1011
Contig ID
                   uC-zmflb73120f10b1
5'-most EST
                   BLASTX
Method
                   g2191135
NCBI GI
                   250
BLAST score
                   3.0e-21
E value
Match length
                   73
                   56
% identity
                   (AF007269) A IG002N01.14 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   270841
Seq. No.
                   28173 1.R1011
Contig ID
5'-most EST
                   ypc700799613.h1
Method
                   BLASTX
NCBI GI
                   q132600
                   545
BLAST score
                   8.0e-56
E value
Match length
                   104
                   100
% identity
NCBI Description RIBOSOME-INACTIVATING PROTEIN PRECURSOR (RRNA
                   N-GLYCOSIDASE) >gi_72361_pir__RLZMRI ribosome-inactivating
protein precursor - maize >gi_168610 (M77122)
                   ribosome-inactivating protein [Zea mays]
Seq. No.
                    270842
                    28173 2.R1011
Contig ID
5'-most EST
                   LIB3151-020-Q1-K1-E3
                   BLASTX
Method
NCBI GI
                   q132600
BLAST score
                   880
                    5.0e-95
E value
```



NCBI Description RIBOSOME-INACTIVATING PROTEIN PRECURSOR (RRNA N-GLYCOSIDASE) >gi_72361_pir__RLZMRI ribosome-inactivating protein precursor - maize >gi_168610 (M77122) ribosome-inactivating protein [Zea mays] 270843 Seq. No. 28178 1.R1011 Contig ID LIB3180-046-P2-M2-H4 5'-most EST BLASTX Method g1237250 NCBI GI 369 BLAST score 3.0e-35 E value 113 Match length 54 % identity NCBI Description (X96784) cytochrome P450 [Nicotiana tabacum] 270844 Seq. No. 28179 1.R1011 Contig ID 5'-most EST LIB3151-008-Q1-K1-H4 270845 Seq. No. 28179 2.R1011 Contig ID LIB3061-045-Q1-K1-D2 5'-most EST 270846 Seq. No. 28203 1.R1011 Contig ID LIB3117-003-Q1-K1-B9 5'-most EST BLASTX Method q16073 NCBI GI BLAST score 190 7.0e-17 E value 56 Match length 74 % identity (X59526) zein protein [Acetabularia mediterranea] NCBI Description 270847 Seq. No. 28215 1.R1011 Contig ID $uC-zm\overline{f}lb73143e12b1$ 5'-most EST Method BLASTX g3036806 NCBI GI BLAST score 274 4.0e-24 E value Match length 79 63 % identity NCBI Description (AL022373) glycine-rich protein [Arabidopsis thaliana] 270848 Seg. No. 28218 1.R1011 Contig ID $uC-zm\overline{f}lmo17067e02b1$ 5'-most EST 270849 Seq. No.

28247 1.R1011 Contig ID

LIB3151-011-Q1-K1-A5 5'-most EST

BLASTX Method g1399917 NCBI GI 325 BLAST score 7.0e-30 E value



```
237
Match length
% identity
                  33
                  (U60144) replication factor C large subunit [Anas
NCBI Description
                  platyrhynchos]
                  270850
Seq. No.
                  28270 1.R1011
Contig ID
5'-most EST
                  LIB3061-030-Q1-K1-F8
                  270851
Seq. No.
                  28280 1.R1011
Contig ID
5'-most EST
                  LIB3151-011-Q1-K1-G12
                  270852
Seq. No.
                  28280 2.R1011
Contig ID
                  uC-zmflmo17047f09a1
5'-most EST
                  270853
Seq. No.
Contig ID
                  28281 1.R1011
                  wyr700235361.h1
5'-most EST
                  270854
Seq. No.
                  28307 1.R1011
Contig ID
5'-most EST
                  LIB3151-012-Q1-K1-C9
                  BLASTX
Method
                  q4455284
NCBI GI
                   250
BLAST score
                   2.0e-21
E value
Match length
                   72
% identity
                   61
                  (AL035527) beta-glucosidase-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   270855
                   28315 1.R1011
Contig ID
                   LIB3152-019-P1-K1-B6
5'-most EST
                   BLASTX
Method
                   g141601
NCBI GI
BLAST score
                   259
                   8.0e-25
E value
                   89
Match length
                   73
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
NCBI Description
                   >gi_82657_pir__S03417 19K zein precursor (clone gZ19AB11) -
                   maize >gi_22543_emb_CAA29340_ (X05911) 19 kd alpha zein (AA
                   1 - 234) [Zea mays]
                   270856
Seq. No.
                   28319 1.R1011
Contig ID
5'-most EST
                   LIB3151-012-Q1-K1-E2
```

Method BLASTN g168665 NCBI GI BLAST score 263 E value 1.0e-146

Match length 298 97 % identity

NCBI Description Maize 16-kDa zein-2 mRNA, complete cds



Seq. No. 270857

Contig ID 28336_1.R1011

5'-most EST LIB3151-012-Q1-K1-H9

Seq. No. 270858

Contig ID 28337 1.R1011

5'-most EST LIB3151-013-Q1-K1-A3

Seq. No. 270859

Contig ID 28363_1.R1011

5'-most EST LIB3151-013-Q1-K1-G5

Method BLASTN
NCBI GI g3108278
BLAST score 74
E value 2.0e-33
Match length 161

% identity 88

NCBI Description Gossypium barbadense clone pXP101 repetitive DNA sequence

Seq. No. 270860

Contig ID 28383 1.R1011

5'-most EST LIB189-022-Q1-E1-D9

Method BLASTX
NCBI GI g431154
BLAST score 560
E value 4.0e-57
Match length 167
% identity 63

NCBI Description (D21813) ORF [Lilium longiflorum]

Seq. No. 270861

Contig ID 28383 2.R1011 5'-most EST wty700166790.h1

Seq. No. 270862

Contig ID 28383_3.R1011

5'-most EST LIB143-028-Q1-E1-F4

Seq. No. 270863

Contig ID 28389_1.R1011 5'-most EST uC-zmroB73028d04b1

Method BLASTX
NCBI GI g2239083
BLAST score 261
E value 1.0e-22
Match length 149
% identity 42

NCBI Description (Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase

[Dianthus caryophyllus] >gi_2239087_emb_CAB06429_ (Z84385)

anthranilate N-hydroxycinnamoyl/benzoyltransferase

[Dianthus caryophyllus]

Seq. No. 270864

Contig ID 28391_1.R1011

5'-most EST LIB3151-014-Q1-K1-B12

Method BLASTX



NCBI GI g2832247 BLAST score 185 E value 9.0e-14 Match length 119 % identity 39

NCBI Description (AF031569) 22-kDa alpha zein 10 [Zea mays]

Seq. No. 270865

Contig ID 28405_1.R1011

5'-most EST LIB3061-003-Q1-K1-C5

Method BLASTX
NCBI GI g118926
BLAST score 722
E value 3.0e-76
Match length 245
% identity 56

NCBI Description DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR

>gi_320600_pir__E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi_227781 prf__1710351E abscisic acid responsive protein E

[Craterostigma plantagineum]

Seq. No. 270866

Contig ID 28406_1.R1011 5'-most EST xmt700262383.h1

Method BLASTX
NCBI GI g3776573
BLAST score 161
E value 7.0e-11
Match length 67
% identity 49

NCBI Description (AC005388) Similar to nodulins and lipase homolog F14J9.5

gi_3482914 from Arabidopsis thaliana BAC gb_AC003970. Alternate first exon from 72258 to 72509. [Arabidopsis

thaliana]

Seq. No. 270867

Contig ID 28406_2.R1011 5'-most EST cyk700051870.f1

Seq. No. 270868

Contig ID 28416_1.R1011 5'-most EST pmx700091029.h1

Seq. No. 270869

Contig ID 28425_1.R1011

5'-most EST LIB3151-014-Q1-K1-G8

Seq. No. 270870

Contig ID 28427_1.R1011 5'-most EST ypc700804737.h1

Method BLASTX
NCBI GI g3075392
BLAST score 713
E value 2.0e-75
Match length 175



% identity (AC004484) putative steroid dehydrogenase [Arabidopsis NCBI Description thaliana] 270871 Seq. No. 28443 1.R1011 Contig ID LIB3151-015-Q1-K1-C12 5'-most EST BLASTX Method g3850576 NCBI GI 604 BLAST score 1.0e-62 E value Match length 208 60 % identity (AC005278) Strong similarity to gb_U04968 nucleotide NCBI Description excision repair protein (ERCC2) from Cricetulus grisseus. [Arabidopsis thaliana] 270872 Seq. No. 28459 1.R1011 Contig ID $1hp70\overline{0}053436.r1$ 5'-most EST BLASTX Method g4097571 NCBI GI BLAST score 144 4.0e-09 E value Match length 61 52 % identity (U64916) GMFP5 [Glycine max] NCBI Description 270873 Seq. No. 28464 1.R1011 Contig ID xjt700094238.h1 5'-most EST BLASTX Method g3790441 NCBI GI 700 BLAST score 7.0e-74E value 183 Match length 81 % identity (AF030515) chaperonin 60 alpha subunit [Canavalia lineata] NCBI Description 270874 Seq. No. 28467 1.R1011 Contig ID uC-zmflmo17271a03b1 5'-most EST BLASTX Method q4240207 NCBI GI 314 BLAST score 1.0e-28 E value 188 Match length 37 % identity (AB020666) KIAA0859 protein [Homo sapiens] NCBI Description 270875 Seq. No. 28486 1.R1011

Contig ID 28486_1.R1011 5'-most EST uC-zmflb73159b11b2



```
Method
                  BLASTX
                  g2213591
NCBI GI
BLAST score
                  262
                  6.0e-23
E value
Match length
                  70
                  71
% identity
                  (AC000348) T7N9.11 [Arabidopsis thaliana]
NCBI Description
                  270877
Seq. No.
                  28505 1.R1011
Contig ID
5'-most EST
                  LIB3151-045-Q1-K1-A6
                  270878
Seq. No.
Contig ID
                  28506 1.R1011
                  LIB3151-016-Q1-K1-E3
5'-most EST
Seq. No.
                  270879
                  28526 1.R1011
Contig ID
5'-most EST
                  uC-zmflmo17097q01b1
Method
                  BLASTX
                  g3193293
NCBI GI
                  165
BLAST score
E value
                  9.0e-11
Match length
                  71
                  55
% identity
                  (AF069298) contains a short region of similarity to another
NCBI Description
                  Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)
                  [Arabidopsis thaliana]
                  270880
Seq. No.
                  28526 3.R1011
Contig ID
                  LIB3151-017-Q1-K1-B1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3193293
BLAST score
                  296
E value
                  9.0e-27
Match length
                  112
% identity
                  (AF069298) contains a short region of similarity to another
NCBI Description
                  Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)
                  [Arabidopsis thaliana]
Seq. No.
                  270881
Contig ID
                  28529 1.R1011
5'-most EST
                  LIB3059-026-Q1-K1-A6
                  BLASTX
Method
NCBI GI
                  q485744
BLAST score
                  287
                  4.0e-31
E value
                  80
Match length
% identity
```

NCBI Description (L32792) pyrophosphatase [Beta vulgaris]

Seq. No. 270882

Contig ID 28533_1.R1011

5'-most EST LIB3151-017-Q1-K1-B9

Method BLASTX

37720

- 1



NCBI GI g1174162 BLAST score 803 E value 7.0e-86 Match length 156 90 % identity (U44976) ubiquitin-conjugating enzyme [Arabidopsis NCBI Description thaliana] >qi 3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana] 270883 Seq. No. Contig ID 28533 2.R1011 5'-most EST uC-zmroteosinte091f10b2 Method BLASTX NCBI GI g1174162 BLAST score 436 E value 5.0e-43 Match length 86 % identity 92 NCBI Description (U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi 3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana] 270884 Seq. No. 28548_1.R1011 Contig ID 5'-most EST LIB3180-002-P1-M1-A1 Method BLASTX NCBI GI g3511236 BLAST score 842 E value 1.0e-90 Match length 180 % identity 90 NCBI Description (AF072725) starch branching enzyme IIb [Zea mays] 270885 Seq. No. 28550_1.R1011 Contig ID 5'-most EST pmx700084813.h1 Method BLASTX NCBI GI g3004560 BLAST score 542 E value 3.0e-55 Match length 163 % identity NCBI Description (AC003673) putative ATP binding protein [Arabidopsis thaliana] Seq. No. 270886 Contig ID 28550_2.R1011 5'-most EST uC-zmroteosinte094c06b2 Method BLASTX NCBI GI q3004560 BLAST score 353

E value 5.0e-64 Match length 212

% identity

(AC003673) putative ATP binding protein [Arabidopsis NCBI Description thaliana]



```
270887
Seq. No.
                   28566 1.R1011
Contig ID
5'-most EST
                   uC-zmflb73099e10b1
Seq. No.
                   270888
Contig ID
                   28576 1.R1011
5'-most EST
                   uC-zmroteosinte063g08b1
                   BLASTX
Method
NCBI GI
                   g3790593
BLAST score
                   172
                   9.0e-12
E value
Match length
                   76
                   43
% identity
                  (AF079185) RING-H2 finger protein RHY1a [Arabidopsis
NCBI Description
                   thaliana]
                   270889
Seq. No.
Contig ID
                   28589 1.R1011
                   xtd70\overline{0}282259.h2
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4038035
BLAST score
                   155
                   5.0e-10
E value
Match length
                   130
                   36
% identity
                  (AC005936) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   270890
Seq. No.
                   28600 1.R1011
Contig ID
5'-most EST
                   LIB3061-044-Q1-K1-A2
Method
                   BLASTX
NCBI GI
                   q3687237
BLAST score
                   228
                   7.0e-19
E value
Match length
                   62
% identity
                   66
                   (AC005169) putative Cys3His zinc-finger protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   270891
Contig ID
                   28602 1.R1011
5'-most EST
                   LIB3151-018-Q1-K1-G6
Seq. No.
                   270892
Contig ID
                   28602 2.R1011
5'-most EST
                   uC-zmflmo17269d01b1
                   270893
Seq. No.
```

Contig ID 28609 1.R1011

5'-most EST LIB3159-001-Q1-K1-G12

Method BLASTX NCBI GI q4140644 BLAST score 394 E value 3.0e-38 Match length 105

79 % identity



```
(AF090447) 22-kDa zein protein 12 [Zea mays]
NCBI Description
                  270894
Seq. No.
                  28624 1.R1011
Contiq ID
                  LIB3151-019-Q1-K1-C11
5'-most EST
                  270895
Seq. No.
                  28624 2.R1011
Contig ID
                  uC-zmflmo17288h01b1
5'-most EST
                   270896
Seq. No.
Contig ID
                  28644 1.R1011
                  LIB3151-019-Q1-K1-F1
5'-most EST
                  270897
Seq. No.
                   28679 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73067h10b1
                   270898
Seq. No.
                   28679 2.R1011
Contig ID
                   uC-zmrob73080c01b1
5'-most EST
                  BLASTX
Method
                   g4510383
NCBI GI
                   850
BLAST score
                   2.0e-91
E value
Match length
                   252
                   69
% identity
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                   270899
Seq. No.
                   28679_3.R1011
Contig ID
                   LIB3151-020-Q1-K1-D5
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4510383
                   297
BLAST score
                   1.0e-26
E value
                   70
Match length
% identity
                   79
                  (AC007017) unknown protein [Arabidopsis thaliana]
NCBI Description
                   270900
Seq. No.
                   28679 4.R1011
Contig ID
5'-most EST
                   wyr700238867.hl
                   BLASTN
Method
NCBI GI
                   g3821780
BLAST score
                   36
                   2.0e-10
E value
Match length
                   48
                   67
% identity
```

NCBI Description Xenopus laevis cDNA clone 27A6-1 Seq. No. 270901

Contig ID 28704_1.R1011 5'-most EST uC-zmflb73359c10a2 Method BLASTX

NCBI GI g4220481 BLAST score 319



```
E value
                   6.0e-29
Match length
                  159
% identity
                  44
                  (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                  270902
Seq. No.
                  28704 2.R1011
Contig ID
                  uC-zmflmo17097c12b1
5'-most EST
                  BLASTX
Method
                  g4220481
NCBI GI
                  175
BLAST score
E value
                  1.0e-12
                  73
Match length
                  49
% identity
                  (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                  270903
Seq. No.
Contig ID
                  28725 1.R1011
5'-most EST
                  LIB3061-049-Q1-K1-H4
                  270904
Seq. No.
                  28726 1.R1011
Contig ID
5'-most EST
                  LIB3151-021-Q1-K1-F5
Method
                  BLASTX
                  q4006922
NCBI GI
BLAST score
                  154
                   4.0e-10
E value
Match length
                   48
% identity
                   56
                  (Z99708) cytochrome P450 like protein [Arabidopsis
NCBI Description
                  thaliana]
                   270905
Seq. No.
                   28739 1.R1011
Contig ID
                  LIB3152-048-P1-K1-B5
5'-most EST
                  BLASTX
Method
NCBI GI
                  g141597
BLAST score
                   202
E value
                   1.0e-15
                   88
Match length
                   57
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi 22545 emb CAA24728 (V01481) reading frame zein [2]
                   [Zea mays]
Seq. No.
                   270906
Contig ID
                   28739 2.R1011
5'-most EST
                  LIB3059-026-Q1-K1-A3
Method
                   BLASTX
NCBI GI
                   a141609
```

NCBI GI g141609
BLAST score 339
E value 1.0e-31
Match length 177

% identity 69

NCBI Description ZEIN-ALPHA PRECURSOR (19 KD) (PMS2) >gi_100944_pir__S15656 zein, 19K - maize >gi_22448 emb_CAA41543 (X58700) 19 kDa



zein [Zea mays]

Seq. No. 270907

Contig ID 28747_1.R1011 5'-most EST uC-zmflb73078e10b2

Method BLASTX
NCBI GI g1723339
BLAST score 336
E value 5.0e-31
Match length 156
% identity 43

NCBI Description HYPOTHETICAL 19.2 KD PROTEIN YCF36 (ORF165)

>gi_2147559_pir__S73194 hypothetical protein 36 - Porphyra
purpurea chloroplast >gi_1276739 (U38804) hypothetical

chloroplast ORF 36. [Porphyra purpurea]

Seq. No. 270908

Contig ID 28755 1.R1011

5'-most EST LIB3136-018-Q1-K1-G4

Method BLASTX
NCBI GI g2961358
BLAST score 1407
E value 1.0e-156
Match length 331
% identity 79

NCBI Description (AL022140) serine/threonine protein kinase like protein

[Arabidopsis thaliana]

Seq. No. 270909

Contig ID 28756_1.R1011

5'-most EST LIB3061-005-Q1-K1-H8

Method BLASTX
NCBI GI g4097547
BLAST score 226
E value 3.0e-18
Match length 68
% identity 63

NCBI Description (U64906) ATFP3 [Arabidopsis thaliana]

Seq. No. 270910

Contig ID 28762_1.R1011 5'-most EST uC-zmflb73076h09b2

Method BLASTX
NCBI GI g1731181
BLAST score 407
E value 3.0e-39
Match length 360
% identity 31

NCBI Description HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II

>gi_3874230_emb_CAA90107_ (Z49909) weak similarity with a
B. Flavum translocation protein (Swiss Prot accession
number P38376); cDNA EST yk220e10.5 comes from this gene

[Caenorhabditis elegans]

Seq. No. 270911

Contig ID 28762_2.R1011 5'-most EST tzu700201949.h1

E value

Match length % identity

2.0e-47 127

69



```
270912
Seq. No.
                  28775 1.R1011
Contig ID
                  LIB3151-022-Q1-K1-H3
5'-most EST
                  270913
Seq. No.
                  28781 1.R1011
Contig ID
                  LIB3151-023-Q1-K1-A1
5'-most EST
                  270914
Seq. No.
Contig ID
                  28793_1.R1011
                  LIB83-004-Q1-E2-E1
5'-most EST
                  270915
Seq. No.
                  28819 1.R1011
Contig ID
                  uC-zmflb73040a11b1
5'-most EST
                  BLASTN
Method
                  q3869069
NCBI GI
                  38
BLAST score
                  2.0e-11
E value
                  102
Match length
                  84
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MEB5, complete sequence [Arabidopsis thaliana]
                  270916
Seq. No.
                   28819 2.R1011
Contig ID
                  uC-zmflmo17421e01a1
5'-most EST
                  BLASTN
Method
                  g2198852
NCBI GI
                   41
BLAST score
                   2.0e-13
E value
                   65
Match length
                   91
% identity
                  Zea mays cystathionine gamma-synthase (CGS1) gene, complete
NCBI Description
                   cds
                   270917
Seq. No.
                   28825 1.R1011
Contig ID
                   yyf700349509.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4455367
BLAST score
                   933
                   1.0e-102
E value
Match length
                   285
% identity
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]
Seq. No.
                   270918
Contig ID
                   28827 1.R1011
                   LIB143-057-Q1-E1-H2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3395938
BLAST score
                   473
```



NCBI Description (AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq. No. 270919

Contig ID 28840_1.R1011 5'-most EST xmt700257332.h1

Method BLASTX
NCBI GI g1723761
BLAST score 362
E value 7.0e-34
Match length 171
% identity 45

NCBI Description HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION

>gi_2132628_pir__S64571 probable membrane protein YGR245c yeast (Saccharomyces cerevisiae) >gi_1323444_emb_CAA97274_

(Z73030) ORF YGR245c [Saccharomyces cerevisiae] >gi 1702955 emb CAA68967 (Y07703) unknown ORF

[Saccharomyces cerevisiae]

Seq. No. 270920

Contig ID 28855_1.R1011 5'-most EST uC-zmroB73014e01b1

Method BLASTX
NCBI GI g1703446
BLAST score 491
E value 2.0e-49
Match length 167
% identity 58

NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)

>gi_1076292_pir__S53127 asparaginase - Arabidopsis thaliana >gi_735918 emb_CAA84367 (Z34884) asparaginase [Arabidopsis

thaliana]

Seq. No. 270921

Contig ID 28864 1.R1011

5'-most EST LIB3151-024-Q1-K1-G1

Method BLASTX
NCBI GI g3983663
BLAST score 702
E value 3.0e-74
Match length 179
% identity 78

NCBI Description (AB011270) importin-beta1 [Oryza sativa]

Seq. No. 270922

Contig ID 28882_1.R1011 5'-most EST xmt700265223.h1

Method BLASTX
NCBI GI g4105681
BLAST score 155
E value 2.0e-33
Match length 338
% identity 23

NCBI Description (AF049348) unknown [Oryza sativa]

Seq. No. 270923

Contig ID 28882_2.R1011



```
5'-most EST
                  LIB3152-056-P1-K1-D8
                  BLASTX
Method
                  q4105681
NCBI GI
BLAST score
                   164
                   5.0e-18
E value
Match length
                  135
% identity
                   20
                  (AF049348) unknown [Oryza sativa]
NCBI Description
                   270924
Seq. No.
Contig ID
                   28895 1.R1011
5'-most EST
                  LIB3151-025-Q1-K1-F9
                   BLASTX
Method
NCBI GI
                   g4587525
BLAST score
                   547
                   3.0e-77
E value
                   277
Match length
% identity
                   51
                  (AC007060) Contains the PF 00650 CRAL/TRIO
NCBI Description
                   phosphatidyl-inositol-transfer protein domain. ESTs
                   gb_T76582, gb_N06574 and gb_Z25700 come from this gene.
                   [Arabidopsis thaliana]
                   270925
Seq. No.
                   28916 1.R1011
Contig ID
5'-most EST
                   ymt700224830.h1
                   270926
Seq. No.
                   28918 1.R1011
Contig ID
5'-most EST
                   qmh700028293.f1
Method
                   BLASTX
NCBI GI
                   q1705930
BLAST score
                   443
E value
                   1.0e-43
Match length
                   123
                   69
% identity
NCBI Description
                  ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1
                   (ENDOPEPTIDASE CLP 1) >gi 1001349_dbj_BAA10836_ (D64006)
                   ATP-dependent protease ClpP [Synechocystis sp.]
                   270927
Seq. No.
Contig ID
                   28918 3.R1011
5'-most EST
                   fdz701164283.h1
                   270928
Seq. No.
                   28920 1.R1011
Contig ID
5'-most EST
                   ceu700423184.h1
Method
                   BLASTX
NCBI GI
                   g1079136
BLAST score
                   246
E value
                   1.0e-20
```

Match length 91 % identity 44

NCBI Description RNA-binding protein cabeza - fruit fly (Drosophila melanogaster) >gi_532788 (U13178) RNA binding protein

[Drosophila melanogaster] >gi 567106 (L37083) RNA binding

protein [Drosophila melanogaster]



Seq. No. 270929

Contig ID 28920 2.R1011

5'-most EST LIB3067-027-Q1-K1-E8

Method BLASTX
NCBI GI g1079136
BLAST score 252
E value 1.0e-21
Match length 91
% identity 46

NCBI Description RNA-binding protein cabeza - fruit fly (Drosophila

melanogaster) >gi_532788 (U13178) RNA binding protein [Drosophila melanogaster] >gi 567106 (L37083) RNA binding

protein [Drosophila melanogaster]

Seq. No. 270930

Contig ID 28926_1.R1011 5'-most EST uC-zmflb73250h05a2

Method BLASTX
NCBI GI g2829894
BLAST score 649
E value 3.0e-67
Match length 521
% identity 38

NCBI Description (AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No. 270931

Contig ID 28939 1.R1011

5'-most EST LIB3068-027-Q1-K1-E1

Seq. No. 270932

Contig ID 28965_1.R1011

5'-most EST LIB3136-025-Q1-K1-E5

Method BLASTX
NCBI GI g4097547
BLAST score 301
E value 6.0e-27
Match length 162
% identity 46

NCBI Description (U64906) ATFP3 [Arabidopsis thaliana]

Seq. No. 270933

Contig ID 28971 1.R1011

5'-most EST LIB3151-029-Q1-K1-C10

Seq. No. 270934

Contig ID 29050_1.R1011

5'-most EST LIB3059-010-Q1-K1-C3

Method BLASTN
NCBI GI g2245648
BLAST score 113
E value 2.0e-56
Match length 191
% identity 84

NCBI Description Zea mays discolored-1 (mutant allele dsc1-Ref::Mul) gene,

partial sequence



Seq. No. 270935 29050 3.R1011 Contig ID LIB143-006-Q1-E1-C7 5'-most EST BLASTX Method NCBI GI q1171965 1429 BLAST score 1.0e-159 E value Match length 319 87 % identity PHOSPHATIDYLINOSITOL 3-KINASE, ROOT ISOFORM (PI3-KINASE) NCBI Description (PTDINS-3-KINASE) (PI3K) (SPI3K-5) >gi_736339 (L27265) phosphatidylinositol 3-kinase [Glycine max] 270936 Seq. No. 29053 1.R1011 Contig ID LIB3151-031-Q1-K1-B4

5'-most EST Method BLASTX q2191171 NCBI GI BLAST score 186 1.0e-13 E value 66 Match length 45 % identity

(AF007270) similar to A. thaliana DI19 mRNA (NID:g469110) NCBI Description

[Arabidopsis thaliana]

270937 Seq. No. 29053 2.R1011 Contig ID 5'-most EST LIB143-018-Q1-E1-B2

270938 Seq. No. 29058 1.R1011 Contig ID uC-zmflmo17330a08b1 5'-most EST

270939 Seq. No. 29074 1.R1011 Contig ID xsy700209514.h1 5'-most EST

BLASTX Method q3924596 NCBI GI BLAST score 296 1.0e-32 E value 116 Match length 73 % identity

(AF069442) putative phospho-ser/thr phosphatase NCBI Description

[Arabidopsis thaliana]

270940 Seq. No.

29074 2.R1011 Contig ID uC-zmflmo17333a06b15'-most EST

BLASTX Method g3924596 NCBI GI 1070 BLAST score 1.0e-117 E value 241 Match length 87 % identity

(AF069442) putative phospho-ser/thr phosphatase NCBI Description

[Arabidopsis thaliana]

Contig ID

5'-most EST Method



```
270941
Seq. No.
                  29075 1.R1011
Contig ID
                  LIB3151-047-P1-K1-G4
5'-most EST
                  BLASTX
Method
                   g1685003
NCBI GI
                   187
BLAST score
                   4.0e-14
E value
                   90
Match length
                   41
% identity
                   (U32643) immediate-early salicylate-induced
NCBI Description
                   glucosyltransferase [Nicotiana tabacum]
                   270942
Seq. No.
                   29094 3.R1011
Contig ID
                   LIB3136-025-Q1-K1-D4
5'-most EST
                   270943
Seq. No.
                   29110 1.R1011
Contig ID
                   LIB3182-004-P2-M1-D5
5'-most EST
                   BLASTN
Method
                   g1037129
NCBI GI
                   376
BLAST score
                   0.0e+00
E value
                   436
Match length
                   97
% identity
                   (gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                   Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                   270944
Seq. No.
                   29114 1.R1011
Contig ID
                   uC-zm\overline{f}lb73307a02b1
5'-most EST
                   BLASTX
Method
                   q116923
NCBI GI
                   492
BLAST score
                   1.0e-49
E value
                   173
Match length
                   54
% identity
                   COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
NCBI Description
                   >gi_111414_pir_S13520 beta-COP protein - rat
                   >gi_55819emb_\overline{CA}A40505_ (X57228) beta COP [Rattus
                   norvegicus]
                   270945
Seq. No.
                   29138 1.R1011
Contig ID
                   LIB3151-044-Q1-K1-D5
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4220523
BLAST score
                   225
E value
                   3.0e-18
                   107
Match length
% identity
NCBI Description (AL035356) putative alliin lyase [Arabidopsis thaliana]
                   270946
Seq. No.
                   29177 1.R1011
```

37731

LIB3151-037-Q1-K1-B2

BLASTX



```
g141597
NCBI GI
                   314
BLAST score
                   2.0e-45
E value
                   131
Match length
                   81
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A30)
NCBI Description
                   >gi_72314_pir__ZIZM3 19K zein precursor (clone A30) - maize
                   >gi_22545_emb_CAA24728_ (V01481) reading frame zein [2]
                   [Zea mays]
                   270947
Seq. No.
                   29185 1.R1011
Contig ID
                   uC-zmroteosinte047d04b1
5'-most EST
                   BLASTX
Method
                   g4467117
NCBI GI
                   436
BLAST score
                   2.0e-42
E value
                   304
Match length
                   38
% identity
                   (AL035538) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   270948
Seq. No.
                   29195 1.R1011
Contig ID
                   qmh700025837.f1
5'-most EST
                   BLASTX
Method
                   g719291
NCBI GI
                   479
BLAST score
                   5.0e-48
E value
                   201
Match length
                   54
% identity
                   (U19134) unknown [Arabidopsis thaliana]
NCBI Description
                   >gi_1095007_prf__2107236A SABRE gene [Arabidopsis thaliana]
                   270949
Seq. No.
                   29197_1.R1011
Contig ID
                   xsy70\overline{0}217410.h1
5'-most EST
Method
                   BLASTX
                   g4262186
NCBI GI
BLAST score
                   1833
                   0.0e + 00
E value
Match length
                   463
                   76
% identity
                   (AC005508) Highly similar to cullin 3 [Arabidopsis
NCBI Description
                   thaliana]
                   270950
Seq. No.
Contig ID
                   29225 1.R1011
5'-most EST
                   xyt700344012.h1
Method
                   BLASTX
                   q3128186
NCBI GI
                   339
BLAST score
                   3.0e - 31
E value
Match length
                   178
% identity
```

Seq. No. 270951

NCBI Description

(AC004521) hypothetical protein [Arabidopsis thaliana]

Match length

% identity

411



```
29231 1.R1011
Contig ID
                  LIB3151-038-Q1-K1-F3
5'-most EST
                  270952
Seq. No.
Contig ID
                  29259 1.R1011
5'-most EST
                  xsy700208627.hl
Seq. No.
                  270953
                  29300 1.R1011
Contig ID
5'-most EST
                  xmt700261064.hl
                  270954
Seq. No.
Contig ID
                  29304 1.R1011
                  LIB3068-009-Q1-K1-H4
5'-most EST
                  BLASTX
Method
                  q1085952
NCBI GI
BLAST score
                  611
                  4.0e-63
E value
Match length
                  147
                  81
% identity
                  hypothetical protein S1 - Phalaris coerulescens
NCBI Description
                  >qi 556831 emb CAA57519 (X81991) S1 [Phalaris
                  coerulescens] >gi 1103489 emb CAA63108 (X92351)
                  self-incompatibility mutant protein [Phalaris coerulescens]
                  270955
Seq. No.
                   29304 2.R1011
Contig ID
5'-most EST
                  LIB3068-031-Q1-K1-C1
Method
                  BLASTN
NCBI GI
                   g556832
BLAST score
                   45
                   6.0e-16
E value
Match length
                  113
% identity
                   89
NCBI Description P.coerulescens S2 gene
                   270956
Seq. No.
                   29321 1.R1011
Contig ID
                   LIB3151-041-Q1-K1-A4
5'-most EST
                   BLASTX
Method
                   g3169719
NCBI GI
                   515
BLAST score
                   4.0e-52
E value
Match length
                   137
                   70
% identity
NCBI Description (AF007109) similar to yeast dcp1 [Arabidopsis thaliana]
                   270957
Seq. No.
                   29322 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17154b01b1
                   BLASTX
Method
                   g2827143
NCBI GI
                   1462
BLAST score
                   1.0e-163
E value
```

NCBI Description (AF027174) cellulose synthase catalytic subunit



[Arabidopsis thaliana]

270958 Seq. No. 29330 1.R1011 Contig ID LIB3060-008-Q1-K1-C1 5'-most EST BLASTX Method g4106061 NCBI GI 218 BLAST score 2.0e-17 E value 71 Match length 61 % identity (AF053318) CCR4-associated factor 1 [Homo sapiens] NCBI Description 270959 Seq. No. 29330 2.R1011 Contig ID yyf700352159.h1 5'-most EST BLASTX Method g4106061 NCBI GI 213 BLAST score 7.0e-17 E value 72 Match length 60 % identity (AF053318) CCR4-associated factor 1 [Homo sapiens] NCBI Description 270960 Seq. No. 29337 1.R1011 Contig ID 5'-most EST uC-zmflb73223g01b2 Method BLASTX g3786005 NCBI GI 223 BLAST score 6.0e-18 E value 53 Match length 75 % identity (AC005499) putative phosphoethanolamine NCBI Description cytidylyltransferase [Arabidopsis thaliana] Seq. No. 270961 29360 1.R1011 Contig ID LIB3151-041-Q1-K1-G3 5'-most EST BLASTX Method q2688299 NCBI GI BLAST score 508 2.0e-51 E value 143 Match length 60 % identity (AE001145) prolyl-tRNA synthetase (proS) [Borrelia NCBI Description burgdorferi] Seq. No. 270962 29370 1.R1011 Contig ID 5'-most EST LIB3151-042-Q1-K1-A1 BLASTX Method NCBI GI g2982459 BLAST score 147

2.0e-09

56 50

E value Match length

% identity



```
(AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  270963
                  29373 1.R1011
Contig ID
                  uwc700152189.h1
5'-most EST
                  BLASTX
Method
                  q2621621
NCBI GI
                  152
BLAST score
                  2.0e-09
E value
                  168
Match length
                   29
% identity
                   (AE000837) cationic amino acid transporter related protein
NCBI Description
                   [Methanobacterium thermoautotrophicum]
                   270964
Seq. No.
Contig ID
                   29391 1.R1011
                  LIB189-008-Q1-E1-D8
5'-most EST
Method
                  BLASTX
                   q4321762
NCBI GI
                   1125
BLAST score
                   1.0e-123
E value
                   311
Match length
% identity
                   73
                  (AF061107) transcription factor MYC7E [Zea mays]
NCBI Description
                   270965
Seq. No.
                   29396 1.R1011
Contig ID
5'-most EST
                   vux700156758.h1
                   BLASTX
Method
                   g2696229
NCBI GI
                   196
BLAST score
                   6.0e-24
E value
                   118
Match length
                   62
% identity
                  (D55712) chitinase [Oryza sativa]
NCBI Description
Seq. No.
                   270966
                   29399 1.R1011
Contig ID
                   uC-zmrob73049e11a1
5'-most EST
Method
                   BLASTX
                   q4191774
NCBI GI
BLAST score
                   415
                   1.0e-40
E value
                   135
Match length
% identity
                   63
                   (AC005917) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   270967
                   29419 1.R1011
Contig ID
5'-most EST
                   LIB3061-025-Q1-K1-A7
                   BLASTX
Method
NCBI GI
                   q2129628
BLAST score
                   202
E value
                   9.0e-16
```

37735

72

57

Match length % identity



ketoconazole resistent protein - Arabidopsis thaliana NCBI Description >gi 928938 emb_CAA61433_ (X89036) ketoconazole resistent protein [Arabidopsis thaliana]

270968 Seq. No. 29433 1.R1011 Contig ID uC-zmflb73222f01b1 5'-most EST

270969 Seq. No.

29440 1.R1011 Contig ID

LIB3061-054-Q1-K1-H2 5'-most EST

BLASTX Method g2894603 NCBI GI 191 BLAST score 3.0e-14E value 93 Match length 39 % identity

(AL021889) putative protein [Arabidopsis thaliana] NCBI Description

270970 Seq. No.

29459 1.R1011 Contig ID

LIB3151-044-Q1-K1-F7 5'-most EST

BLASTX Method g1370160 NCBI GI 852 BLAST score 2.0e-91 E value 208 Match length % identity 82

NCBI Description (Z73958) RAB11J [Lotus japonicus]

270971 Seq. No.

29472 1.R1011 Contig ID 5'-most EST tzu700202569.h1

270972 Seq. No.

29473 1.R1011 Contig ID uC-zmflmo17202h10b1

5'-most EST

270973 Seq. No.

29473 3.R1011 Contig ID

LIB3180-005-P2-M1-G9 5'-most EST

BLASTX Method NCBI GI g461033 363 BLAST score 2.0e-34 E value 151 Match length 48 % identity

NCBI Description (S68015) c6.1A [human, Peptide, 324 aa] [Homo sapiens]

270974 Seq. No.

Contig ID 29473 4.R1011

uC-zmflmo17130b05b1 5'-most EST

270975 Seq. No.

29480 1.R1011 Contig ID

LIB3151-045-Q1-K1-B8 5'-most EST



Seq. No. 270976

Contig ID 29499_1.R1011

5'-most EST $uC-zm\overline{f}lm017214b05b1$

Method BLASTX
NCBI GI g1705677
BLAST score 494
E value 6.0e-50
Match length 111
% identity 82

NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG

>gi_2118115_pir__S60112 cell division control protein CDC48
homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell

division cycle protein [Arabidopsis thaliana]

Seq. No. 270977

Contig ID 29513_1.R1011 5'-most EST uC-zmflB73046e09b1

Seq. No. 270978

Contig ID 29513_2.R1011 5'-most EST pmx700088613.h1

Method BLASTX
NCBI GI g2739431
BLAST score 482
E value 4.0e-48
Match length 243
% identity 42

NCBI Description (U70368) hematopoietic-specific IL-2 deubiquitinating

enzyme [Mus musculus]

Seq. No. 270979

Contig ID 29513_3.R1011 5'-most EST pmx700083983.h1

Seq. No. 270980

Contig ID 29513_10.R1011 5'-most EST rvt700552954.h1

Seq. No. 270981

Contig ID 29519_1.R1011

5'-most EST uC-zmroteosinte120d08b2

Method BLASTX
NCBI GI g4204304
BLAST score 776
E value 1.0e-82
Match length 201
% identity 74

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 270982

Contig ID 29520 1.R1011 5'-most EST uC-zmflb73065b08b1

Method BLASTX
NCBI GI g3786009
BLAST score 1113
E value 1.0e-122



```
Match length
                  281
% identity
                  (AC005499) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  270983
                  29520 2.R1011
Contig ID
                  uwc700154359.h1
5'-most EST
Method
                  BLASTX
                  a3786009
NCBI GI
BLAST score
                  159
                  2.0e-10
E value
                  50
Match length
% identity
                  70
                  (AC005499) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  270984
Contig ID
                  29521 1.R1011
5'-most EST
                  uC-zmflmo17122f11b1
Method
                  BLASTX
                  q2130052
NCBI GI
BLAST score
                  2161
                  0.0e+00
E value
                   456
Match length
% identity
                  86
                  xylose isomerase (EC 5.3.1.5) - barley
NCBI Description
                   >gi 1296809 emb CAA64545 (X95257) xylose isomerase
                   [Hordeum vulgare]
Seq. No.
                   270985
Contig ID
                   29521 2.R1011
5'-most EST
                  bdu700383182.h1
                  BLASTX
Method
NCBI GI
                   g2130052
BLAST score
                   371
                   2.0e-35
E value
Match length
                  84
                   86
% identity
                  xylose isomerase (EC 5.3.1.5) - barley
NCBI Description
                   >gi 1296809 emb CAA64545 (X95257) xylose isomerase
                   [Hordeum vulgare]
                   270986
Seq. No.
                   29521 3.R1011
Contig ID
                   yyf700349932.h1
5'-most EST
Method
                   BLASTX
                   g2130051
NCBI GI
BLAST score
                   340
                   7.0e-32
E value
                   78
Match length
                   77
% identity
                  xylose isomerase (EC 5.3.1.5) - barley
NCBI Description
                   >gi 1296807 emb CAA64544 (X95256) xylose isomerase
```

Seq. No. 270987 Contig ID 29525 1.R1011

isomerase [Hordeum vulgare]

[Hordeum vulgare] >gi 1588664 prf 2209268A xylose

Seq. No.

270994



```
LIB3151-046-Q1-K1-E1
5'-most EST
                  270988
Seq. No.
                   29543 1.R1011
Contig ID
                  LIB3151-046-Q1-K1-H5
5'-most EST
                  BLASTX
Method
                   q4521249
NCBI GI
BLAST score
                   474
                   2.0e-47
E value
                   174
Match length
                   56
% identity
                  (AB013912) DNA helicase [Mus musculus]
NCBI Description
                   270989
Seq. No.
                   29555 1.R1011
Contig ID
                   LIB3062-031-Q1-K1-D12
5'-most EST
Seq. No.
                   270990
                   29591 1.R1011
Contig ID
                   uC-zmflb73182h05b1
5'-most EST
                   270991
Seq. No.
                   29669 1.R1011
Contig ID
                   LIB3182-001-P1-M1-A11
5'-most EST
                   BLASTX
Method
                   q4056613
NCBI GI
BLAST score
                   826
                   9.0e-89
E value
Match length
                   157
                   97
% identity
                  (AF067400) Scl1 protein [Zea mays]
NCBI Description
                   270992
Seq. No.
                   29672 1.R1011
Contig ID
                   LIB3151-050-P1-K1-B5
5'-most EST
                   BLASTX
Method
                   g4512685
NCBI GI
                   177
BLAST score
                   2.0e-27
E value
                   109
Match length
                   53
 % identity
                   (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087)
                   hypothetical protein [Arabidopsis thaliana]
                   270993
 Seq. No.
                   29678 1.R1011
 Contig ID
 5'-most EST
                   LIB3180-045-P2-M2-H12
                   BLASTX
 Method
                   q4097547
 NCBI GI
                   273
 BLAST score
                   6.0e-24
 E value
 Match length
                   67
                   76
 % identity
 NCBI Description (U64906) ATFP3 [Arabidopsis thaliana]
```



Contig ID 29700_1.R1011 5'-most EST uC-zmflb73152b05b1

Seq. No. 270995

Contig ID 29700_2.R1011 5'-most EST uwc700149875.h1

Seq. No. 270996

Contig ID 29700_3.R1011

5'-most EST LIB3156-012-Q1-K1-D3

Seq. No. 270997

Contig ID 29701_1.R1011

5'-most EST LIB3151-050-P1-K1-G5

Seq. No. 270998

Contig ID 29702 1.R1011 5'-most EST xsy700214016.h1

Method BLASTX
NCBI GI g4544445
BLAST score 691
E value 6.0e-73
Match length 183
% identity 77

NCBI Description (AC006592) putative pyrophosphate--fructose 6-phosphate

1-phosphotransferase [Arabidopsis thaliana]

Seq. No. 270999

Contig ID 29704 1.R1011

5'-most EST uC-zmflmo17015c12b1

Seq. No. 271000

Contig ID 29706_1.R1011

5'-most EST LIB3062-008-Q1-K1-G10

Seq. No. 271001

Contig ID 29715_1.R1011 5'-most EST qmh700030565.f1

Seq. No. 271002

Contig ID 29756_1.R1011

5'-most EST uC-zmflm017212g06b1

Method BLASTX
NCBI GI g4206196
BLAST score 186
E value 3.0e-13
Match length 224

% identity 32

NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana]

Seq. No. 271003

Contig ID 29824 1.R1011

5'-most EST LIB3068-008-Q1-K1-F2

Seq. No. 271004

Contig ID 29825_1.R1011 5'-most EST uC-zmflb73233f10b1



```
BLASTX
Method
                    q82308
NCBI GI
BLAST score
                    665
                    7.0e-70
E value
Match length
                    126
                    93
% identity
                    myb protein 308 - garden snapdragon
NCBI Description
                    271005
Seq. No.
                    29825 2.R1011
Contig ID
                    uC-zm\overline{f}1b73008g11b1
5'-most EST
                    BLASTX
Method
                    g82308
NCBI GI
                    708
BLAST score
                    7.0e-75
E value
                    139
Match length
% identity
                    91
                    myb protein 308 - garden snapdragon
NCBI Description
                    271006
Seq. No.
                    29825 3.R1011
Contig ID
                    wyr700242984.hl
5'-most EST
                    BLASTX
Method
NCBI GI
                    g127579
                    438
BLAST score
                    2.0e-70
E value
                    172
Match length
                    78
% identity
                    MYB-RELATED PROTEIN HV1 >gi_82423_pir__S04896 transforming
NCBI Description
                    protein (myb) homolog (clone Hv1) - barley
                     >gi 2130044 pir__S61506 Myb1 protein - barley
                     >gi_19051_emb_CAA50222 (X70877) MybHv1 [Hordeum vulgare]
>gi_19053_emb_CAA50224 (X70879) MybHv1 [Hordeum vulgare]
                     >gi_22703\overline{0}_pr\overline{f}_161341\overline{2}A myb-related gene Hv1 [Hordeum
                     vulgare var. distichum]
                     271007
Seq. No.
                     29825 4.R1011
Contig ID
                     LIB3151-057-Q1-K1-E8
5'-most EST
                     BLASTX
Method
                     g2605617
NCBI GI
                     551
BLAST score
                     2.0e-56
E value
                     167
Match length
                     62
 % identity
 NCBI Description (D88617) OSMYB1 [Oryza sativa]
                     271008
 Seq. No.
                     29825 5.R1011
 Contig ID
 5'-most EST
                     LIB3062-010-Q1-K1-A1
                     BLASTX
 Method
                     g2605617
 NCBI GI
                     598
 BLAST score
                     3.0e-62
 E value
```

37741

115

NCBI Description (D88617) OSMYB1 [Oryza sativa]

Match length % identity



```
271009
Seq. No.
                  29830 1.R1011
Contig ID
                  LIB3151-057-Q1-K1-F3
5'-most EST
                  BLASTX
Method
                  g1730777
NCBI GI
                  357
BLAST score
                  2.0e-48
E value
                  251
Match length
                  45
% identity
                  HYPOTHETICAL 119.3 KD PROTEIN IN FPR1-TOM22 INTERGENIC
NCBI Description
                  REGION >gi_1078050_pir__S55151 probable membrane protein
                  YNL132w - yeast (Saccharomyces cerevisiae)
                  >gi_854505_emb_CAA86893_ (Z46843) orf16 [Saccharomyces
                  cerevisiae] >gi_1302072_emb_CAA96014_ (Z71408) ORF_YNL132w
                  [Saccharomyces cerevisiae]
                  271010
Seq. No.
                  29845 1.R1011
Contig ID
                  fwa700101803.hl
5'-most EST
                  BLASTX
Method
                  g4454017
NCBI GI
                  160
BLAST score
                  6.0e-11
E value
                  45
Match length
                  69
% identity
                  (AL035396) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  271011
Seq. No.
                  29851 1.R1011
Contig ID
5'-most EST
                  LIB148-003-Q1-E1-B12
                  BLASTX
Method
                  g2827623
NCBI GI
                  198
BLAST score
                  4.0e-15
E value
                  60
Match length
                   62
% identity
                  (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
                  271012
Seq. No.
                   29867 1.R1011
Contig ID
5'-most EST
                  rv1700457807.h1
Method
                  BLASTX
                  q4585907
NCBI GI
                   761
BLAST score
                   5.0e-81
E value
Match length
                   188
% identity
NCBI Description (AC006298) unknown protein [Arabidopsis thaliana]
                   271013
Seq. No.
                   29869 1.R1011
Contig ID
5'-most EST
                   LIB3151-058-Q1-K1-E3
```

Method BLASTX
NCBI GI g3023929
BLAST score 1160
E value 1.0e-127

300 Match length % identity HISTONE DEACETYLASE 1 (HD1) >qi 2791684 (AF039751) histone NCBI Description deacetylase-1; HD-1 [Gallus gallus] >gi 2829214 (AF044169) erythrocyte histone deacetylase [Gallus gallus] 271014 Seq. No. 29874 1.R1011 Contig ID 5'-most EST ntr700071920.h1 Method BLASTX NCBI GI g3023275 BLAST score 384 4.0e-37 E value 124 Match length 62 % identity ALPHA-GLUCOSIDASE PRECURSOR (MALTASE) NCBI Description >gi_2130027_pir__S65057 alpha-glucosidase (EC 3.2.1.20) barley >qi 944901 (U22450) alpha-glucosidase [Hordeum vulgare] 271015 Seq. No. 29876_1.R1011 Contig ID 5'-most EST uC-zmflB73007g02b1 BLASTX Method g166410 NCBI GI BLAST score 504 E value 6.0e-51 Match length 125 73 % identity NCBI Description (L07291) Alfin-1 [Medicago sativa] 271016 Seq. No.

Contig ID 29877 1.R1011

5'-most EST LIB3151-058-Q1-K1-G1

Seq. No. 271017

Contig ID 29880 1.R1011

5'-most EST LIB3060-041-Q1-K1-B7

Seq. No. 271018

Contig ID 29890 1.R1011

5'-most EST uC-zmroteosinte068c07b1

271019 Seq. No.

29897 1.R1011 Contig ID

5'-most EST uC-zmflb73149a06b1 Method BLASTX

NCBI GI g4585977 BLAST score 444 6.0e-44E value 125 Match length % identity

(AC005287) Unknown protein [Arabidopsis thaliana] NCBI Description

271020 Seq. No.

Contig ID 29903 1.R1011 uC-zmflb73066c02b1 5'-most EST



Method BLASTX
NCBI GI g2829927
BLAST score 506
E value 5.0e-51
Match length 239
% identity 48

NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No. 271021

Contig ID 29919 1.R1011 5'-most EST xsy700212087.h1

Seq. No. 271022

Contig ID 29942 1.R1011

5'-most EST LIB3136-040-P1-K1-D5

Seq. No. 271023

Contig ID 29943 1.R1011

5'-most EST LIB3180-046-P2-M2-E3

Seq. No. 271024

Contig ID 29954 1.R1011

5'-most EST uC-zmroteosinte061a10b2

Method BLASTX
NCBI GI g541816
BLAST score 922

E value 1.0e-100 Match length 211 % identity 82

NCBI Description protein kinase - common ice plant >gi_457689_emb_CAA82990_

(Z30329) protein kinase [Mesembryanthemum crystallinum]

Seq. No. 271025

Contig ID 29956 1.R1011

5'-most EST LIB189-010-Q1-E1-A6

Seq. No. 271026

Contig ID 29978_1.R1011

5'-most EST LIB3151-062-Q1-K1-B12

Method BLASTN
NCBI GI g2655290
BLAST score 34
E value 1.0e-09
Match length 86
% identity 85

NCBI Description Oryza sativa germin-like protein 4 (GER4) mRNA, complete

cds

Seq. No. 271027

Contig ID 29994_1.R1011 5'-most EST bdu700383137.h1

Method BLASTX
NCBI GI g1245182
BLAST score 1869
E value 0.0e+00
Match length 430
% identity 78



```
NCBI Description (U49398) sterol delta-7 reductase [Arabidopsis thaliana]
Seq. No.
                  271028
                  29999 1.R1011
Contig ID
                  uC-zmflmo17103e09b1
5'-most EST
                  271029
Seq. No.
                  29999 2.R1011
Contig ID
                  LIB3159-015-Q1-K1-B12
5'-most EST
                   271030
Seq. No.
                   30000 1.R1011
Contig ID
                  LIB3180-038-P2-M2-H1
5'-most EST
                   BLASTX
Method
                   q3402487
NCBI GI
BLAST score
                   200
E value
                   1.0e-15
Match length
                   105
% identity
                   45
                  (AB015138) Vacuolar proton pyrophosphatase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   271031
                   30039 1.R1011
Contig ID
5'-most EST
                   hvj700621162.h1
                   271032
Seq. No.
Contig ID
                   30047 1.R1011
5'-most EST
                   LIB3152-001-Q1-K1-G5
                   271033
Seq. No.
                   30059 1.R1011
Contig ID
                   uC-zm\overline{f}lmo17152e11b1
5'-most EST
                   BLASTN
Method
                   g3821780
NCBI GI
                   36
BLAST score
                   1.0e-10
E value
                   48
Match length
% identity
                   67
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   271034
Seq. No.
                   30060 1.R1011
Contig ID
                   LIB3152-002-Q1-K1-B4
5'-most EST
                   271035
Seq. No.
                   30061 1.R1011
Contig ID
5'-most EST
                   LIB3068-057-Q1-K1-B5
```

271036 Seq. No.

30070 1.R1011 Contig ID

LIB3180-029-P2-M2-F11 5'-most EST

271037 Seq. No.

30070 2.R1011 Contig ID

LIB3180-027-P2-M2-A9 5'-most EST



```
Seq. No.
                   271038
                   30073 1.R1011
Contig ID
                  hbs701182052.h1
5'-most EST
                   BLASTX
Method
                   g2281089
NCBI GI
                   380
BLAST score
                   2.0e-36
E value
                   79
Match length
                   91
% identity
                   (AC002333) Sm protein F isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   271039
                   30097_1.R1011
Contig ID
                   wen700332547.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4432814
                   414
BLAST score
                   7.0e-40
E value
                   306
Match length
                   33
% identity
                  (AC006593) unknown protein [Arabidopsis thaliana]
NCBI Description
                   271040
Seq. No.
                   30104 1.R1011
Contig ID
                   LIB3152-003-P1-K1-D1
5'-most EST
                   271041
Seq. No.
Contig ID
                   30130 1.R1011
                   xmt70\overline{0}264770.h1
5'-most EST
                   BLASTX
Method
                   q1370172
NCBI GI
                   709
BLAST score
                   1.0e-74
E value
                   209
Match length
                   67
% identity
                  (Z73935) RAB1X [Lotus japonicus]
NCBI Description
                   271042
Seq. No.
                   30176 1.R1011
Contig ID
                   LIB3069-009-Q1-K1-D3
5'-most EST
                   271043
Seq. No.
Contig ID
                   30182 1.R1011
5'-most EST
                   pwr700451595.hl
                   271044
Seq. No.
                   30191_1.R1011
Contig ID
5'-most EST
                   LIB3180-053-P2-M1-C11
                   BLASTX
Method
                   q141617
NCBI GI
BLAST score
                   289
                   6.0e-26
E value
```

Match length 104 % identity 58

ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1) NCBI Description

>gi_100941_pir__S12140 zein Zc1 - maize
>gi_100945_pir__B29017 zein 2 - maize



>gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays] >gi 168666 (M16460) 16-kDa zein protein [Zea mays]

271045 Seq. No. 30210 1.R1011 Contig ID 5'-most EST wyr700236843.h1

271046 Seq. No.

30240 1.R1011 Contig ID

5'-most EST LIB3068-047-Q1-K1-E9

BLASTX Method g2621324 NCBI GI BLAST score 179 2.0e-22 E value Match length 133 47 % identity

NCBI Description (AE000813) conserved protein [Methanobacterium

thermoautotrophicum]

271047 Seq. No.

30240 2.R1011 Contig ID 5'-most EST uC-zmflb73203d04a1

271048 Seq. No.

30245 1.R1011 Contig ID

uC-zmflmo17269c02b1 5'-most EST

Method BLASTN g2062705 NCBI GI BLAST score 36 2.0e-10 E value Match length 36

100 % identity

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 271049

30247 1.R1011 Contig ID $xdb70\overline{0}341946.h1$ 5'-most EST

Method BLASTX NCBI GI q2934885 BLAST score 288 2.0e-25 E value 81 Match length 73 % identity

NCBI Description (L28004) TGACG-motif-binding factor [Glycine max]

271050 Seq. No.

30249 1.R1011 Contig ID 5'-most EST wen700334249.h1

Seq. No. 271051

Contig ID 30256 1.R1011 5'-most EST uC-zmflb73152g04b1

Method BLASTX NCBI GI g544184 BLAST score 666 E value 5.0e-70

Match length 176



5'-most EST uC-zmflmo17292c01b1
Method BLASTX
NCBI GI g3288823
BLAST score 694
E value 8.0e-73
Match length 189
% identity 73

NCBI Description (AF063852) FUS5 [Arabidopsis thaliana]

Seq. No. 271053
Contig ID 30261 2.R1011

5'-most EST LIB3137-057-Q1-K1-A2

Seq. No. 271054

Contig ID 30261_3.R1011 5'-most EST uC-zmflb73137e10a1

Method BLASTX
NCBI GI g3288823
BLAST score 203
E value 6.0e-34
Match length 126
% identity 59

NCBI Description (AF063852) FUS5 [Arabidopsis thaliana]

Seq. No. 271056

Contig ID 30263_1.R1011 5'-most EST xmt700263672.h1

Method BLASTX
NCBI GI g2501197
BLAST score 285
E value 2.0e-25
Match length 47
% identity 100

NCBI Description GAMMA-ZEATHIONIN

Seq. No. 271057

Contig ID 30271 2.R1011 5'-most EST gwl700613288.h1

Method BLASTX
NCBI GI g4586107
BLAST score 347
E value 1.0e-32
Match length 118
% identity 15



NCBI Description (AL049638) putative disease resistance protein [Arabidopsis thaliana]

Seq. No. 271058

Contig ID 30285_1.R1011 5'-most EST fwa700101161.h1

Method BLASTX
NCBI GI g409756
BLAST score 257
E value 1.0e-21
Match length 198
% identity 32

NCBI Description (L25643) ATP/GTP nucleotide-binding protein [Leishmania

infantum]

Seq. No. 271059

Contig ID 30285 2.R1011

5'-most EST uC-zmflmo17219d03b1

Seq. No. 271060

Contig ID 30285_3.R1011 5'-most EST yyf700350457.h1

Seq. No. 271061

Contig ID 30285_4.R1011 5'-most EST cjh700195328.h1

Seq. No. 271062

Contig ID 30309_1.R1011 5'-most EST uC-zmflb73152h12b1

Method BLASTX
NCBI GI g416583
BLAST score 191
E value 6.0e-14
Match length 204
% identity 32

NCBI Description ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE)

(ACYL-ACTIVATING ENZYME) >gi_396404 (U00006) acetyl-CoA sythetase [Escherichia coli] >gi_1790505 (AE000480)

acetyl-CoA synthetase [Escherichia coli]

Seq. No. 271063

Contig ID 30323_1.R1011

5'-most EST uC-zmflmo17307h07b1

Method BLASTX
NCBI GI g3080418
BLAST score 216
E value 4.0e-17
Match length 111
% identity 42

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 271064

Contig ID 30353 1.R1011

5'-most EST LIB3137-058-Q1-K1-E9

Method BLASTX NCBI GI g3869088

37749

....



BLAST score 1169 1.0e-128 E value 224 Match length 99 % identity

(AB019427) elongation factor-1 alpha [Nicotiana paniculata] NCBI Description

271065 Seq. No.

30365 1.R1011 Contig ID pmx700082389.h15'-most EST

BLASTX Method g4406770 NCBI GI BLAST score 1168 1.0e-128 E value 314 Match length % identity 67

(AC006836) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 271066

30368 1.R1011 Contig ID

LIB3152-014-P1-K1-F9 5'-most EST

271067 Seq. No.

30368 2.R1011 Contig ID hvj700619154.hl 5'-most EST

271068 Seq. No.

30382 1.R1011 Contig ID

5'-most EST LIB3061-053-Q1-K1-H9

Method BLASTX g2118425 NCBI GI 250 BLAST score 3.0e-21E value 73 Match length 66

% identity

subtilisin/chymotrypsin inhibitor - maize NCBI Description

>gi_475253_emb_CAA55588_ (X78988) proteinase inhibitor [Zea

mays] >gi_475922_emb_CAA49593_ (X69972) proteinase inhibitor [Zea mays] >gi_559538_emb_CAA57677_ (X82187) substilin /chymotrypsin-like inhibitor [Zea mays]

271069 Seq. No.

Contig ID 30386 1.R1011 5'-most EST xjt700094629.h1

271070 Seq. No.

30391 1.R1011 Contig ID 5'-most EST $zuv70\overline{0}354617.h1$

Seq. No. 271071

30416 1.R1011 Contig ID

uC-zmflmo17019g06a1 5'-most EST

BLASTX Method NCBI GI q3080413 BLAST score 515 6.0e-52 E value Match length 171 % identity 58



```
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
                  271072
Seq. No.
                  30432 1.R1011
Contiq ID
                  uC-zmrob73050a04b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3451075
                  412
BLAST score
                  3.0e-40
E value
                  123
Match length
                  64
% identity
                  (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
                  271073
Seq. No.
                  30437 1.R1011
Contig ID
                  uC-zmflb73018d07b1
5'-most EST
                  BLASTX
Method
                  g2367392
NCBI GI
                  415
BLAST score
                  1.0e-55
E value
                  246
Match length
                   47
% identity
                  (U82513) random slug cDNA25 protein [Dictyostelium
NCBI Description
                  discoideum]
                   271074
Seq. No.
Contig ID
                   30437 2.R1011
                  uC-zmflb73192f12b1
5'-most EST
                   271075
Seq. No.
                   30452 1.R1011
Contig ID
                   LIB3137-005-Q1-K1-F5
5'-most EST
                   BLASTX
Method
NCBI GI
                   q3892708
                   548
BLAST score
E value
                   5.0e-56
Match length
                   192
% identity
                   52
                  (AL033545) putative protein [Arabidopsis thaliana]
NCBI Description
                   271076
Seq. No.
Contig ID
                   30463 1.R1011
                   xmt700266090.h1
5'-most EST
                   271077
Seq. No.
                   30465 1.R1011
Contig ID
5'-most EST
                   uC-zmroteosinte025f11b1
Method
                   BLASTX
NCBI GI
                   q2129753
BLAST score
                   759
E value
                   6.0e-81
Match length
                   168
% identity
                   83
                   threonine synthase (EC 4.2.99.2) precursor - Arabidopsis
NCBI Description
                   thaliana (fragment) >gi_1448917 (L41666) threonine synthase
```

37751

[Arabidopsis thaliana]



```
271078
Seq. No.
                  30470 1.R1011
Contig ID
                  LIB3152-018-P1-K1-E3
5'-most EST
                  271079
Seq. No.
                  30483 1.R1011
Contig ID
                  LIB143-041-Q1-E1-C2
5'-most EST
                  BLASTX
Method
                  q4325372
NCBI GI
                  208
BLAST score
                  4.0e-16
E value
                  88
Match length
                  48
% identity
                  (AF128396) contains similarity to protein disulfide
NCBI Description
                  isomerases [Arabidopsis thaliana]
                  271080
Seq. No.
                  30483 2.R1011
Contig ID
                  rv1700457711.h1
5'-most EST
                  271081
Seq. No.
                  30487 1.R1011
Contig ID
                  LIB3152-019-P1-K1-A3
5'-most EST
                  271082
Seq. No.
                  30502 1.R1011
Contig ID
5'-most EST
                  uC-zmroB73015a10b1
                  BLASTX
Method
                  g2224931
NCBI GI
                  518
BLAST score
                   1.0e-52
E value
Match length
                   139
                   66
% identity
                   (AF004215) ethylene-insensitive3-like3 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   271083
                   30507 1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17294f11b1
                   BLASTX
Method
                   q3080397
NCBI GI
BLAST score
                   250
                   3.0e-21
E value
                   57
Match length
                   79
% identity
NCBI Description (AL022603) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   271084
Contig ID
                   30522 1.R1011
                   LIB36-013-Q1-E1-H3
```

5'-most EST

BLASTX Method NCBI GI q400983 BLAST score 261 1.0e-22 E value Match length 125 50 % identity

NCBI Description 50S RIBOSOMAL PROTEIN L11, CHLOROPLAST PRECURSOR (CL11)



271085

>gi_279648_pir__R5SP11 ribosomal protein L11 precursor spinach >gi_21313_emb_CAA39950_ (X56615) ribosomal protein
L11 [Spinacia oleracea]

30534 1.R1011 Contig ID LIB3061-031-Q1-K1-D8 5'-most EST BLASTX Method g3236247 NCBI GI 274 BLAST score 3.0e-24E value Match length 144 47 % identity

Seq. No.

NCBI Description (AC004684) SCARECROW-like protein [Arabidopsis thaliana]

Seq. No. 271086

Contig ID 30536 1.R1011

5'-most EST LIB143-054-Q1-E1-F12

Method BLASTX
NCBI GI g4240120
BLAST score 338
E value 1.0e-31
Match length 98

% identity 61 NCBI Description (AB007801) cytochrome b5 [Arabidopsis thaliana]

Seq. No. 271087

Contig ID 30547_1.R1011 5'-most EST zuv700353841.h1

Method BLASTX NCBI GI g131755 BLAST score 693 E value 5.0e-73

Match length 175 % identity 75

NCBI Description PPLZ12 PROTEIN >gi_81843_pir__S14688 hypothetical protein

pPLZ12 - large-leaved lupine >gi_19501_emb_CAA36070_ (X51768) pPLZ12 gene product (AA 1-184) [Lupinus

polyphyllus]

Seq. No. 271088

Contig ID 30561_1.R1011

5'-most EST LIB3152-021-P1-K1-E1

Seq. No. 271089

Contig ID 30567_1.R1011 5'-most EST tfd700569901.h1

Seq. No. 271090

Contig ID 30570_1.R1011 5'-most EST tzu700204831.h1

Method BLASTX
NCBI GI g2459421
BLAST score 316
E value 4.0e-29
Match length 98
% identity 59



```
(AC002332) putative calcium-binding EF-hand protein
NCBI Description
                   [Arabidopsis thaliana]
                  271091
Seq. No.
                  30589 1.R1011
Contig ID
                  uC-zmflm017212f02b1
5'-most EST
Method
                  BLASTX
                  g3702339
NCBI GI
BLAST score
                  659
E value
                  8.0e-69
                  279
Match length
                   48
% identity
                  (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                  271092
Seq. No.
                  30592 1.R1011
Contig ID
                  LIB3152-022-P1-K1-D2
5'-most EST
                  BLASTX
Method
                  g4581111
NCBI GI
BLAST score
                  204
                   9.0e-16
E value
Match length
                  192
                   30
% identity
                  (AC005825) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   271093
                   30608 1.R1011
Contig ID
5'-most EST
                   fwa700098853.h1
                   271094
Seq. No.
Contig ID
                   30615 1.R1011
                  LIB3152-023-P1-K1-B2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2832247
BLAST score
                   142
E value
                   9.0e-09
Match length
                   42
% identity
                   71
                 (AF031569) 22-kDa alpha zein 10 [Zea mays]
NCBI Description
Seq. No.
                   271095
                   30615 2.R1011
Contig ID
5'-most EST
                   xmt700261901.h1
Method
                   BLASTX
NCBI GI
                   q629529
BLAST score
                   150
E value
                   3.0e-16
Match length
                   89
                   53
% identity
NCBI Description
                  late embryogenic abundant protein - Arabidopsis thaliana
                   >qi 289199 (L16946) late embryoqenic abundant protein
                   [Arabidopsis thaliana] >qi 289201 (L17001) late embryogenic
```

Seq. No. 271096

Contig ID 30615_3.R1011

abundant protein [Arabidopsis thaliana]



5'-most EST nbm700475004.h1

Method BLASTN
NCBI GI g22270
BLAST score 130
E value 6.0e-67
Match length 221
% identity 94

NCBI Description Maize mRNA from an embryogenic abscisic acid-inducible gene

Seq. No. 271097

Contig ID 30639 1.R1011

5'-most EST LIB3061-030-Q1-K1-D5

Method BLASTX
NCBI GI g100905
BLAST score 657
E value 6.0e-69
Match length 168
% identity 79

NCBI Description Opaque-2 protein - maize

Seq. No. 271098

Contig ID 30652_1.R1011 5'-most EST uC-zmflb73031h06b1

Method BLASTX
NCBI GI g1169228
BLAST score 315
E value 2.0e-28
Match length 99
% identity 63

NCBI Description RNA HELICASE-LIKE PROTEIN DB10 >qi 1084413 pir S42639

helicase-like protein - Wood tobacco

>gi_563986_dbj_BAA03763_ (D16247) RNA helicase like protein

DB10 [Nicotiana sylvestris]

Seq. No. 271099

Contig ID 30652_2.R1011 5'-most EST uC-zmflmo17037f07b1

Method BLASTX
NCBI GI g3149952
BLAST score 704
E value 2.0e-74
Match length 180

% identity 74

NCBI Description (AB010259) DRH1 [Arabidopsis thaliana]

Seq. No. 271100

Contig ID 30652_3.R1011 5'-most EST wty700164258.h1

Seq. No. 271101

Contig ID 30671 1.R1011

5'-most EST LIB3062-025-Q1-K1-D2

Method BLASTX
NCBI GI g118171
BLAST score 324
E value 8.0e-30
Match length 83



% identity 76 CYSTEINE PROTEINASE INHIBITOR-II (ORYZACYSTATIN-II) NCBI Description >gi 100692 pir A38375 oryzacystatin II - rice >gi_169803 (J05595) oryzacystatin-II [Oryza sativa] 271102 Seq. No. 30671 2.R1011 Contig ID $uC-zm\overline{f}lmo17175e09b1$ 5'-most EST BLASTX Method NCBI GI g2583133 BLAST score 309 8.0e-28 E value 215 Match length % identity 34 (AC002387) unknown protein [Arabidopsis thaliana] NCBI Description 271103 Seq. No. 30671 3.R1011 Contig ID LIB3066-034-Q1-K1-A10 5'-most EST BLASTX Method g2583133 NCBI GI BLAST score 203 E value 1.0e-15 Match length 86 48 % identity (AC002387) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 271104 30671 5.R1011 Contig ID 5'-most EST xsy700214530.h1 BLASTN Method NCBI GI g169802 41 BLAST score E value 8.0e-14 Match length 89 87 % identity NCBI Description Rice oryzacystatin-II mRNA, complete cds Seq. No. 271105 30695 1.R1011 Contig ID uC-zmflb73200d03b1 5'-most EST Method BLASTX NCBI GI g3128218 BLAST score 1303 1.0e-144 E value Match length 396 % identity NCBI Description (AC004077) putative end13 protein [Arabidopsis thaliana]

Seq. No. 271106

Contig ID 30720_1.R1011

5'-most EST LIB3152-028-P1-K1-C7

Seq. No. 271107

Contig ID 30720_2.R1011

5'-most EST LIB3152-050-P1-K1-F5



```
271108
Seq. No.
Contig ID
                  30784 1.R1011
                  LIB3060-044-Q1-K1-F9
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2829868
BLAST score
                  195
                   5.0e-14
E value
Match length
                   495
                   25
% identity
                  (AC002396) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   271109
Contig ID
                   30814 1.R1011
5'-most EST
                   tzu700204546.h1
                   271110
Seq. No.
Contig ID
                   30820 1.R1011
5'-most EST
                   ymt700218879.h1
Seq. No.
                   271111
                   30821 1.R1011
Contig ID
                   wyr700239503.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4646203
                   273
BLAST score
                   5.0e-47
E value
                   203
Match length
                   48
% identity
                   (AC007230) Belongs to PF 00026 Eukaryotic aspartyl protease
NCBI Description
                   family. [Arabidopsis thaliana]
                   271112
Seq. No.
                   30833 1.R1011
Contig ID
                   uC-zmflmo17163f01b1
5'-most EST
                   BLASTX
Method
                   g4455323
NCBI GI
                   1741
BLAST score
                   0.0e + 00
E value
Match length
                   621
                   57
% identity
                  (AL035525) aminopeptidase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   271113
Seq. No.
                   30833 2.R1011
Contig ID
                   LIB189-006-Q1-E1-A3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4455323
                   287
BLAST score
                   2.0e-25
E value
                   116
Match length
% identity
                   (AL035525) aminopeptidase-like protein [Arabidopsis
NCBI Description
                   thaliana]
```

37757

271114

30838_1.R1011

Seq. No.

Contig ID

E value

Match length

4.0e-55



```
uC-zmflb73190g06b1
5'-most EST
                  271115
Seq. No.
                  30855 1.R1011
Contig ID
5'-most EST
                  cyk700048154.fl
                  BLASTX
Method
                  g2982311
NCBI GI
                  718
BLAST score
                  1.0e-75
E value
                  233
Match length
                   57
% identity
                  (AF051240) probable ubiquitin-conjugating enzyme E2 [Picea
NCBI Description
                  mariana]
                   271116
Seq. No.
                  30855 2.R1011
Contig ID
                  LIB3062-002-Q1-K2-B7
5'-most EST
                  BLASTX
Method
                  g2982311
NCBI GI
BLAST score
                   216
                   2.0e-17
E value
                   49
Match length
                   78
% identity
                  (AF051240) probable ubiquitin-conjugating enzyme E2 [Picea
NCBI Description
                  mariana]
Seq. No.
                   271117
                   30863 1.R1011
Contig ID
                   tzu700201845.hl
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1403522
                   368
BLAST score
                   3.0e - 35
E value
                   114
Match length
                   60
% identity
                  (X57187) chitinase [Phaseolus vulgaris]
NCBI Description
                   271118
Seq. No.
                   30865 1.R1011
Contig ID
5'-most EST
                   LIB3068-025-Q1-K1-H9
                   BLASTX
Method
NCBI GI
                   g1731426
BLAST score
                   1141
                   1.0e-125
E value
Match length
                   204
                   99
% identity
                   ZEAMATIN PRECURSOR >gi 459170 (U06831) unnamed protein
NCBI Description
                   product [Zea mays]
                   271119
Seq. No.
Contig ID
                   30865 2.R1011
                   LIB3152-033-P1-K1-A4
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1731426
                   537
BLAST score
```



88 % identity ZEAMATIN PRECURSOR >gi 459170 (U06831) unnamed protein NCBI Description product [Zea mays] 271120 Seq. No. 30867 1.R1011 Contig ID 5'-most EST LIB3152-033-P1-K1-B3 271121 Seq. No. 30886 1.R1011 Contig ID 5'-most EST LIB3137-049-Q1-K1-C2 271122 Seq. No. 30898 1.R1011 Contig ID rvt700551528.h1 5'-most EST BLASTX Method q4263521 NCBI GI 630 BLAST score 1.0e-65 E value Match length 215 57 % identity (AC004044) putative WD-repeat protein [Arabidopsis NCBI Description thaliana] Seq. No. 271123 30920 1.R1011 Contig ID 5'-most EST LIB3067-031-Q1-K1-F4 Method BLASTX g431162 NCBI GI BLAST score 237 2.0e-34 E value Match length 142 53 % identity NCBI Description (D21822) ORF [Lilium longiflorum] Seq. No. 271124 Contig ID 30920 2.R1011 5'-most EST uC-zmrob73012h03b1 Method BLASTX NCBI GI q4432841 BLAST score 970 E value 1.0e-105 Match length 323 % identity NCBI Description (AC006283) hypothetical protein [Arabidopsis thaliana] Seq. No. 271125 Contig ID 30928 1.R1011 5'-most EST LIB3156-001-Q1-K1-G6 Seq. No. 271126

Contig ID 30936_1.R1011

5'-most EST LIB143-034-Q1-E1-H1

Method BLASTX
NCBI GI g3123056
BLAST score 158
E value 3.0e-10



Match length 111 % identity 36

NCBI Description HYPOTHETICAL PROTEIN KIAA0039 >gi_436222_dbj_BAA05039_

(D26018) KIAA0039 [Homo sapiens]

Seq. No. 271127

Contig ID 30945 1.R1011

5'-most EST uC-zmflmo17043h03a1

Method BLASTX
NCBI GI g2129880
BLAST score 967
E value 1.0e-134
Match length 318
% identity 80

NCBI Description cytochrome P450 - garden pea >gi 1360118_emb_CAA89260_

(Z49263) cytochrome P450 [Pisum sativum]

Seq. No. 271128

Contig ID 30947_1.R1011 5'-most EST pmx700086591.h1

Seq. No. 271129

Contig ID 30949_1.R1011 5'-most EST pmx700083242.h1

Method BLASTX
NCBI GI 9733554
BLAST score 364
E value 3.0e-34
Match length 112
% identity 59

NCBI Description (U23450) similar to RNA-binding protein [Caenorhabditis

elegans]

Seq. No. 271130

Contig ID 30952_1.R1011

5'-most EST LIB3152-035-P1-K1-D11

Method BLASTX
NCBI GI g3880563
BLAST score 401
E value 7.0e-39
Match length 199
% identity 42

NCBI Description (Z78018) predicted using Genefinder; similar to

serine/threonine kinase; cDNA EST yk353d10.5 comes from

this gene [Caenorhabditis elegans]

Seq. No. 271131

Contig ID 30958_1.R1011

5'-most EST LIB3152-035-P1-K1-F12

Seq. No. 271132

Contig ID 30975 1.R1011

5'-most EST LIB3068-050-Q1-K1-B8

Seq. No. 271133

Contig ID 30975_2.R1011 5'-most EST uC-zmflb73064b08b1



```
271134
Seq. No.
                  30980 1.R1011
Contig ID
                  uC-zmrob73036e06b1
5'-most EST
                  BLASTX
Method
                  g3123908
NCBI GI
                  482
BLAST score
                  8.0e-49
E value
                  140
Match length
                  66
% identity
                  (AF038392) pre-mRNA splicing factor [Homo sapiens]
NCBI Description
                  271135
Seq. No.
                  31000 1.R1011
Contig ID
                  LIB3152-039-P1-K1-B9
5'-most EST
Seq. No.
                  271136
                  31011 1.R1011
Contig ID
                  LIB3152-039-P1-K1-E5
5'-most EST
                  BLASTX
Method
                  g224508
NCBI GI
                  255
BLAST score
                  4.0e-22
E value
                  94
Match length
                  92
% identity
NCBI Description zein A20 [Zea mays]
Seq. No.
                  271137
                  31026 1.R1011
Contig ID
                  vux700157384.h1
5'-most EST
                  271138
Seq. No.
                  31034 1.R1011
Contig ID
                  ymt700220089.h1
5'-most EST
                  271139
Seq. No.
Contig ID
                  31039 1.R1011
5'-most EST
                  LIB3152-040-P1-K1-D11
                   271140
Seq. No.
                   31054 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73092a08b2
Method
                   BLASTX
NCBI GI
                   q600872
BLAST score
                   664
                   1.0e-69
E value
Match length
                   142
% identity
                   89
                   (U17897) starch branching enzyme I [Zea mays] >gi 3309178
NCBI Description
                   (AF072724) starch branching enzyme I [Zea mays]
Seq. No.
                   271141
```

Contiq ID

31054 2.R1011 $qmh70\overline{0}027301.f1$ 5'-most EST

BLASTX Method NCBI GI q600872 BLAST score 433



E value 1.0e-42 110 Match length 79 % identity (U17897) starch branching enzyme I [Zea mays] >gi_3309178 NCBI Description (AF072724) starch branching enzyme I [Zea mays] 271142 Seq. No. 31060 1.R1011 Contig ID uC-zmflb73223c01b2 5'-most EST BLASTX Method g1742187 NCBI GI 179 BLAST score 2.0e-12 E value Match length 140 33 % identity NCBI Description (D90771) ORF ID:o260#14; similar to [SwissProt Accession Number P11666] [Escherichia coli] >gi_1742198_dbj_BAA14933_ (D90772) ORF ID:0260#14; similar to [SwissProt Accession Number P11666] [Escherichia coli] >gi 1787591 (AE000231) orf, hypothetical protein [Escherichia coli] 271143 Seq. No. 31063 1.R1011 Contig ID tzu700201877.h1 5'-most EST BLASTX Method g2914706 NCBI GI 928 BLAST score E value 1.0e-100 219 Match length 80 % identity (AC003974) putative homeobox protein [Arabidopsis thaliana] NCBI Description Seq. No. 271144 31063 2.R1011 Contig ID 5'-most EST uC-zmflb73050g09b1 BLASTX Method NCBI GI g2914706 761 BLAST score 7.0e-81 E value 175 Match length 82 % identity (AC003974) putative homeobox protein [Arabidopsis thaliana] NCBI Description 271145 Seq. No. 31063 3.R1011 Contig ID LIB3067-016-Q1-K1-E8 5'-most EST Method BLASTX

Method BLASTX
NCBI GI g2494115
BLAST score 444
E value 1.0e-43
Match length 117
% identity 74

NCBI Description (AC002376) Strong similarity to Arabidopsis ATHSAR1

(gb_M90418). ESTs gb_T44122, gb_N65276, gb_AA041135 come from

this gene. [Arabidopsis thaliana]

Seq. No. 271146

BLAST score

E value

344

4.0e-32



```
Contig ID
                  31063 5.R1011
                  uwc700153125.h1
5'-most EST
                  BLASTX
Method
                  g3298555
NCBI GI
BLAST score
                  180
                  2.0e-13
E value
                  41
Match length
                  80
% identity
                  (AC004681) putative homeobox protein, 3' partial
NCBI Description
                   [Arabidopsis thaliana]
                  271147
Seq. No.
                  31095 1.R1011
Contig ID
5'-most EST
                  LIB3152-042-P1-K1-A3
                  BLASTX
Method
                  q82659
NCBI GI
                   338
BLAST score
                   1.0e-31
E value
                   116
Match length
                   64
% identity
                  19K zein precursor (clone Z4) - maize
NCBI Description
                   >gi_4388702_emb_CAA24719_ (V01472) zein [Zea mays]
                   271148
Seq. No.
                   31096 1.R1011
Contig ID
5'-most EST
                   cjh700194215.h1
                   271149
Seq. No.
                   31106 1.R1011
Contig ID
                   LIB3152-042-P1-K1-C9
5'-most EST
                   BLASTN
Method
                   g666088
NCBI GI
BLAST score
                   71
                   1.0e-31
E value
                   268
Match length
                   82
% identity
NCBI Description S.bicolor mRNA for p-(S)-hydroxymandelonitrile lyase
                   271150
Seq. No.
Contig ID
                   31112 1.R1011
                   LIB3152-042-P1-K1-E10
5'-most EST
Method
                   BLASTX
                   q4376872
NCBI GI
BLAST score
                   375
                   7.0e-36
E value
Match length
                   174
% identity
                   45
                  (AE001642) Sugar Nucleotide Phosphorylase [Chlamydia
NCBI Description
                   pneumoniae]
Seq. No.
                   271151
Contig ID
                   31142 1.R1011
                   LIB3152-043-P1-K1-F12
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3641868
```



```
109
Match length
                   61
% identity
                  (AJ011012) hypothetical protein [Cicer arietinum]
NCBI Description
                  271152
Seq. No.
                  31164 1.R1011
Contig ID
                  uC-zmflmo17202c08b1
5'-most EST
                  BLASTX
Method
                  g3702327
NCBI GI
                  517
BLAST score
                   4.0e-52
E value
Match length
                  266
% identity
                  45
                  (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  271153
                   31164 2.R1011
Contig ID
                  LIB3061-040-Q1-K1-D11
5'-most EST
                  BLASTX
Method
                  q3702327
NCBI GI
                   280
BLAST score
                   8.0e-25
E value
Match length
                   68
                   78
% identity
                  (AC005397) unknown protein [Arabidopsis thaliana]
NCBI Description
                   271154
Seq. No.
Contig ID
                   31173 1.R1011
                  LIB3059-017-Q1-K1-H3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2921823
                   259
BLAST score
E value
                   4.0e-22
                   89
Match length
                   61
% identity
                  (AF046934) shoot-forming PKSF1 [Paulownia kawakamii]
NCBI Description
Seq. No.
                   271155
Contig ID
                   31173 2.R1011
                   uC-zmflmo17376d06a1
5'-most EST
                   271156
Seq. No.
                   31173 3.R1011
Contig ID
                   tzu700203638.h1
5'-most EST
Method
                   BLASTX
                   g2921823
NCBI GI
BLAST score
                   160
E value
                   6.0e-11
Match length
                   68
% identity
                  (AF046934) shoot-forming PKSF1 [Paulownia kawakamii]
NCBI Description
```

Seq. No. 271157

Contig ID 31177_1.R1011

5'-most EST LIB3152-044-P1-K1-F6

Method BLASTX NCBI GI g3559816



BLAST score 2003 E value 0.0e+00 Match length 444 % identity 86

NCBI Description (Y15782) transketolase 2 [Capsicum annuum]

Seq. No. 271158

Contig ID 31191 1.R1011

5'-most EST LIB3152-045-P1-K1-B7

Seq. No. 271159

Contig ID 31191_2.R1011

5'-most EST uC-zmflmo17283a05b1

Seq. No. 271160

Contig ID 31203_1.R1011

5'-most EST LIB31 $\overline{5}$ 9-008-Q1-K1-G6

Method BLASTX
NCBI GI g3273243
BLAST score 463
E value 4.0e-46

Match length 141 % identity 67

NCBI Description (AB004660) NLS receptor [Oryza sativa]

>gi_3273245_dbj_BAA31166 (AB004814) NLS receptor [Oryza

sativa]

Seq. No. 271161

Contig ID 31203_2.R1011 5'-most EST xsy700209191.h1

Method BLASTX
NCBI GI g3273243
BLAST score 351
E value 4.0e-33
Match length 113

% identity 65

NCBI Description (AB004660) NLS receptor [Oryza sativa]

>gi_3273245_dbj_BAA31166_ (AB004814) NLS receptor [Oryza

sativa]

Seq. No. 271162

Contig ID 31205_1.R1011 5'-most EST LIB36-010-Q1-E1-H6

Method BLASTX
NCBI GI g3763917
BLAST score 790
E value 2.0e-84
Match length 209
% identity 74

NCBI Description (AC004450) hypothetical protein [Arabidopsis thaliana]

>gi_4531438_gb_AAD22123.1_AC006224_5 (AC006224)

hypothetical protein [Arabidopsis thaliana]

Seq. No. 271163

Contig ID 31209_1.R1011 5'-most EST hbs701180894.h1



Seq. No. 271164

Contig ID 31218_1.R1011

5'-most EST LIB3152-046-P1-K1-B11

Seq. No. 271165

Contig ID 31227 1.R1011

5'-most EST LIB3136-054-Q1-K1-G4

Seq. No. 271166

Contig ID 31227_2.R1011 5'-most EST uC-zmflb73057g10a2

Seq. No. 271167

Contig ID 31240 1.R1011

5'-most EST LIB3061-035-Q1-K1-A8

Method BLASTX
NCBI GI g452519
BLAST score 153
E value 3.0e-09
Match length 257
% identity 26

NCBI Description (D26362) similar to Human homolog of Drosophila female

sterile homeotic mRNA (HUMFSHG) [Homo sapiens]

Seq. No. 271168

Contig ID 31264 1.R1011

5'-most EST LIB3152-047-P1-K1-F10

Method BLASTX
NCBI GI g3831462
BLAST score 221
E value 8.0e-18
Match length 142
% identity 42

NCBI Description (AC005700) hypothetical protein [Arabidopsis thaliana]

Seq. No. 271169

Contig ID 31269_1.R1011 5'-most EST uC-zmflb73303a03b1

Seq. No. 271170

Contig ID 31293 1.R1011

5'-most EST LIB3136-008-Q1-K1-G8

Seq. No. 271171

Contig ID 31298_1.R1011 5'-most EST rvt700552615.h1

Method BLASTX
NCBI GI g3355487
BLAST score 204
E value 8.0e-16
Match length 185
% identity 31

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 271172

Contig ID 31302_1.R1011 5'-most EST uC-zmflm017025g01b1



```
BLASTX
Method
NCBI GI
                   q3176664
                   236
BLAST score
E value
                   3.0e-19
Match length
                   193
                   33
% identity
                   (ACO04393) Contains similarity to beta scruin gb_Z47541
NCBI Description
                   from Limulus polyphemus. ESTs gb_T04493 and gb_AA585955
                   come from this gene. [Arabidopsis thaliana]
                   271173
Seq. No.
                   31315 1.R1011
Contig ID
5'-most EST
                   xjt700093113.h1
                   271174
Seq. No.
                   31316 1.R1011
Contig ID
```

5'-most EST LIB1 $4\overline{3}$ -040-Q1-E1-B1 Seq. No. 271175

Contig ID 31320_1.R1011

5'-most EST LIB143-067-Q1-E1-B8 Method BLASTX

Method BLASTX
NCBI GI g3193303
BLAST score 226
E value 3.0e-18
Match length 105
% identity 45

NCBI Description (AF069298) similar to several proteins containing a tandem

repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807); partial CDS [Arabidopsis

thaliana]

Seq. No. 271176

Contig ID 31322_1.R1011 5'-most EST fdz701165648.h1

Method BLASTN
NCBI GI g168677
BLAST score 39
E value 2.0e-12
Match length 55
% identity 93

NCBI Description Maize 19 kDa zein mRNA, clone cZ19C1, complete cds

Seq. No. 271177

Contig ID 31348 1.R1011

5'-most EST LIB3061-046-Q1-K1-B9

Method BLASTX
NCBI GI g1167955
BLAST score 327
E value 4.0e-30
Match length 145
% identity 48

NCBI Description (U43497) putative 32.7 kDa jasmonate-induced protein

[Hordeum vulgare] >gi 2465428 (AF021257) 32 kDa protein

[Hordeum vulgare]

Seq. No. 271178



```
Contig ID
                  31367 1.R1011
                  xmt700258162.h1
5'-most EST
Method
                  BLASTX
                  q2911059
NCBI GI
BLAST score
                  287
                  2.0e-25
E value
Match length
                  107
% identity
                   51
                  (ALO21961) putative protein [Arabidopsis thaliana]
NCBI Description
                   271179
Seq. No.
Contig ID
                   31378 1.R1011
                  LIB3180-038-P2-M2-F2
5'-most EST
                   271180
Seq. No.
                   31392 1.R1011
Contig ID
                  LIB3152-051-P1-K1-D7
5'-most EST
                   271181
Seq. No.
                   31405 1.R1011
Contig ID
                  LIB3060-019-Q1-K1-C4
5'-most EST
Seq. No.
                   271182
                   31405 2.R1011
Contig ID
                   wyr700238452.h1
5'-most EST
                   271183
Seq. No.
Contig ID
                   31405 3.R1011
                   LIB3152-051-P1-K1-H4
5'-most EST
                   271184
Seq. No.
                   31416 1.R1011
Contig ID
                   LIB3137-018-Q1-K1-A1
5'-most EST
                   BLASTX
Method
                   g2262105
NCBI GI
BLAST score
                   243
                   4.0e-26
E value
Match length
                   112
% identity
                   58
                  (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   271185
Contig ID
                   31423 1.R1011
5'-most EST
                   uC-zmrob73071f01b1
                   BLASTX
Method
NCBI GI
                   g126201
BLAST score
                   990
E value
                   1.0e-162
                   388
Match length
% identity
                   78
```

NCBI Description

3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi_81676_pir__S20510 3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor -rape >gi_17827_emb_CAA42596_ (X59970) 3-isopropylmalate

dehydrogenase [Brassica napus]

Seq. No.

```
31423 3.R1011
       Contig ID
                          xjt700096012.h1
       5'-most EST
                          271187
       Seq. No.
                          31423 5.R1011
       Contig ID
                          xsy700213068.hl
       5'-most EST
                          BLASTX
       Method
                          g1903021
       NCBI GI
                          174
       BLAST score
                          2.0e-12
       E value
       Match length
                          47
                          74
       % identity
                         (Y10216) hypothetical 3-isopropylmalate dehydrogenase
       NCBI Description
                          [Arabidopsis thaliana]
                          271188
       Seq. No.
Contig ID
                          31425 1.R1011
                          LIB3152-053-P1-K1-E8
       5'-most EST
                          BLASTX
       Method
                          g2809251
       NCBI GI
       BLAST score
                          241
                          1.0e-20
       E value
```

% identity 52 NCBI Description (AC002560) F21B7.20 [Arabidopsis thaliana]

 Seq. No.
 271189

 Contig ID
 31454_1.R1011

 5'-most EST
 LIB3061-054-Q1-K1-B1

 Method
 BLASTX

 NCBI GI
 g4587597

 BLAST score
 649

83

BLAST score 649 E value 1.0e-67 Match length 248 % identity 52

Match length

NCBI Description (AC006951) putative MAP kinase phosphatase [Arabidopsis

thaliana]

Seq. No. 271190

Contig ID 31454_3.R1011 5'-most EST xsy700211247.h1

Method BLASTX
NCBI GI g4587597
BLAST score 277
E value 2.0e-24
Match length 75
% identity 69

NCBI Description (AC006951) putative MAP kinase phosphatase [Arabidopsis

thaliana]

Seq. No. 271191

Contig ID 31456_1.R1011 5'-most EST LIB3152-054-P1-K1-E12

Seq. No. 271192

Contig ID 31479_1.R1011

5'-most EST LIB3152-056-P1-K1-C10



```
Method
                   BLASTX
                   g3482919
NCBI GI
                   497
BLAST score
                   3.0e-50
E value
                   120
Match length
                   77
% identity
                   (AC003970) Putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   271193
Seq. No.
                   31491 1.R1011
Contig ID
                   nbm70\overline{0}477954.h1
5'-most EST
Method
                   BLASTX
                   g2623199
NCBI GI
                   1431
BLAST score
                   1.0e-166
E value
Match length
                   305
                   93
% identity
                   (AF030290) protein phosphatase X isoform 2 [Arabidopsis
NCBI Description
                   thaliana]
                   271194
Seq. No.
                   31491 2.R1011
Contig ID
                   uC-zmflmo17235f03b1
5'-most EST
Method
                   BLASTX
                   g1346780
NCBI GI
                   288
BLAST score
                   2.0e-25
E value
Match length
                   113
                   93
% identity
                   SERINE/THREONINE PROTEIN PHOSPHATASE PP-X ISOZYME 2
NCBI Description
                   >gi_629550_pir__S42559 phosphoprotein phosphatase (EC
                   3.1-3.16) \overline{X}-2 (clone EP128) - Arabidopsis thaliana
                   >gi 397590_emb_CAA80312_ (Z22596) protein phosphatase
                   [Arabidopsis thaliana]
Seq. No.
                   271195
                   31495 1.R1011
Contig ID
5'-most EST
                   uC-zmroteosinte036c07b1
                   271196
Seq. No.
                   31496 1.R1011
Contig ID
5'-most EST
                   LIB3152-056-P1-K1-G2
                   271197
Seq. No.
                   31528 1.R1011
Contig ID
                   LIB3181-003-P1-K2-G8
5'-most EST
                   BLASTX
Method
NCBI GI
                   q82659
                   524
BLAST score
E value
                   3.0e-53
                   186
Match length
```

% identity 65
NCBI Description 19K zein precursor (clone Z4) - maize
>qi 4388702 emb CAA24719 (V01472) zein [Zea mays]

Seq. No. 271198

Contig ID 31550 1.R1011

NCBI Description

```
LIB3180-050-P2-M1-E4
5'-most EST
                  271199
Seq. No.
                  31572 1.R1011
Contig ID
5'-most EST
                  LIB3154-001-Q1-K1-B4
Seq. No.
                  271200
                  31607 1.R1011
Contig ID
5'-most EST
                  LIB3154-001-Q1-K1-E10
                  271201
Seq. No.
Contig ID
                  31625 1.R1011
5'-most EST
                  LIB3154-001-Q1-K1-H2
Method
                  BLASTX
NCBI GI
                  q131432
BLAST score
                  440
E value
                  1.0e-43
Match length
                  127
                  66
% identity
NCBI Description LITHOSTATHINE PRECURSOR (PANCREATIC STONE PROTEIN) (PSP)
                  (PANCREATIC THREAD PROTEIN) (PTP) (ISLET OF LANGERHANS
                  REGENERATING PROTEIN) (REG) (ISLET CELLS REGENERATION
                  FACTOR) (ICRF) >gi_108847_pir__A37194 pancreatic thread
                  protein precursor - bovine >gi 163649 (M59794) pancreatic
                  thread protein [Bos taurus]
Seq. No.
                  271202
Contig ID
                  31673 1.R1011
5'-most EST
                  LIB3154-011-Q1-K1-B11
                  271203
Seq. No.
Contig ID
                  31682 1.R1011
                  LIB3154-004-Q1-K1-D11
5'-most EST
Method
                  BLASTX
NCBI GI
                  q118926
BLAST score
                  145
E value
                  4.0e-09
Match length
                  48
                  56
% identity
NCBI Description
                  DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR
                  >gi 320600 pir E45509 desiccation-related protein (clone
                  PCC13-62) - Craterostigma plantagineum >gi 167479 (M62991)
                  dessication-related protein [Craterostigma plantagineum]
                  >gi_227781_prf__1710351E abscisic acid responsive protein E
                  [Craterostigma plantagineum]
Seq. No.
                  271204
Contig ID
                  31686 1.R1011
                  LIB3180-003-P2-M1-D10
5'-most EST
Method
                  BLASTN
NCBI GI
                  g1037129
BLAST score
                  217
E value
                  1.0e-119
                  373
Match length
% identity
                  90
```

Tuxpeno CMS 450, mRNA Partial, 1889 nt]

(gamma-zeinA)=opaque2 modifier {5' region} [Zea mays=maize,



Seq. No. 271205

Contig ID 31734_1.R1011 5'-most EST xjt700096570.h1

Method BLASTX
NCBI GI g3176691
BLAST score 364
E value 3.0e-34
Match length 213
% identity 43

NCBI Description (AC003671) Contains homology to serine/threonine protein kinase gb X99618 from Mycobacterium tuberculosis. ESTs

gb F14403, gb_F14404, and gb_N96730 come from this gene.

[Arabidopsis thaliana]

Seq. No. 271206

Contig ID 31734_2.R1011 5'-most EST nbm700465566.h1

Method BLASTX
NCBI GI g3176691
BLAST score 163
E value 2.0e-11
Match length 57
% identity 49

NCBI Description (AC003671) Contains homology to serine/threonine protein

kinase gb_X99618 from Mycobacterium tuberculosis. ESTs gb F14403, gb_F14404, and gb_N96730 come from this gene.

[Arabidopsis thaliana]

Seq. No. 271207

Contig ID 31739_1.R1011 5'-most EST uC-zmflb73245h10b2

Method BLASTX
NCBI GI g3859116
BLAST score 533
E value 2.0e-54
Match length 134
% identity 79

NCBI Description (AF031609) unknown [Oryza sativa]

Seq. No. 271208

Contig ID 31782 1.R1011

5'-most EST LIB3154-010-Q1-K1-E1

Seq. No. 271209

Contig ID 31807_1.R1011

5'-most EST LIB3180-029-P2-M2-B10

Method BLASTX
NCBI GI g3763845
BLAST score 382
E value 9.0e-37
Match length 114
% identity 64

NCBI Description (AB018375) early nodulin [Oryza sativa]

>gi_3763847_dbj_BAA33814 (AB018376) early nodulin [Oryza

sativa]



Seq. No. 271210

Contig ID 31807 2.R1011

5'-most EST LIB3059-012-Q1-K1-A2

Method BLASTN
NCBI GI g3763846
BLAST score 51
E value 1.0e-19
Match length 131
% identity 85

NCBI Description Oryza sativa OsENOD93a mRNA for early nodulin, complete cds

Seq. No. 271211

Contig ID 31820_1.R1011

5'-most EST LIB3154-013-Q1-K1-B11

Seq. No. 271212

Contig ID 31846_1.R1011

5'-most EST LIB189-009-Q1-E1-A9

Method BLASTN
NCBI GI g3821780
BLAST score 37
E value 3.0e-11
Match length 49
% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 271213

Contig ID 31849 1.R1011

5'-most EST uC-zmflmo17070c03a1

Seq. No. 271214

Contig ID 31849_2.R1011 5'-most EST LIB83-014-Q1-E1-A8

Seq. No. 271215

Contig ID 31859 1.R1011

5'-most EST LIB3156-002-Q1-K1-H12

Seq. No. 271216

Contig ID 31861_1.R1011 5'-most EST tfd700571682.h1

Method BLASTX
NCBI GI g4558664
BLAST score 228
E value 1.0e-18
Match length 131
% identity 40

NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]

Seq. No. 271217

Contig ID 31878_1.R1011

5'-most EST LIB3156-002-Q1-K1-G10

Seq. No. 271218

Contig ID 31881_1.R1011 5'-most EST uC-zmflmo17297e04b1

Method BLASTX



NCBI GI g3377820 BLAST score 174 E value 2.0e-12 Match length 46 % identity 76

NCBI Description (AF076275) contains similarity to coatomer zeta chains

[Arabidopsis thaliana]

Seq. No. 271219

Contig ID 31881 2.R1011

5'-most EST uC-zmflmo17180e02b1

Method BLASTX
NCBI GI g3377820
BLAST score 359
E value 1.0e-33
Match length 123
% identity 61

NCBI Description (AF076275) contains similarity to coatomer zeta chains

[Arabidopsis thaliana]

Seq. No. 271220

Contig ID 31881_3.R1011

5'-most EST uC-zmroteosinte045b0.6b2

Method BLASTX
NCBI GI g3377820
BLAST score 320
E value 6.0e-36
Match length 139
% identity 62

NCBI Description (AF076275) contains similarity to coatomer zeta chains

[Arabidopsis thaliana]

Seq. No. 271221

Contig ID 31892_1.R1011 5'-most EST kyv700142520.h1

Method BLASTX
NCBI GI g3024516
BLAST score 431
E value 2.0e-42
Match length 125

Match length 125 % identity 68

NCBI Description RAS-RELATED PROTEIN RAB11C >gi_2160157 (AC000132) Strong

similarity to A. thaliana ara-2 (gb_ATHARA2). ESTs ab ATTS2483 gb_ATTS2484 gb_AA042159 come from this

gb_ATTS2483,gb_ATTS2484,gb_AA042159 come from this gene.
[Arabidopsis thaliana] >gi_2231303 (U74669) ras-related

small GTPase [Arabidopsis thaliana]

Seq. No. 271222

Contig ID 31893 1.R1011

5'-most EST LIB3156-002-Q1-K2-D11

Seq. No. 271223

Contig ID 31897_1.R1011 5'-most EST xmt700265420.h1

Seq. No. 271224

Contig ID 31911 1.R1011



5'-most EST wty700163529.h1

Method BLASTX
NCBI GI g629669
BLAST score 319
E value 6.0e-29
Match length 337
% identity 29

NCBI Description hypothetical protein - tomato

Seq. No. 271225

Contig ID 31911_2.R1011

5'-most EST LIB3158-018-Q1-K1-G7

Seq. No. 271226

Contig ID 31913 1.R1011

5'-most EST LIB3156-002-Q1-K1-B2

Method BLASTX
NCBI GI g2529662
BLAST score 464
E value 3.0e-46
Match length 105
% identity 86

NCBI Description (AC002535) putative small nuclear ribonucleoprotein, Sm D2

[Arabidopsis thaliana] >gi_3738278 (AC005309) putative small nuclear ribonucleoprotein, Sm D2 [Arabidopsis

thaliana]

Seq. No. 271227

Contig ID 31914 1.R1011

5'-most EST LIB3181-007-P1-K2-C7

Seq. No. 271228

Contig ID 31921_1.R1011 5'-most EST qmh700025868.f1

Method BLASTX
NCBI GI g4115936
BLAST score 986
E value 1.0e-107
Match length 228
% identity 81

NCBI Description (AF118223) No definition line found [Arabidopsis thaliana]

Seq. No. 271229

Contig ID 31921 2.R1011

5'-most EST LIB1 $4\overline{3}$ -024-Q1-E1-A1

Method BLASTX
NCBI GI g4115936
BLAST score 175
E value 2.0e-12
Match length 40
% identity 80

NCBI Description (AF118223) No definition line found [Arabidopsis thaliana]

Seq. No. 271230

Contig ID 31921_3.R1011 5'-most EST nbm700473317.h1

Method BLASTX



```
g4115936
NCBI GI
BLAST score
                   306
                   4.0e-28
E value
Match length
                   66
% identity
                   85
                  (AF118223) No definition line found [Arabidopsis thaliana]
NCBI Description
                  271231
Seq. No.
Contig ID
                   31931_1.R1011
5'-most EST
                  uC-zmflb73107h03a2
                  BLASTN
Method
NCBI GI
                  g3511235
BLAST score
                  44
                  2.0e-15
E value
Match length
                   48
% identity
                   98
                  Zea mays starch branching enzyme IIb (ae) gene, complete
NCBI Description
                   271232
Seq. No.
Contig ID
                   31945_1.R1011
5'-most EST
                  dyk700102338.h1
                   271233
Seq. No.
Contig ID
                   31954 1.R1011
5'-most EST
                  LIB3136-003-Q1-K1-G11
Method
                  BLASTX
NCBI GI
                   g2944178
BLAST score
                   417
E value
                   2.0e-53
Match length
                   169
% identity
                   67
                  (AF007778) trehalose-6-phosphate phosphatase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   271234
Contig ID
                   31954 2.R1011
5'-most EST
                   cyk700047339.f1
Method
                   BLASTX
NCBI GI
                   q3892714
BLAST score
                   526
E value
                   1.0e-53
Match length
                   156
% identity
                   67
NCBI Description
                  (AL033545) trehalose-6-phosphate phosphatase - like protein
                   [Arabidopsis thaliana]
Seq. No.
                   271235
Contig ID
                   31967 1.R1011
                   LIB3156-002-Q1-K1-B7
5'-most EST
Method
                   BLASTX
NCBI GI
                   q1345132
```

BLAST score 880
E value 5.0e-95
Match length 223

% identity 78

NCBI Description (U47029) ERECTA [Arabidopsis thaliana]



>gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase
[Arabidopsis thaliana] >gi_3075386 (AC004484) receptor
protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No. 271236

Contig ID 31968 1.R1011

5'-most EST LIB3156-002-Q1-K1-B9

Seq. No. 271237

Contig ID 31974_1.R1011 5'-most EST wyr700240543.h1

Seq. No. 271238

Contig ID 31974_2.R1011 5'-most EST nbm700469715.h1

Seq. No. 271239

Contig ID 31974 4.R1011 5'-most EST qmh700026520.f1

Seq. No. 271240

Contig ID 31974_5.R1011

5'-most EST LIB3156-002-Q1-K1-A9

Seq. No. 271241

Contig ID 31977_1.R1011 5'-most EST hvj700624603.h1

Method BLASTX
NCBI GI g4006874
BLAST score 486
E value 1.0e-48
Match length 172

% identity 59

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

Seq. No. 271242

Contig ID 31981_1.R1011

5'-most EST LIB3136-026-Q1-K1-B5

Method BLASTX
NCBI GI g3287695
BLAST score 890
E value 2.0e-95
Match length 398
% identity 52

NCBI Description (AC003979) Similar to hypothetical protein C34B7.2

gb_1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis

thaliana]

Seq. No. 271243

Contig ID 31981_2.R1011 5'-most EST dyk700102644.h1

Seq. No. 271244

Contig ID 31981 3.R1011

5'-most EST LIB31 $\overline{5}$ 8-018-Q1-K1-B4

Seq. No. 271245



89

% identity

```
31981 4.R1011
Contig ID
                  uC-zm\overline{f}lmo17282c09b1
5'-most EST
                   271246
Seq. No.
                   31994 1.R1011
Contig ID
                  LIB3156-001-Q1-K1-F6
5'-most EST
Method
                  BLASTX
                   g2281088
NCBI GI
BLAST score
                   518
                   2.0e-52
E value
Match length
                   251
                   46
% identity
                   (AC002333) indole-3-acetate beta-glucosyltransferase isolog
NCBI Description
                   [Arabidopsis thaliana]
                   271247
Seq. No.
                   32001 1.R1011
Contig ID
                   LIB3156-001-Q1-K1-G5
5'-most EST
                   BLASTN
Method
                   g22553
NCBI GI
                   34
BLAST score
                   1.0e-09
E value
                   34
Match length
                   100
% identity
                  Tomato 25S ribosomal RNA gene
NCBI Description
                   271248
Seq. No.
Contig ID
                   32007 1.R1011
5'-most EST
                   xsy700210865.hl
                   BLASTX
Method
                   g3834302
NCBI GI
                   409
BLAST score
                   5.0e-40
E value
Match length
                   123
                   64
% identity
                   (ACO05679) Similar to gb_D45384 vacuolar H+-pyrophosphatase
NCBI Description
                   from Oryza sativa. ESTs gb_F14272 and gb F14273 come from
                   this gene. [Arabidopsis thaliana]
                   271249
Seq. No.
                   32017 1.R1011
Contig ID
5'-most EST
                   fwa700097896.hl
                   271250
Seq. No.
                   32041 1.R1011
Contig ID
                   ymt700223074.h1
5'-most EST
Seq. No.
                   271251
Contig ID
                   32067 1.R1011
                   hbs701182076.h1
5'-most EST
                   BLASTN
Method
                   q399647
NCBI GI
BLAST score
                   54
                   3.0e-21
E value
Match length
                   102
```

NCBI Description Lycopersicon esculentum (DB244) meloidogyne-induced giant

% identity

NCBI Description

thaliana]



cell protein mRNA, 3' end

Seq. No. 271252 32068 1.R1011 Contig ID $uC-zm\overline{f}lmo17337h11a1$ 5'-most EST BLASTN Method q18731 NCBI GI 45 BLAST score 8.0e-16 E value 101 Match length 86 % identity Soybean RPB1-B1 gene for the largest subunit of RNA NCBI Description polymerase II (EC 2.7.7.6) Seq. No. 271253 32069 1.R1011 Contig ID LIB3136-022-Q1-K1-G2 5'-most EST Method BLASTX q4512671 NCBI GI 177 BLAST score 1.0e-12 E value 118 Match length % identity 39 (AC006931) unknown protein [Arabidopsis thaliana] NCBI Description 271254 Seq. No. 32069_2.R1011 Contig ID 5'-most EST LIB3068-033-Q1-K1-C8 271255 Seq. No. 32069 3.R1011 Contig ID uC-zmflb73131b07b2 5'-most EST 271256 Seq. No. 32069 7.R1011 Contig ID 5'-most EST uC-zmflb73228d02a1 Seq. No. 271257 32069 8.R1011 Contig ID LIB3136-001-P1-K1-H11 5'-most EST 271258 Seq. No. 32089 1.R1011 Contig ID 5'-most EST uC-zmflmo17235a08b1 271259 Seq. No. Contig ID 32089 2.R1011 5'-most EST uC-zmflmo17215g03b1 Method BLASTX g4580398 NCBI GI 772 BLAST score 4.0e-82 E value Match length 196

(ACO07171) putative protein kinase APK1A [Arabidopsis



Contig ID 32091 1.R1011

5'-most EST LIB3156-012-Q1-K1-E5

Seq. No. 271261

Contig ID 32098 1.R1011

5'-most EST LIB3156-003-Q1-K1-C1

Method BLASTX
NCBI GI g1076781
BLAST score 426
E value 7.0e-42
Match length 194
% identity 49

NCBI Description transcription factor HBP-la(c14) - wheat

>gi 497895 dbj BAA02304 (D12920) transcription factor

HBP-la(c14) [Triticum aestivum]

Seq. No. 271262

Contig ID 32101 1.R1011

5'-most EST uC-zmroteosinte022d09b1

Method BLASTX
NCBI GI g400578
BLAST score 274
E value 8.0e-24
Match length 109
% identity 47

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 18 KD SUBUNIT PRECURSOR

(COMPLEX I-18 KD) (CI-18 KD) (COMPLEX I-AQDQ) (CI-AQDQ) >gi_346531_pir__S28240 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-18(IP) - bovine >gi 226 emb CAA44900

(X63215) NADH dehydrogenase [Bos taurus]

Seq. No. 271263

Contig ID 32101 2.R1011 5'-most EST wyr700243913.h1

Method BLASTX
NCBI GI g400578
BLAST score 171
E value 2.0e-15
Match length 109
% identity 41

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 18 KD SUBUNIT PRECURSOR

(COMPLEX I-18 KD) (CI-18 KD) (COMPLEX I-AQDQ) (CI-AQDQ) >gi_346531_pir__S28240 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-18(IP) - bovine >gi_226 emb CAA44900

(X63215) NADH dehydrogenase [Bos taurus]

Seq. No. 271264

Contig ID 32104_1.R1011

5'-most EST LIB3137-007-Q1-K1-D12

Seq. No. 271265

Contig ID 32107_1.R1011 5'-most EST uer700580550.h1

Method BLASTX
NCBI GI g2459442
BLAST score 221



```
E value 1.0e-17
Match length 66
% identity 67
NCBI Description (AC0023 thalian
```

ICBI Description (AC002332) putative DNA-binding protein PD1 [Arabidopsis thaliana]

Seq. No. 271266

Contig ID 32110_1.R1011 5'-most EST dyk700104573.h1

Method BLASTN
NCBI GI g4218534
BLAST score 41
E value 9.0e-14
Match length 123
% identity 90

NCBI Description Triticum sp. mRNA for GRAB1 protein

Seq. No. 271267

Contig ID 32121 1.R1011

5'-most EST LIB3156-003-Q1-K1-F7

Method BLASTX
NCBI GI g2335055
BLAST score 159
E value 4.0e-15
Match length 87
% identity 52

NCBI Description (AD001530) putative [Homo sapiens]

Seq. No. 271268

Contig ID 32125_1.R1011

5'-most EST LIB3156-003-Q1-K1-G2

Method BLASTX
NCBI GI g3522937
BLAST score 177
E value 1.0e-12
Match length 152
% identity 37

NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

Seq. No. 271269

Contig ID 32126_1.R1011 5'-most EST ceu700424005.h1

Method BLASTX
NCBI GI g2118425
BLAST score 248
E value 6.0e-21
Match length 60
% identity 80

NCBI Description subtilisin/chymotrypsin inhibitor - maize

>gi_475253_emb_CAA55588_ (X78988) proteinase inhibitor [Zea

mays] >gi_475922_emb_CAA49593 (X69972) proteinase inhibitor [Zea mays] >gi_559538_emb_CAA57677 (X82187) substilin /chymotrypsin-like inhibitor [Zea mays]

Seq. No. 271270

Contig ID 32126 2.R1011

5'-most EST LIB3156-003-Q1-K1-G3



Method BLASTN
NCBI GI g475252
BLAST score 45
E value 5.0e-16
Match length 121
% identity 85

NCBI Description Z.mays MPI gene

Seq. No. 271271

Contig ID 32131_1.R1011 5'-most EST gct701173355.h2

Seq. No. 271272

Contig ID 32132_1.R1011

5'-most EST LIB143-067-Q1-E1-E7

Method BLASTX
NCBI GI g2618689
BLAST score 1103
E value 1.0e-121
Match length 250
% identity 84

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 271273

Contig ID 32169_1.R1011 5'-most EST rv1700457365.h1

Method BLASTN
NCBI GI g2832242
BLAST score 737
E value 0.0e+00
Match length 845
% identity 97

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

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Seq. No. 271274 Contig ID 32172 1.R1011

5'-most EST LIB3156-004-Q1-K1-E9

Seq. No. 271275

Contig ID 32173_1.R1011 5'-most EST kem700610896.h1

Method BLASTX
NCBI GI g3413697
BLAST score 161
E value 6.0e-11
Match length 91
% identity 36

NCBI Description (AC004747) SF16-like protein, 5' partial [Arabidopsis

thaliana]

Seq. No. 271276

Contig ID 32175_1.R1011

5'-most EST uC-zmflmo17175h04b1

Method BLASTX
NCBI GI g2245136
BLAST score 1303
E value 1.0e-144



Match length 367 % identity 66 NCBI Description (Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana] Seq. No. 271277 Contig ID 32175 2.R1011 LIB3067-051-Q1-K1-B5 5'-most EST Method BLASTX g2245136 NCBI GI BLAST score 287 E value 1.0e-25 Match length 90 63 % identity (Z97344) trehalose-6-phosphate synthase homolog NCBI Description [Arabidopsis thaliana] Seq. No. 271278 Contig ID 32176 1.R1011 LIB3156-004-Q1-K1-F4 5'-most EST 271279 Seq. No. Contig ID 32178 1.R1011 5'-most EST LIB3068-007-Q1-K1-E7 Method BLASTX NCBI GI q4218120 BLAST score 404 E value 1.0e-38 Match length 361 32 % identity (AL035353) Proline-rich APG-like protein [Arabidopsis NCBI Description thaliana] 271280 Seq. No. 32193 1.R1011 Contig ID $clt70\overline{0}045967.f1$ 5'-most EST Seq. No. 271281 32194 1.R1011 Contig ID 5'-most EST xdb700337474.h1 271282 Seq. No. 32194 2.R1011 Contig ID 5'-most EST LIB3156-004-Q1-K1-H7 271283 Seq. No. Contig ID 32201 1.R1011

5'-most EST uC-zmflm017026h02b1

Method BLASTX
NCBI GI g216965
BLAST score 193
E value 2.0e-14
Match length 138
% identity 35

NCBI Description (D10387) aspartokinase I-homoserine dehydrogenase I

[Serratia marcescens]



```
271284
Seq. No.
Contig ID
                   32221 1.R1011
5'-most EST
                   LIB3062-033-Q1-K1-D6
Seq. No.
                   271285
Contig ID
                   32222 1.R1011
                   uC-zmflmo17023f03b1
5'-most EST
                   BLASTX
Method
                   q1362093
NCBI GI
                   620
BLAST score
                   2.0e-64
E value
                   183
Match length
                   63
% identity
                   hypothetical protein (clone TPP15) - tomato (fragment)
NCBI Description
                   >gi 924632 (U20595) unknown [Solanum lycopersicum]
Seq. No.
                   271286
                   32222 2.R1011
Contig ID
5'-most EST
                   uwc700153874.hl
                   BLASTN
Method
                   q1103627
NCBI GI
BLAST score
                   35
                   5.0e-10
E value
Match length
                   59
                   90
% identity
                  Z.mays Fer1 gene
NCBI Description
Seq. No.
                   271287
Contig ID
                   32222 3.R1011
                   uC-zmf1b73227f01a1
5'-most EST
                   271288
Seq. No.
Contig ID
                   32222 4.R1011
5'-most EST
                   wty700166410.h1
Method
                   BLASTX
NCBI GI
                   g1362093
BLAST score
                   393
                   3.0e - 38
E value
Match length
                   94
                   71
% identity
                   hypothetical protein (clone TPP15) - tomato (fragment)
NCBI Description
                   >gi 924632 (U20595) unknown [Solanum lycopersicum]
                   271289
Seq. No.
                   32224 1.R1011
Contig ID
                   z1a70\overline{0}379722.h1
5'-most EST
                   BLASTX
Method
```

g2342735 NCBI GI BLAST score 419

5.0e-41 E value 120 Match length % identity 72

(AC002341) unknown protein [Arabidopsis thaliana] NCBI Description

271290 Seq. No.

32242 1.R1011 Contig ID nbm700464910.h1 5'-most EST

Contig ID

271297

32280 1.R1011



```
271291
Seq. No.
Contig ID
                  32246 1.R1011
                  LIB143-048-Q1-E1-G10
5'-most EST
Method
                  BLASTX
                  g3367522
NCBI GI
BLAST score
                  166
                  1.0e-11
E value
Match length
                   67
% identity
                   45
                   (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                   271292
Seq. No.
Contig ID
                   32247 1.R1011
                   ceu700429657.h1
5'-most EST
Seq. No.
                   271293
                   32249 1.R1011
Contig ID
                   LIB3136-020-Q1-K1-B1
5'-most EST
Method
                   BLASTX
                   g4115371
NCBI GI
BLAST score
                   769
                   1.0e-81
E value
Match length
                   262
% identity
                   61
                  (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                   271294
Seq. No.
                   32259 1.R1011
Contig ID
                   fC-zmle700444786a4
5'-most EST
                   BLASTX
Method
NCBI GI
                   g3551958
                   469
BLAST score
                   7.0e-47
E value
Match length
                   141
                   63
% identity
                  (AF082032) senescence-associated protein 12 [Hemerocallis
NCBI Description
                   hybrid cultivar]
                   271295
Seq. No.
Contig ID
                   32260 1.R1011
                   uC-zmflb73362e10a2
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4580990
BLAST score
                   674
E value
                   2.0e-70
Match length
                   463
% identity
                   33
                  (AF120335) putative transposase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   271296
Contig ID
                   32267 1.R1011
5'-most EST
                   LIB3156-007-Q1-K1-A10
```



```
uC-zmromo17112f06a1
5'-most EST
Seq. No.
                   271298
                   32284 1.R1011
Contig ID
                   yyf700350736.h1
5'-most EST
Seq. No.
                   271299
                   32294 1.R1011
Contig ID
                   uC-zmroB73015e02b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2414622
BLAST score
                   549
                   7.0e-56
E value
Match length
                   182
                   56
% identity
                  (Z99259) conserved protein [Schizosaccharomyces pombe]
NCBI Description
                   271300
Seq. No.
Contig ID
                   32294 2.R1011
5'-most EST
                   yne700379364.h1
Seq. No.
                   271301
                   32294 3.R1011
Contig ID
5'-most EST
                   uwc700153421.h1
Method
                   BLASTN
NCBI GI
                   g2828011
BLAST score
                   41
E value
                   2.0e-13
Match length
                   48
                   96
% identity
                   Zea mays starch synthase I precursor (Ss1) mRNA, nuclear
NCBI Description
                   gene encoding plastid protein, complete cds
                   271302
Seq. No.
                   32312 1.R1011
Contig ID
                   nwy70\overline{0}447681.h1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4262143
                   344
BLAST score
                   3.0e - 32
E value
                   145
Match length
% identity
                   48
                  (AC005275) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   271303
Seq. No.
                   32314_1.R1011
Contig ID
5'-most EST
                   uC-zmflmo17101fl0b1
Method
                   {\tt BLASTX}
                   g3242704
NCBI GI
BLAST score
                   166
                   2.0e-11
E value
Match length
                   66
% identity
                   45
                  (AC003040) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

32314_2.R1011

271304

Seq. No.

Contig ID

NCBI GI

E value

BLAST score

g1168646

4.0e-52

517



```
uC-zmflmo17198b06b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g3242704
BLAST score
                  547
                  1.0e-55
E value
Match length
                  247
% identity
                  43
                  (AC003040) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  271305
Seq. No.
                  32323 1.R1011
Contig ID
                  fC-zmro700450908f1
5'-most EST
                  BLASTX
Method
NCBI GI
                  q3334222
BLAST score
                  673
E value
                  6.0e-71
                  149
Match length
% identity
                  86
                  4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD)
NCBI Description
                  >gi 2695710 emb CAA04245 (AJ000693)
                  4-hydroxyphenylpyruvate dioxygenase [Hordeum vulgare]
Seq. No.
                  271306
                  32326 1.R1011
Contig ID
5'-most EST
                  LIB3156-007-Q1-K1-H6
Method
                  BLASTX
                  g2245030
NCBI GI
BLAST score
                  330
                  6.0e-31
E value
                  89
Match length
                  66
% identity
                  (Z97341) apetala2 domain TINY homolog [Arabidopsis
NCBI Description
                  thaliana]
                   271307
Seq. No.
                  32329 1.R1011
Contig ID
5'-most EST
                  LIB3062-012-Q1-K1-G8
Seq. No.
                  271308
                  32341 1.R1011
Contig ID
                  uC-zmflb73202d09b1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q585748
BLAST score
                   999
                   1.0e-108
E value
                   253
Match length
% identity
                  74
                  PHYTOENE SYNTHASE PRECURSOR >gi_413732 (L25812) phytoene
NCBI Description
                  synthase [Arabidopsis thaliana]
                   271309
Seq. No.
Contig ID
                   32343 1.R1011
5'-most EST
                  LIB3137-036-01-K1-D11
Method
                  BLASTX
```



Match length 293 % identity 36 NCBI Description GTP-

GTP-BINDING PROTEIN ERA HOMOLOG (BEX PROTEIN) >gi_606745 (U18532) Bex [Bacillus subtilis] >gi_1303826_dbj_BAA12482_ (D84432) YqfH [Bacillus subtilis] >gi_2634961_emb_CAB14458_

(Z99116) GTP-binding protein [Bacillus subtilis]

>gi 2634975 emb CAB14471_ (Z99117) GTP-binding protein

[Bacillus subtilis]

Seq. No.

Contig ID 32344 1.R1011

5'-most EST LIB83-016-Q1-E1-B12

271310

Seq. No. 271311

Contig ID 32348_1.R1011 5'-most EST wyr700236190.h1

Method BLASTX
NCBI GI g1402918
BLAST score 1037
E value 1.0e-113
Match length 300
% identity 66

NCBI Description (X98320) peroxidase [Arabidopsis thaliana]

>gi 1429215 emb CAA67310 (X98774) peroxidase ATP6a

[Arabidopsis thaliana]

Seq. No. 271312

Contig ID 32348_2.R1011

5'-most EST uC-zmroteosinte004c07b1

Method BLASTX
NCBI GI g1402918
BLAST score 457
E value 2.0e-45
Match length 140
% identity 64

NCBI Description (X98320) peroxidase [Arabidopsis thaliana]

>gi 1429215 emb_CAA67310_ (X98774) peroxidase ATP6a

[Arabidopsis thaliana]

Seq. No. 271313

Contig ID 32348_6.R1011 5'-most EST dyk700104030.h1

Seq. No. 271314

Contig ID 32356_1.R1011

5'-most EST LIB3156-008-Q1-K1-C8

Seq. No. 271315

Contig ID 32356_2.R1011 5'-most EST uC-zmflb73149c02a1

Seq. No. 271316

Contig ID 32363_1.R1011 5'-most EST uC-zmflmo17332b11a1

Seq. No. 271317

Contig ID 32365_1.R1011



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5'-most EST
                   nwy700447049.h1
Seq. No.
                   271318
                   32366 2.R1011
Contig ID
                   LIB3156-008-Q1-K1-D9
5'-most EST
Seq. No.
                   271319
                   32368 1.R1011
Contig ID
                   uC-zm\overline{f}lmo17309g02b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1724114
BLAST score
                   432
                   5.0e-45
E value
Match length
                   199
                   56
% identity
NCBI Description
                   (U80041) Af10-protein [Avena fatua]
                   271320
Seq. No.
                   32369 1.R1011
Contig ID
                   fC-zmst700622384g1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g4589852
BLAST score
                   537
                   1.0e-54
E value
Match length
                   165
                   61
% identity
                   (AB025968) cycloartenol synthase [Glycyrrhiza glabra]
NCBI Description
                   271321
Seq. No.
                   32371 1.R1011
Contig ID
                   LIB3156-008-Q1-K1-E2
5'-most EST
                   271322
Seq. No.
                   32386 1.R1011
Contig ID
                   zuv700356675.hl
5'-most EST
                   {\tt BLASTX}
Method
                   g1899175
NCBI GI
BLAST score
                   643
                   6.0e-67
E value
Match length
                   167
                   75
% identity
                   (U90262) calcium-dependent calmodulin-independent protein
NCBI Description
                   kinase CDPK [Cucurbita pepo]
Seq. No.
                   271323
                   32411_1.R1011
Contig ID
5'-most EST
                   hbs701181445.h1
Method
                   BLASTX
NCBI GI
                   q4056437
BLAST score
                   169
                   9.0e-12
E value
                   81
Match length
                   48
% identity
                   (AC005990) Strong similarity to PFAM PF 00069 Eukaryotic
NCBI Description
                   protein kinase domain. [Arabidopsis thaliana]
```



Contig ID 32417_1.R1011 5'-most EST hbs701183928.h1

Method BLASTX
NCBI GI g3292823
BLAST score 283
E value 3.0e-25
Match length 112
% identity 47

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 271325

Contig ID 32419 1.R1011

5'-most EST uC-zmroteosinte008e09b1

Method BLASTX
NCBI GI g4467122
BLAST score 657
E value 7.0e-69
Match length 205
% identity 61

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 271326

Contig ID 32426 1.R1011

5'-most EST uC-zmflmo17044f11b1

Seq. No. 271327

Contig ID 32437_1.R1011 5'-most EST uC-zmrob73077h12b1

Method BLASTX
NCBI GI g3548806
BLAST score 588
E value 3.0e-60
Match length 261
% identity 44

NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]

Seq. No. 271328

Contig ID 32442_1.R1011 5'-most EST yyf700347835.h1

Method BLASTX
NCBI GI g3879561
BLAST score 262
E value 1.0e-22
Match length 189
% identity 31

NCBI Description (Z81117) cDNA EST yk416a1.3 comes from this gene; cDNA EST

yk466h2.3 comes from this gene; cDNA EST yk273e2.3 comes from this gene; cDNA EST yk475e12.3 comes from this gene; cDNA EST yk416a1.5 comes from this gene; cDNA EST yk4

Seq. No. 271329

Contig ID 32448_1.R1011 5'-most EST LIB36-019-Q1-E1-C9

Seq. No. 271330

Contig ID 32448 2.R1011

5'-most EST LIB3136-020-Q1-K1-G11



Contig ID 32452_1.R1011 5'-most EST yne700379076.h1

Seq. No. 271332

Contig ID 32453 1.R1011

5'-most EST uC-zmroteosinte042f02b1

Method BLASTX
NCBI GI g2226329
BLAST score 476
E value 1.0e-47
Match length 129
% identity 71

NCBI Description (AF001634) physical impedance induced protein [Zea mays]

Seq. No. 271333

Contig ID 32453_2.R1011 5'-most EST ntr700073036.h1

Method BLASTX
NCBI GI g2226329
BLAST score 377
E value 5.0e-36
Match length 126
% identity 62

NCBI Description (AF001634) physical impedance induced protein [Zea mays]

Seq. No. 271334

Contig ID 32455 1.R1011

5'-most EST uC-zmflm017026d02b1

Method BLASTX
NCBI GI g3075394
BLAST score 1854
E value 0.0e+00
Match length 534
% identity 68

NCBI Description (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis

thaliana] >gi 3559809 emb CAA09311 (AJ010713) fiddlehead

protein [Arabidopsis Thaliana]

Seq. No. 271335

Contig ID 32455_2.R1011

5'-most EST uC-zmflmo17042g03b1

Method BLASTX
NCBI GI g3075394
BLAST score 347
E value 3.0e-45
Match length 144
% identity 67

NCBI Description (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis

 $\verb|thaliana| > \verb|gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead| \\$

protein [Arabidopsis thaliana]

Seq. No. 271336

Contig ID 32467_1.R1011 5'-most EST hvj700620760.h1



Seq. No. 271337 Contig ID 32478 1.R1011 uC-zmflb73266e08a2 5'-most EST Method BLASTX NCBI GI q483410 BLAST score 301 4.0e-27 E value Match length 86 % identity 76 (L01496) calmodulin-binding protein [Zea mays] NCBI Description 271338 Seq. No. Contig ID 32478 2.R1011 5'-most EST uC-zmflb73137d03a1 BLASTX Method NCBI GI q483410 BLAST score 204 2.0e-18 E value Match length 57 89 % identity (L01496) calmodulin-binding protein [Zea mays] NCBI Description Seq. No. 271339 Contig ID 32486 1.R1011 5'-most EST uC-zmflb73196g11b1 Seq. No. 271340 Contig ID 32495 1.R1011 5'-most EST LIB3156-010-Q1-K1-A3 271341 Seq. No. 32499 1.R1011 Contig ID uC-zmflb73115b11a1 5'-most EST 271342 Seq. No. 32502 1.R1011 Contig ID xmt700263008.h1 5'-most EST BLASTX Method NCBI GI g2505870 BLAST score 1466 E value 1.0e-163 Match length 481 63 % identity (Y12227) hypothetical protein [Arabidopsis thaliana] NCBI Description 271343 Seq. No. 32502_2.R1011 Contig ID 5'-most EST LIB36-002-Q1-E1-E11 Seq. No. 271344 32502 3.R1011 Contig ID 5'-most EST LIB3066-026-Q1-K1-H4

Method BLASTX
NCBI GI g2505870
BLAST score 454
E value 3.0e-45
Match length 116



% identity NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana] 271345 Seq. No. 32502 5.R1011 Contig ID uer700580927.h1 5'-most EST BLASTN Method NCBI GI g22330 35 BLAST score 2.0e-10 E value 39 Match length 97 % identity NCBI Description Z.mays Zmhox1a mRNA for homeobox protein Seq. No. 271346 32509 1.R1011 Contig ID 5'-most EST uC-zmroteosinte021e12b1 Method BLASTX q3668093 NCBI GI 735 BLAST score 5.0e-78 E value Match length 181 75 % identity NCBI Description (AC004667) unknown protein [Arabidopsis thaliana] Seq. No. 271347 32512 1.R1011 Contig ID 5'-most EST LIB3156-010-Q1-K1-C11 Seq. No. 271348 32520 1.R1011 Contig ID 5'-most EST wty700164891.h1 271349 Seq. No. Contig ID 32523 1.R1011 5'-most EST LIB3156-010-Q1-K1-D3 Method BLASTX NCBI GI g2252632 BLAST score 189 5.0e-14 E value Match length 78 % identity 51 (U95973) Barley Mlo protein isolog [Arabidopsis thaliana] NCBI Description Seq. No. 271350 32528 1.R1011 Contig ID pmx700085990.h1 5'-most EST Method BLASTX g4584110 NCBI GI BLAST score 330 2.0e-30 E value Match length 120 53 % identity (AJ133639) SAH7 protein [Arabidopsis thaliana] NCBI Description

Seq. No. 271351

Contig ID 32537_1.R1011